

Jarrell, Noble

From: Jiang, Dong
Sent: Tuesday, February 28, 2006 11:52 AM
To: Jarrell, Noble
Subject: 10/616,788

Please search 1) SEQ ID NO:1 (nt)
2) SEQ ID NO:2 (aa) - standard & against nt
databases.

- issued & Pub.
- commercial

Please send results on paper to Dong Jiang in REM 4D70 (mail
stop REM 4C70).

Thank you very much.

Dong

Dong Jiang

AU1646
REM - 4D70
571-272-0872
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Noble 2NA
1AA
Jan 31/2/06
SPR computer
SONC

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 07:09:08 ; Search time 1261 Seconds
(without alignments)
4839.652 Million cell updates/sec

Title: US-10-616-788-2
Perfect score: 3948
Sequence: 1 MAP10LQCSVFYFTNACNG.....SCRADLCGRSTDLHAVAP 738

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :
Published Applications NA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3948	100.0	3083	3	US-09-809-567-1 Sequence 1, Appli
2	3948	100.0	3083	5	US-10-216-156-1 Sequence 1, Appli
3	3948	100.0	3083	7	US-10-616-788-1 Sequence 1, Appli
4	3948	100.0	3083	8	US-10-842-006-3 Sequence 3, Appli
5	3918	99.2	2341	3	US-09-912-157-7 Sequence 7, Appli
6	3918	99.2	2341	7	US-10-717-282-7 Sequence 7, Appli
7	3908	99.0	4477	8	US-10-842-006-1 Sequence 1, Appli

8	3908	99.0	4477	8	US-10-608-449-1	5/100	Sequence 1, Appli
9	3901	98.6	2383	3	US-09-912-157-1	7/0	Sequence 1, Appli
10	3901	98.6	2383	7	US-10-717-282-1		Sequence 1, Appli
11	3891	98.6	2383	3	US-09-912-157-4		Sequence 4, Appli
12	3891	98.6	2383	7	US-10-717-282-4		Sequence 4, Appli
13	3857	97.7	4392	7	US-10-343-348-15		Sequence 15, Appli
14	3835.5	97.2	2786	3	US-09-863-818A-9		Sequence 9, Appli
15	3835.5	97.2	2786	8	US-10-749-144-9		Sequence 9, Appli
16	3835.5	97.2	2786	8	US-10-924-667-9		Sequence 9, Appli
17	3706	93.9	2894	8	US-10-104-047-1429		Sequence 1429, Ap
18	3706	93.9	4508	8	US-10-608-449-3		Sequence 3, Appli
19	3690	93.5	2319	3	US-09-874-503-17		Sequence 17, Appli
20	3690	93.5	2319	3	US-09-747-259-17		Sequence 17, Appli
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22	3690	93.5	2319	5	US-10-000-157-17		Sequence 17, Appli
23	3690	93.5	2319	6	US-10-410-927-17		Sequence 17, Appli
24	3690	93.5	2319	6	US-10-410-374-17		Sequence 17, Appli
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39	2649	67.1	2217	7	US-10-717-282-13		Sequence 13, Appli
40	1345.5	34.1	1723	7	US-10-616-788-18		Sequence 18, Appli
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45	321.5	8.1	3120	5	US-10-207-655-106		Sequence 106, App

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09809567
; Patent No. US20020045213A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shugan
; TITLE OR INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (22)..(2235)
US-09-809-567-1
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Pred. No.: 0
Score: 3948.00
Percent Similarity: 100.0%
Best local Similarity: 100.0%
Query Match: 100.0%
Length: 3083
Matches: 738
Conservative: 0
Mismatch: 0
Indels: 0

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QY 21 SerGlnLeuAlaValAlaAlaGlySerGlyValArgAlaTrrGlyValAspThrCyGly 40
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QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrrAsnIleThrPheLeuTyr 60
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QY 61 AspAsnCySerThrThrTyrrLeuAsnProValGlyValAlaIleAlaAspAlaGlnAsn 80
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QY 81 IleThrIleSerGlnTyrrAlaCySerHisAspGlnValAlaValThrIleLeuTrrSerPro 100
DB 262 ATCAACCATCAGCCAGATGCTGTGCTGATGACCAAGTGGCAGTCACTCTTGTGCTCCCA 321
QY 101 G1ValAlaLeuGlyIleGluPheLeuGlyPheArgValIleLeuGlnGluLeuLeuSer 120
DB 322 GGGGCTCTCGGATCGAATTCCTGAAAGATTTGGGTAATCTGGAGAGCTTAAGTGC 381
QY 121 G1GlyValArgGlnCySerGlnLeuIleLeuValAspProIyGlnLeuAsnSerSerPhe 140
DB 382 GAGGGAAGACAGTGCACAACTGATCTTAAGGATCCGAAGCAGCTCAACAGTACGCTTC 441
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QY 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCyAlaAspProGlyProGlnSerAsp 600
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QY 621 GlnSerGlnHisGlyGlyLeuAspGlnAspGlyGlnAlaAspProAlaLeuAspGlySer 640
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 ; Sequence 1, Application US/10216156
 ; Publication No. US20030099980A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jinq, Shuguan
 ; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
 ; FILE REFERENCE: 0101736916A
 ; CURRENT APPLICATION NUMBER: US/10/216,156
 ; CURRENT FILING DATE: 2002-08-08
 ; PRIOR APPLICATION NUMBER: US/09/809,567
 ; PRIOR FILING DATE: 2001-03-15
 ; PRIOR APPLICATION NUMBER: 09/724,460
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 60/189,816
 ; PRIOR FILING DATE: 2000-03-16
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 3083
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (22)..(2235)
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 Score: 3948.00 Matches: 738
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 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
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 Qy 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuGlyTrpAlaIleThrPheLeuTyr 60
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 Qy 61 AspAsnGlyThrThrTyrLeuAsnProValGlyLeuHisValIleAlaAspAlaGlnAsn 80
 Db 202 GACAAATGTGACCACTACTGTAATCCAGTGGGAAAGCATGTGATGCTGACGCCCAAT 261
 Qy 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrSerPro 100
 Db 262 ATCCACATCCAGCCAGTATGCTGCCATGACCAAGTGGCAGTCACATTTCTTGTCCCA 321
 Qy 101 GAlaLeuGlyIleGlnPheLeuGlyPheArgValIleLeuGlnGluLeuLeuSer 120
 Db 322 GGGGCGCTCGGCATCGAATTCCTGAAGAGATTGGGTAAATACGAGAGAGCTGAAGTCG 381
 Qy 121 GluGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerPhe 140
 Db 382 GAGGGAAGACAGTCCCAACAACTGATTTAAAGATCCGAAGCAGCTCAACAGTAGCTTC 441
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 Qy 241 ProPheLysArgLysThrCysLysGlnGlnIleThrThrGlnThrThrSerCysLeuLeu 260
 Db 742 CTTTCAGGAAAGACCTGTAAAGAGAGCAACATACAGAGACAGCAGCTGCTCTT 801
 Qy 261 GlnAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspThrAsnThrArg 280
 Db 802 CAATATTTCTCAGGCGATTAATTAATTAATGAGCTGTGATGACATTAACAACAAGA 861
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 Qy 421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisLysGlyGly 440
 Db 1282 GTTGTGTTCCAAAGTATGAAGTACTTGTGCAAGAAAGAACTCAAAACCAAGAGGT 1341
 Qy 441 GAlaArgGlySerGlyLysGlyGlnPheLeuValAlaValSerAlaIleAlaGlnLys 460
 Db 1342 GGGCGAGCTCGGGAAAGAGAGCTTCTCTGTGGCGGTGTGACGCAATTCGCCAAGAG 1401
 Qy 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
 Db 1402 CTCGCGCAGGCAAGCAGAGTTCCTCGCGGCGCTCAGCAAGTTATTCGCGCTACTTT 1461
 Qy 481 AspTyrSerCysGlyGlyAspValProGlyTyrLeuAspLeuSerThrLysTyrArgLeu 500
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DB 1702 GAAAGAGATTCGTCCTTCCTTCATCCCTCCATCGGCTACCGGAGGACGTCCTGAG 1761
QY 581 LysPheArgSerG1YLeuVal1LeuAsnArgVal1MetCyAsnProG1YProG1YLeuSerAsp 600
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DB 1822 TTTGCTTAAAGTAAAGTAAAGGCGCTGTTCTTGCGGCAACCGGACGACGCTCCAGAC 1881
QY 621 G1N1SerG1NH1sG1YG1YLeuArgG1N1eArgG1YG1N1AArgProAlaLeuArgG1YSer 640
DB 1882 GAGAGTACGATGCGGCGCTGACCAAGACGCGGAGGCGCGCTGCGCTTGACGATAGC 1941
QY 641 AlaAlaLeuG1N1ProLeuLeuH1eThrVal1YVal1AG1YSerProSerAspMetProArg 660
DB 1942 GCGCGCTGCAACCCCTGCTGACACGCTGAAACCGGAGGCGCTTGACATCCCGG 2001
QY 661 AspSerG1YLeuYrAspSerSerVal1ProSerSerG1N1eLeuSerLeuProLeuMetG1N 680
DB 2002 GACTCAGCATCTATGACTGCTGTCGCTCATCCAGCTGTCTTGCGCATGATGAA 2061
QY 681 G1YLeuSerThrArgG1N1ThrG1N1ThrSerSerLeuThrG1N1SerValSerSerSer 700
DB 2062 GAGCTCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2121
QY 701 G1YLeuG1YG1N1G1N1ProProAlaLeuProSer1YLeuLeuSerSerG1YSerCyS 720
DB 2122 GCGCTGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2181
QY 721 LysAlaAspLeuG1YCySArgSerTyrThrAspG1N1eH1sAlaVal1APro 738
DB 2182 AAGGACATCTTGCTGCGGACGACGACGACGACGACGACGACGACGACGACGACG 2235
RESULT 3
US-10-616-788-1
; Sequence 1, Application US/10616788
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/39525
; CURRENT APPLICATION NUMBER: US/10/616, 788
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(2235)
US-10-616-788-1

Pred. No.: 0
Score: 3948.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 7
Gaps: 0
US-10-616-788-2 (1-738) x US-10-616-788-1 (1-3083)
QY 1 MetAlaProThrLeuG1N1eUcySerVal1PheThrVal1AsnAlaCyLeuAsnG1Y 20
DB 22 ATGCGCCCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 81
QY 21 SerG1N1eUAlaVal1Ala1AG1YG1YSerG1YArgAla1ArgP1YVal1AspThrCySg1Y 40
DB 82 TCCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 141
QY 41 TrpArgG1YVal1G1YProAlaSerArgAsnSerG1YLeuTyrAsn11eThrPheTy 60
DB 142 TGGAGGGAGTGGGCGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 201
QY 61 AspAsnCySerThrThrTyLeuAsnProVal1G1YLeuH1sVal11eAlaAspAlaG1N1Asn 80
DB 202 GACAAATTGTAACAACCTTGAATCCAGTGGAGACATGATGATTCGACGCCAGAAAT 261
QY 81 11eThr11eSerG1N1YrAlaCyS1H1sAspG1N1Val1AlaVal1Thr11eLeuTyrSerPro 100
DB 262 ATCAACATGACACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 321
QY 101 G1YAlaLeuG1Y11eG1N1PheLeu1Yg1YPheArgVal11eLeuG1N1eUcySer 120
DB 322 GGGGCGCTGCGGCTGCAATTCGAAAGATTCGGGTAATTCGAGGAGGCTGAAAGTCG 381
QY 121 G1N1G1YArgG1N1G1N1G1N1eU11eU1YAspPro1Yg1N1eUAsnSerSerPhe 140
DB 382 GAGGAGAGAGAGGACCAACATGATTCGAAAGATTCGAAAGATTCGAAAGATTCG 441
QY 141 LysArgThrG1YMetG1N1SerG1N1ProPheLeuAsnMetLysPheG1N1ThrAspTyrPhe 160
DB 442 AAAAGAACTGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 501
QY 161 Val1YVal1AProPheProSer11eYAsnG1N1SerAntYrH1sProPhePhe 180
DB 502 GTAAGGATGTCCTTTCTTCATTAATAAAGAAAGCAATTAACCACTTTCTTTCTTT 561
QY 181 ArgThrArgAlaCyAsnProLeuLeuG1N1ProAspAsnLeuAlaCyLeuAspProPheTyr 200
DB 562 AGAACCAGACCTGTGACCTGTGTACAGCCGACCAATCTAGCTTGTAACCTTCTG 621
QY 201 LysProArgAsnLeuAsn11eSerG1NH1sG1YSerAspMetG1N1A1SerPheAspH1s 220
DB 622 AAGCTTCGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 681
QY 221 AlaProH1sAsnPheG1YPheArgPheTyLeuH1sTyTyLeu1Yg1YSerG1Y 240
DB 682 GACCGGACAACTTCGCGCTTCGTTCTTCACTTCACTTCACTTCACTTCACTTCACTT 741
QY 241 ProPhe1YArgG1YSerThrCyS1Yg1N1G1N1ThrG1N1ThrThrSerCyS1eU1eU 260
DB 742 CTTTCAAGGAAAGACCTGTAAAGGAGAACTAACAAGACGACGACGACGACGACG 801
QY 261 G1N1AsnVal1SerProG1YAspTyr11e11eG1N1eUVal1AspAspThrAsnThrArg 280
DB 802 CAATAATTTCTCAAGGAGTTATATATATGACGCTGATGATACATAACAACAAGA 861
QY 281 LysValMetH1sTyTyAlaLeu1YProVal1H1sSerProTyrAlaG1YPro11eArgAla 300
DB 862 AAGTATGATCATATGCTTAAAGCAGTGCATCCCGGCGGCGGCGGCGGCGGCGGCGG 921
QY 301 MetAla11eThrVal1ProLeuVal1Val11eSerAlaPheAlaThrLeuPheThrVal1Met 320
DB 922 ATGGCATCAAGATGCACTGTATGCTATTCGCAATTCGCGACGCTTCCTTCACGTCGATG 981

QY	321	CysAsglyValysGlnGlnGlnAsnLeuYSerThrAlaAspGlnGlnSerSerIser	340
Db	992	TGCCCAAGAACCAACAGAAATATTATTATCACTTAAAGTAAGAGCTCTAAGTC	1044
QY	341	SerThrYrThrAlaAlaLeuProAlaArgIuaArgLeuArgProArgProValPheLeu	360
Db	1042	TCCAATATCACTGCAGCACTCCCAAGAGAGAGCTCCGGCCGGCCGAAGGCTTTTCTC	1104
QY	361	CysYrYSerSerLysAspGlyGlnAsnThrSmetAsnValValGlnCysPheAlaYrPhe	380
Db	1102	TGCTATTCTCAAGTAAAGATGGCCAGATCACTAAGATGTCGTCAAGTGTTCCTCAATTC	1164
QY	381	LeuGlnAspPheCysGlyCysGluValAlaLeuAspLeuTrpGlnAspPheSerLeuCys	400
Db	1162	CTCCAGCACTCTGTGGCTGTAGAGGTGGCTGTGACCTGTGGAAAGACTTCAGCCCTGTG	1222
QY	401	ArgGlnGlyGlnArgIuTrpValIleGlnYsrIleHISGlnSerGlnPheIleIleVal	420
Db	1222	AGAGAGGGCCAGAGAGATGGGTATCCAGAGATCCAGAGATCCCAAGTCACTATTGTG	1282
QY	421	ValCysSerLysGlyMetLysYrPheValAspLysLysAsnYrLysHISLysGlyGly	440
Db	1282	GTTGTCTCCAAGGATATAGATCACTTGTGGCAAGAAAGACTAACAACAAGAGAGT	1344
QY	441	GlyArgGlySerGlyLysGlyGlnLeuPheLeuValAlaValSerAlaIleAlaGlnLys	460
Db	1342	GGCCAGGCTCGGGGAAAGAGAGCTCTTCGTGGGGCGGTATCGCAATGGCCCAAAAG	1404
QY	461	LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValYrPhe	480
Db	1402	CTCCGCCAGGCCAAGACAGATTCGTCCCGGGGCTCAACAGTTATTCGGCTCTAATTT	1462
QY	481	AspYrYSerCysGlnGlyAspValProGlyIleLeuAspLeuSerThrLysYrArgLeu	500
Db	1462	GATTATTCTCGAGAGAGACGTCCTCCGGATCTTAAGACTGAATACCAAGTACAGACTC	1522
QY	501	MetAspAsnLeuProGlnLeuCysSerThrAlaMetHISerArgAspHISGlyLeuGlnGly	520
Db	1522	ATGACAAATCTTCTCACTCTGTGTCCACTCCGACTCCGAGACACAGGCTCTCAAGAG	1582
QY	521	ProGlyGlnHISThrArgGlnGlySerArgAsnYrPheArgSerLysSerGlyArg	540
Db	1582	CCGGGGCAGCACCCGACAGGGCGAGAGAGAACTATCTCCGAGCAATGCAGGCCGG	1644
QY	541	SerLeuYrValAlaIleCysAsnMetHISGlnPheIleAspGlnGlyProAspYrPhe	560
Db	1642	TCCCATATGCTCGCACTTTTGCAATGACCCAGTTATTGACAGAGAGCCGAGCTGTTC	1702
QY	561	GlnLysGlnPheValProPheHISProProPoleuAspYrArgGlnProValLeuGln	580
Db	1702	GAAAAAGAGTTCGTCCCTTCATCTCTCCACTCCGACCTCCGAGACAGTCTTGGAG	1762
QY	581	LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGlnSerAsp	600
Db	1762	AAATTGATTGGGCTTGTGGTTTAAATAGTCAATGTCMAACAGAGGCTGAGAGTAAAC	1822
QY	601	PheCysLeuLysValGlnAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHIS	620
Db	1822	TTTGCGCTAAAGGTAGAGGCGCTGTTCCTGGGGCAACCGAGCAAGCCGACTCCAGAC	1882
QY	621	GlnSerGlnHISGlyGlyLeuAspGlnAspGlyAlaArgProAlaLeuAspGlySer	640
Db	1882	GAGAGTCAGCATGGGGGCTGTGACCAACGCGGAGGCGCCGGCTGTGACCGTAGTC	1944
QY	641	AlaAlaLeuGlnProLeuLeuHISThrValLysValAspYsrProSerAspMetProArg	660
Db	1942	GCCGCGCTGCACCCCTGCTGCAACGGTGAAGCCGGGAGCCCTTCGGACATGGCGGG	2002
QY	661	AspSerGlyIleYrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGln	680
Db	2002	GACTCAGGCACTATGACTCGCTGTGGCCCTCATCCGAGAGCTGTCTCTGCACTAATGAA	2062
QY	681	GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSerSer	700

DB	2062	GGAGCTCTGACGGACCAAGAAACGCTTCTCCGACGGAAGCCTGCTCTCTTCA	2112
QY	701	GIyleuGIyGIuGIuProProAlaIeuProSerLyLeuIeuSerGIySerCys	7205
DB	2122	GGCCCTGGGTGAGAGGAACCTCTCTCCCTTCTTCCAAAGCTCTCTCTTGGGTATGC	2185
QY	721	LyAlaAaPLeuGIyCyAaRgSerTyThrAaPLeuIeuHAlaValAlaPro	738
DB	2182	AAAGCAATCTTGCTGTGCGGACGATACACTGATGAATCCACGGCGTCCGCCCT	2235
RESULT 4			
US-10-842-006-3			
; Sequence 3, Application US/10842006			
; Publication No. US20040235104A1			
; GENERAL INFORMATION:			
; APPLICANT: Yang, Ruey-Bing			
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses			
; TITLE OF INVENTION: Therefore			
; FILE REFERENCE: MP103-071P1RM			
; CURRENT APPLICATION NUMBER: US/10/842,006			
; CURRENT FILING DATE: 2004-05-07			
; PRIOR APPLICATION NUMBER: 60/469522			
; PRIOR FILING DATE: 2003-05-08			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 3			
; LENGTH: 3083			
; TYPE: DNA			
; ORGANISM: Homo Sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (22) .. (2241)			
US-10-842-006-3			
Alignment Scores:			
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Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	8	Gaps:	0
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QY	1	MetaLaProTLeuGIuIeuCysSerValPhePheThrValAsnAlaCysLeuAnGIy	20
DB	22	ATGGCCCGCTGGCTGCAGCTCTGCTCCGCTCTTTACGCTCAACCCCTCCCAACGGC	81
QY	21	SerGIuIeuAlaValAlaAlaGIyGIySerGIyAaRgAlaATPGLyValAspThrCysGIy	40
DB	82	TGCGAGCTGGCTGTGGCGCTGGCGGGTCCGGCCCGCGCTGGGGCGTGCACACTGTGGC	141
QY	41	ThraPrgLyValAlGIyProAlaSerTyrgAnSerGIyLeuTyAsnIleThrPheTySer	60
DB	142	TGGAGGGAGTGGGGCCGACGCCAGAAACAGTGGGCTGTAAACATCACTTCAATAT	201
QY	61	AaPaNcYsThrThrTyLeuAnProValGIyLyShIaValIleAlaAspAlaGlnAn	80
DB	202	GACATTTTACCACTTACTTGAATCCAGTGGGGAACATGTGATTCCTACGCCCGAGAT	261
QY	81	IleThrIleSerGIuTyAlaCyAaHlaAaPGLaValAlaValThrIleLeuTySerPro	100
DB	262	ATCACCATCACCGATATGCTTGCATGACCAAGTGGCAGTCAACATTTCTTGGTCCCA	321
QY	101	GIyAlaIeuGIyIleGIuPheIeuIyGIyPheAaRgValIleIeuGIuIeuIySer	120
DB	322	GGGGCCCTCGGCATCGAATTCCTGAAGAGATTTGGGGTAATCTGGAGAGCTGAAGTGC	381
QY	121	GIuGIyAaRgIuGIyGIuIleuIleuIyAaPProLyGIuIeuAnSerSerPhe	140
DB	382	GAGGGAACAGTGCACCAACTGATTTCTTAAAGATCCGAGCACTCAACATGACTTC	441

QY 141 LysArgThrGlyMetGluSerGlnProPheLeuAenMetLysPheGluThrAspTyrPhe 160
 Db 442 AAAAGAACTGGAAATGGAATCTCAACCTTCTCTGATATGAAATTGAAACGAGTTATTTC 501
 QY 161 ValLysValValProPheProSerIleLysAenGluSerAenTyrHisProPhePhe 180
 Db 502 GTAAAGGTGTGCTTTCTCTTCTCAATTAACAAACAAAGCAATTCACCTTCTCTCTT 561
 QY 181 ArgThrArgLysAenPheLeuLeuGlnProAenAenLysCysLysProPheThr 200
 Db 562 AGAACCCGAGCTGTGACCTGTGTACAGCCGAGCAATCTAGCTTGTAAACCTTCTG 621
 QY 201 LysProArgAenLeuAenLysSerGlnHisGlySerAenMetGlnValSerPheAenHis 220
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 Db 682 GCAACGCAACACTTCGGCTTCCTGTTCTTCTATCTTCACTCAAGCTCAAGCAGAAAGA 741
 QY 241 ProPheLysArgLysThrCysLysGlnGluLysThrGluLysThrThrSerCysLeuLeu 260
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 QY 261 GlnAenValSerProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrArg 280
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 QY 281 LysValMetHisTyrValLeuLysProValHisSerProTyrAlaGlyProIleArgAla 300
 Db 862 AAATGTATGCAATATGCTTAAACCCAGTGCATCCCGTGGCGGCGCCATCAGAGCC 921
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 Db 922 ATGGCCATCACAAGGCCATGTAGTCATATCGGACCTTCCGAGCTTCACTGATAG 981
 QY 321 CysArgLysLysGlnGlnLysAenIleTyrSerHisLeuAspGluGluSerSerGlySer 340
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 QY 341 SerThrTyrThrAlaAlaLeuProArgGluArgLeuArgProArgProLysValPheLeu 360
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 QY 361 CysTyrSerSerLysAenPheGlyGlnAenHisMetAenValValGlnCysPheAlaTyrPhe 380
 Db 1102 TGCTATTCAGTAAGATGSCCAAGATCAATGAATGCTGCTCCAGTGTTCCTACTTC 1161
 QY 381 LeuGlnAenPheCysGlyCysGluValAlaLeuAenPheLysPheGluAenPheSerLeuCys 400
 Db 1162 CTCAGAGACTTCTGTGCTGTGAGTGTGCTGTGAGACTGTGTGAGAGACTTCAAGCTCTGT 1221
 QY 401 ArgGlnGlyGlnArgGluTyrValIleGlnLysIleHisGluSerGlnPheIleIleVal 420
 Db 1222 AGAAGAGGCGAGAGATGAGTGTATCCAGAGATCCAGAGTCCAGTTCATCATTTGTG 1281
 QY 421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAenTyrLysHisLysGlyGly 440
 Db 1282 GTTGTTCCAAAGGTATGAACTTGTGTGAGCAAGAACTCAACCAACAAAGAGAGT 1341
 QY 441 GlyArgLysSerGlyLysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLys 460
 Db 1342 GGGCGAGGCTCGGGAGAGAGAGACTTCTGCTGTGCGGTGTGAGCCATTTGCCGAAAG 1401
 QY 461 LeuArgGlnAlaLysSerSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
 Db 1402 CTCGGCAGGCGCAAGAGATTCGTCGCGCGCTCAGCAAGTTATATCGCGTCTACTTT 1461
 QY 481 AspTyrSerCysGluGlyAspValProGlyLysLeuAenPheLysThrLysTyrArgLeu 500
 Db 1462 GATTATTCCTGCGAGGAGAGAGTCCCGGTATCTTAGCCGTGATACCAAGTACAGACTC 1521
 QY 501 MetAenAenLeuProGlnLeuCysSerHisLeuHisSerArgAenHisGlyLeuGlnGlu 520

Db 1522 ATGAGCAATCTTCTCAGCTCTGTTCACCTGCACTCCGAGAGACCGGCTCCAGAG 1581
 QY 521 ProGlyGlnHisThrArgGlnGlySerArgArgAenTyrPheArgSerLysSerGlyArg 540
 Db 1582 CCGGGGAGAGACCGGAGCAGGGGAGAGAAAGAACTTACTTCCGAGCAAGTACAGGCGGG 1641
 QY 541 SerLeuTyrValAlaIleCysAenMetHisGlnPheIleAspGluGluProAspTyrPhe 560
 Db 1642 TCCCTATAGCTCCCACTTGTGAAATGCAATGCAACATTTATTAACAAGAGCCGACTGTTTC 1701
 QY 561 GlnLysGlnPheValProPheHisProProProLeuArgTyrArgGluProValLeuGlu 580
 Db 1702 GAAAGCAGTGTCTTCCCTTCCATCTCTCCACTGCGCTACCGGAGCGCAGCTTGGAG 1761
 QY 581 LysPheAenPheSerLysLeuValLeuAenAenValMetCysLysAspProGlyLysSerAsp 600
 Db 1762 AAATTTGATTCGGGCTTGTGTTTAAATGATGATATGCAAAACAGAGGCTTGAGAGTAC 1821
 QY 601 PheCysLeuLysValGlnAlaProValLeuGlyValaThrGlyProAlaAspSerGlnHis 620
 Db 1822 TTTGCTTAAGGTAGAGGCGCTGTCTTGGGGCAACCGAGACCACTCCAGCAC 1881
 QY 621 GluSerGlnHisGlyGlyLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySer 640
 Db 1882 GAGAGTCAGATGCGGGGCTGAGACAAAGCGGGAGCGCGGCTGCTGACGGTAGC 1941
 QY 641 AlaAlaLeuGlnProLeuLeuHisThrValLysValGlySerProSerAenMetProArg 660
 Db 1942 GCGCGCTGCAACCCCTGTGCAACAGGTAAAGCGCGAGCCCTTCGACATGCGCGG 2001
 QY 661 AspSerGlyIleTyrAspSerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680
 Db 2002 GACTCAGGATCTATGACTGTGTGTGCTTCAATCCAGAGTGTCTTGCACATGAGAA 2061
 QY 681 GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSerSer 700
 Db 2062 GAGCTCGACGAGCAGACAGACAGAAAGCTTCTTCCCTGACGAGAGCGGTCTCTTCA 2121
 QY 701 GlyLeuGlyGlnGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
 Db 2122 GGGCTGGTGAAGAGAACTCTGCTGCTTCTTCCAAAGCTCTCTTCTGTGGGTCAATGC 2181
 QY 721 LysAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
 Db 2182 AAAGCAGATCTTGTGTGCGCAGACTACATGATGAATCCAGCGGCTGCGCCT 2235

RESULT 5
 US-09-912-157-7
 : Sequence 7, Application US/09912157
 : Patent No. US20020165348A1
 : GENERAL INFORMATION:
 : APPLICANT: Presnell, Scott R.
 : APPLICANT: Kuestner, Rolf E.
 : APPLICANT: Gao, Zeren
 : TITLE OF INVENTION: Human Cytokine Receptor
 : FILE REFERENCE: 00-49
 : CURRENT APPLICATION NUMBER: US/09/912,157
 : CURRENT FILING DATE: 2001-07-23
 : NUMBER OF SEQ ID NOS: 13
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 7
 : LENGTH: 2341
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (86)...(2302)
 US-09-912-157-7
 Alignment Scores:
 Pred. No.: 0 Length: 2341
 Score: 3918.00 Matches: 734

Percent Similarity: 99.6%
 Best Local Similarity: 99.5%
 Query Match: 99.2%
 DB: 3
 Gaps: 0

US-10-616-788-2 (1-738) x US-09-912-157-7 (1-2341)

1 MetAlaProTLPLeuGlnLeuCySeSerValPhePheThrValAlaAlaCysLeuAlaGly 20
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 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyValArgAlaTrpGlyValAspThrCysGly 40
 146 TCGCAGCTGGCTGGCGCGTGGCGGGTCCGGCGCGCGCGGGCGCGGCAACCTGGTGGC 205
 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTrpAlaIleThrPheLeuTyr 60
 206 TGGAGGGGAGTGGGGCCAGCCAGCAAAACAGTGGCTGTACAAATCACTTCAAAATAT 265
 61 AspAsnCySeThrThrTyrLeuAsnProValGlyLysHISValIleAlaAspAlaGlnAsn 80
 266 GACATTTGTACACTTCTTGAATTCAGTGGGAAAGATGTGATTGCTGACGCCAGAT 325
 81 IleThrIleSerGlnTyrAlaCysHISAspGlnValAlaValThrIleLeuTrpSerPro 100
 326 ATCAACATCAGCCAGTATGCTTGGCATGACCAAGTGGCAGTCACTTCTTGGTCCCA 385
 101 GlyAlaLeuGlyIleGluPheLeuGlyPheArgValIleLeuGlnGlnLeuLysSer 120
 386 GGGGCGCTCGGCACTGAAATCTTGAAGAGATTTGGGTAAATACGTGAGAGCTGAAGTGG 445
 121 GlnGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
 446 GAGGAAAGACAGTGCACAACTGATTTAAAGATCCGAAAGCAGTCAACAGTAGTTC 505
 141 LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGlnThrAspTyrPhe 160
 506 AAAAGAACTGGAAATGGAATCTCACTTCTGAAATGAAATTTGAAACGATTAATTC 565
 161 ValLysValValProPheProSerIleLysAsnGlnSerAsnTyrHISProPhePhe 180
 566 GTAAAGGTGTCCCTTTCTTCCATTTAAACCAAGCAATATCCACCTTCTTCTT 625
 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
 626 AGAACCCGAGCTGTGACCTGTGTGTAACGCCGGAACATCTAGCTTGAACCTTGTGG 685
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 686 AACCTCGGAACCTGAACATCAGCCAGCATGCTCCGACATGCAAGTGTCTCTTCAACAT 745
 221 AlaProHISAsnPheGlyPheArgPheTyrIleuHISGlyTyrLysLeuLysHISGlnGly 240
 746 GCACCCGACAACTTCCGCTTCCGTTCTTCTTCACTTCACTAACAGCTCAAGCAGAGGA 805
 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrThrGlnThrThrSerCysLeuLeu 260
 806 CTTTCAAGGGAAGACCTTGAAGCAGAGCAAACTACAGAGACGACCACTGCTCTT 865
 261 GlnAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspThrAsnThrArg 280
 866 CAABAATTTCTCTCAAGGAGTTATATATATATGAGTGGATGACATTAACAAACAGA 925
 281 LysValMetHISGlyTyrAlaLeuLysProValHISerProTrpAlaGlyProIleArgAla 300
 926 AAAGTATGATATATGCTTAAAGCCAGTGCATCCCGGTGGCGGCCCATCAGAGCC 985
 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 986 GTGGCCATCAACAGTCACTGTAGTCAATACGCAATTCGCAAGCTTCACTGATATG 1045
 321 CysArgLysLysGlnGlnGlnLeuIleTyrSerHISLeuAspGlnGlnSerSerGlnSer 340

1046 TGCCGAGAAAGCAACAAATAATATATTCATTTAGATGAGAGAGCTGAGTCT 1105
 341 SerThrTyrThrAlaAlaLeuProArgLysLeuArgProArgProLysValPheLeu 360
 1106 TCCACATACACTGACAGCTCCCAAGAGAGAGGCTCCGGCCGCGCGCAAGTCTTCTC 1165
 361 CysTyrSerSerLysAspGlyGlnAsnHISMetAsnValValGlnCysPheAlaTyrPhe 380
 1166 TGCATTTCCAGTAAGATGGCCAGATACATGAAATTCCTCCAGTGTTCCTTACTTC 1225
 381 LeuGlnAspPheCysGlyCysGlnValAlaLeuAspLeuTrpGlnAspPheSerLeuCys 400
 1226 CTCAGGACTTCTGTGCTGAGAGTGGCTTGACCTGTGGACCTGTGGAAAGACTTCAAGCTCTGT 1285
 401 ArgGlnGlyLysArgGlyLysValIleGlnLysIleHISGlnSerGlnPheIleVal 420
 1286 AGAAGAGGAGAGAGATGGGTCTACAGAAATTCACAGATCCCAAGTTCATCATATGTG 1345
 421 ValCysSerLysGlyMetLysTyrPheValAspLysValAsnTyrLysHISLysGlyGly 440
 1346 GTTTGTTCCAAAGGTATGAATCTTTGTGACAAAGAAATCTACAAACAAAGAGT 1405
 441 GlyArgGlySerGlyLysGlnLeuPheLeuValAlaValSerAlaIleAlaGlnLys 460
 1406 GCGCGAGCTCGGGAAAGAGAGCTCTTCTGGTGGCGGTGACCATTTGCCGAAAG 1465
 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
 1466 CTCGCGCAGGCCAAGCAGAGTTCGTCCGCGCGCTCAGCAAGTTATGCGCGTCACTTT 1525
 481 AspTyrSerCysGlnGlyAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeu 500
 1526 GATTATTCCTGCAAGGAGAGCTCCCGGTATCTTAACCTGATCAAGTAAAGTACAGCTC 1585
 501 MetAspAsnLeuProGlnLeuCysSerHISLeuHISerArgAspHISGlyLeuGlnGly 520
 1586 ATGACAACTTCTCTGAGCTGTGTCCACTTGCACCTCCGAGACCAAGCGCTCAAGAG 1645
 521 ProGlyGlnHISThrArgGlnLysSerArgAsnTyrPheArgSerLysSerGlyArg 540
 1646 CCGGGGAGACACCGGACAGGGCAGAGAAAGAACTTCCGAGCAAGTCAAGCGCGG 1705
 541 SerLeuTyrValAlaIleCysAsnMetHISGlnPheIleAspGlnGlnProAspTrpPhe 560
 1706 TCCCTTACCTCCCATTTGCAACATGACCAAGTATATACAGAGGCCCACTGATTC 1765
 561 GlnLysGlnPheValProPheHISProProProLeuArgTyrArgLysProValLeuGln 580
 1766 GAABAAGAGTTCCTTCCCTTCCATCTCTCCACTGCGCTACCGGAGCGAGCTTGGAG 1825
 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGlyLysAsp 600
 1826 AAATTTGATTCGGGCTTGTTTAAATGATGTCATGTGCAAAACAGAGGCTGAGAGTGAAC 1885
 601 PheCysLeuLysValGlnValProValLeuGlyAlaThrGlyProAlaAspSerGlnHIS 620
 1886 TTCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGGCAACCGGACCAAGCCACTCCAGCAC 1945
 621 GlnSerGlnHISGlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
 1946 GAGAGTCAAGATGGGGCTTGGACCAAGAGCGGAGAGCCCGCTGCTTGAACGTAGC 2005
 2006 GCGGCTCGAACCTCTGTCGACACGAGTGAAGCGGAGCGCCCTCGAGCATGCGCGG 2065
 661 AspSerGlyIleTyrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGln 680
 2066 GACTCAGGCACTATATACCTGTGTGCTCTTCACTGAGTGTCTTGGCACTGAATGAA 2125
 681 GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerSerSer 700
 2126 GACCTTCAAGGACCAAGCAAGAACTCTTCCCTTACCGAGAGCTGTCTCTCTTCA 2185

Db 1586 ATGACATCTTCTCAGCTGTTCCACTTGACCTCCGAGACCAAGCCGCTCCAGAG 1645
 Qy 521 Proglnglnhsthrarglngllyserargargantyrpheargserlyserglyarg 540
 Db 1646 CCGGGGAGGACGACGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1705
 Qy 541 SerleutyralalalalecyasamechisaglnpheleapagluglnproaspTrophe 560
 Db 1706 TCCCTTAATGCTGCGCATTTGCAATGCAAGATTATTAAGAGAGAGCCGACCTGATTC 1765
 Qy 561 Glulysglnphevalprophehproproleuarglyarggluprovalleugln 580
 Db 1766 GAAAGAGAGTTCGTTCCCTTCATCTCTCAGCTGCGCTACCGGAGCCAGTCTGGAG 1825
 Qy 581 Lyspheaspseryglyleuvalleuamaspvalmetcyalybproglyprogluserasp 600
 Db 1826 AATATTGATTCGGCTTGTTTAAATGATGTCATGTCAGAACAGAGGCTGAGAGTGAC 1885
 Qy 601 PheCysleuysvalglualaProvalleuglnvalthrglyproalaspserglinhis 620
 Db 1886 TTCTGCTTAAGGTAGAGGCGGCTGTTCTTGCGGACCGAGACCGAGCTCCAGAC 1945
 Qy 621 Gluserglnhsglyglyleuaspglaspglylualargproalaleuaspglyser 640
 Db 1946 GAGAGTACAGATGGGGGCTTGACCAAGACGGGAGGCGCGCTTGACCGTATGC 2005
 Qy 641 AlalaleuglnproleuLeuHisThrValylalaglyserProseraspmetProarg 660
 Db 2006 GCCCCCTGCAACCCCTGCTGACACAGGTGAAACCGGCGAGCCCTCGACATCCGCGG 2065
 Qy 661 AspseryglyleuyraaspseryvalproserserglyleuSerleuProleuMetGlu 680
 Db 2066 GACTCAGGACATGATGACTCTGTGTGCTCTCATCCAGCTGTCTGCACTAATGAA 2125
 Qy 681 GlyleuserThraapglnthrgluthrserSerleuthrgluserValserSerSer 700
 Db 2126 GAGTCTCGACGAGCAAGCAAGACGCTTCCCTGACGAGAGCGTCTCTCTTCA 2185
 Qy 701 GlyleugllyglugluproproalaleuProserlyleuLeuSerSerGlySerCys 720
 Db 2186 GGCCTGGGTGAGGAGAACCTCTGCTTCTTCAAGCTCTCTTCTGCGGTATGC 2245
 Qy 721 LysalaspheuglycyargserlyThraapgluLeuHisalavalalapro 738
 Db 2246 AAGGACATCTGTGTCGCGAGCTACATGATGAATCCACGCGGTGCGCT 2299

RESULT 7

US-10-842-006-1
 ; Sequence 1, Application US/10842006
 ; Publication No. US20040235104A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yang, Ruey-Bing
 ; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
 ; TITLE OF INVENTION: Therefor
 ; FILE REFERENCE: MP103-071P1M
 ; CURRENT APPLICATION NUMBER: US/10/842,006
 ; CURRENT FILING DATE: 2004-05-07
 ; PRIOR APPLICATION NUMBER: 60/469522
 ; PRIOR FILING DATE: 2003-05-08
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PasteSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 4477
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (90)...(2309)
 ; US-10-842-006-1

Alignment Scores:

Pred. No.: 0 Length: 4477
 Score: 3908.00 Matches: 732

Percent Similarity: 99.5%
 Best Local Similarity: 99.2%
 Query Match: 8
 Gaps: 0

Conservative: 2
 Mismatches: 4
 Indels: 0

US-10-616-788-2 (1-738) x US-10-842-006-1 (1-4477)

Qy 1 MetAlaProtrpleuglnleuCyserValPhehethrValaenAlaCyaleuAnGly 20
 Db 90 ATGGCCCGGCGGCGAGCTCTGCTCGTCTTTCAGGCAAGCCCTGCTCAAGCGC 149
 Qy 21 SerGlnleuAlaValAlaAGlyGlySerGlyArgAlaTArgValAlaSerThyCysGly 40
 Db 150 TCGAGCTGCTGCGCGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 209
 Qy 41 TrpArgGlyValGlyProalaspseraspserglyleuTyraenillethrpheleTyx 60
 Db 210 TGAAGGAGTGGGCGGCGAGCAAGAGTGGGCTGTACATCACTCAATAT 269
 Qy 61 AspasncCythrThrTrpTrleuaspProvalGlylyshisValillealaspAlaGlnasn 80
 Db 270 GACAAATGTACCACTTCTGAAATCCAGTGGGAGAGATGATGCTGAGCGCCAGAT 329
 Qy 81 IlerthrlleSerGlnTyralaCyehisaspGlnValAlaValThrilleleuTrpSerPro 100
 Db 330 ATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGACATTCCTTTGGTCCCA 389
 Qy 101 GlyAlaleuglylleglupheleuLyaglyPhehArgValilleleuglulLeuLyser 120
 Db 390 GGGGCTCGGACATCGAATTCCTGAAAGATTCGGGTAAATACGAGAGCTGAATCG 449
 Qy 121 GlulysarglnCynglnglnleuLleuLeuYasProlysglnleuaspSerSerPhe 140
 Db 450 GAGGAGAGACAGTGCACCAACATGATTCGAAAGATCCGAGACGCTCAACAGTACGCTTC 509
 Qy 141 LysArgThrGlyMetGlnserGlnProPheleuaspMetLysPheGlnThrAspTyPhe 160
 Db 510 AAGAACTGATGATGATGATCTCACTTCTGAAATGAAATGAAACGATTAATTC 569
 Qy 161 VallyseValValProPheProserlleyasnglnSeranTyriaspPhePhe 180
 Db 570 GTAAAGTGTTCCTTTCTTCCTCAATTAAAGCAATTAACACCTTTCTTCTT 629
 Qy 181 ArgThrArgAlaCyasPheLeuLeuGlnProaspPheLeuAlaCyalybProPheTrp 200
 Db 630 AGAACCCGAGCTGTGACCTGTGTACAGCGGACCAATCACTTGTAAACCTTCTGCG 689
 Qy 201 LysProArgaspLeuaspLeuaspserGlnHisGlyseraspMetGlnValserPheaspHis 220
 Db 690 AAGCTCGAAGCTGAAATCAAGCAGCATGCTCGGACATGAGGTGCTCTGACAC 749
 Qy 221 AlaProHisaspPheGlyPheArgPhePheTyrlleuHisTyrllyleuLyshisGlyGly 240
 Db 750 GACCGGACAACTTCGCTTCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 809
 Qy 241 ProPheLyasArglyshThrCyalybGlnGlnGlnThrThrGlnThrThrSerCyaleuLeu 260
 Db 810 CTTTCAAGCGAAGAGACTGCTGAGCAGAGCAAACTACAGAGATGACAGCTGCTCTT 869
 Qy 261 GlaspaspValserProgllyaspTyrlleilleGlnleuValaspaspThrThrThrArg 280
 Db 870 CAATATGTTCTCCAGGGAGATTAATTAATGAGTGTGTGATGACATTAACAACAAGA 929
 Qy 281 LysValMetHisTyralaleuLyasProValHiserProTrpAlaGlyProleargAla 300
 Db 930 AAGGTATGATTAATGCTTAAGCCAGTGCATCCCGTGGGCGGCGCCATCAGAGCC 989
 Qy 301 MetAlaIleThrValProleuValValilleSerAlaPheAlaThrleuPheThrValMet 320
 Db 990 GTGGCATACAGAGGACATGCTGATGATTCGCAATTCGCGACGCTTCACTGATG 1049
 Qy 321 CyasArglyshGlnGlnGlnleuaspLeyserHisleuaspGlnGlnGlnSer 340

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Db      1050 TGGCGGAGAGCAAGCAAGAAATATATATTCACATTAGATGAGAGCTGTGACTT 1109
Qy      341  SerThrThrPrlaalaLeuProArgLysArgLeuArgProArgProLysValPheLeu 360
Db      1110 TCCACATACCTGACAGACTCCCAAGAGAGGCTCCGGCCCGCCGAGAGCTTTCTC 1169
Qy      361  CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheValaTyrPhe 380
Db      1170 TGGCTATTCCAGTAAAGATGGCGAGATCATGAAATGTCTGCTTCAGTGTTCGCTACTTC 1229
Qy      381  LeuGlnAspPheCysGlyCysGluValAlaLeuAspLeuTPrGluAspPheSerLeuCys 400
Db      1230 CTCACAGACTTCTGTGCTGTGAGAGTGTCTGTGACCTGTGGAGAGACTTCAGCTTGT 1289
Qy      401  ArgGluGlyGlnArgGluTPrValIleGlnLysIleHisGlnSerGlnPheIleVal 420
Db      1290 AGAGAGGCGAGAGAGATGGGTCTATCCAGAGATCCAGAGTCCAGTTTCATATTGTG 1349
Qy      421  ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisLysGlyGly 440
Db      1350 GTTTGTTCCAAAGATAGAGATCTTTGTGACAGAGAGAGACTCAAAACCAAGAGAGT 1409
Qy      441  GlyArgGlySerGlyLysGlyGlyLysLeuPheLeuValAlaValSerAlaIleAlaGlnLys 460
Db      1410 GGGCGAGGCTCGGGGAAAGAGAGCTCTCTGTGGCGGTGTGAGCCATTCGCGAAAG 1469
Qy      461  LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
Db      1470 CTCGCGAGGCGAGAGAGAGTTCGCGCGGCTGACAGAGATTTATCGCGTACTTT 1529
Qy      481  AspTyrSerCysGluGlyAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeu 500
Db      1530 GATTATTCTCGCGAGGAGAGCTCCCGGTATCTTAACCTGATACCAAGTACAGACTC 1589
Qy      501  MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
Db      1590 ATGACACATCTCTCTGACTGTCTTCCACTGCACTCCGAGACCGGCTCCAGAG 1649
Qy      521  ProGlnGlnHisPheArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArg 540
Db      1650 CCGGGGAGAGACAGACAGGCGAGAGAGAGAACTCTCCGAGACAGAGTCAAGGCGG 1709
Qy      541  SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGluGluProAspTyrPhe 560
Db      1710 TCCCTAATGCTCGCATTTTGCAACATGACCAAGTTTATGACAGAGAGCCGACTGTT 1769
Qy      561  GlnLysGlnPheValProPheHisProProProLeuArgTyrArgGluProValLeuGln 580
Db      1770 GAAAGAGAGTTCGTTCTCTCCATCTCTCCACTGCGCTAACCGGAGCCAGTCTTGAG 1829
Qy      581  LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGlnSerAsp 600
Db      1830 AAATTATTCGGGCTGTGTTTAAATGATGATCATGTGCAAAACAGGAGCTCGAAGTAC 1889
Qy      601  PheCysLeuLysValGlnAlaProValLeuGlyValaThrGlyProAlaAspSerGlnHis 620
Db      1890 TTCTGCTTAAAGATAGAGGCGGCTGTCTTGCGGCAACCGGACAGCGACTCCACAGAC 1949
Qy      621  GlnSerGlnHisGlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
Db      1950 GAGAGTCAAGATGGGGCTGAGCAAGACCGGAGGCGCGCTCTTGAGGAGTTCG 2009
Qy      641  AlaAlaLeuGlnProLeuLeuHisThrValLysValaGlySerProSerArgPheProArg 660
Db      2010 GCCGCCCTCGAACCCCTGCTGACACAGGTGAAACCGGACGCTCTGAGCATGCGCGG 2069
Qy      661  AspSerGlyIleTyrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGln 680
Db      2070 GACTCAGGCACTATGACTCTGTCTGCTCTCAACCAAGCTGTCTGTGCCACTGATGAA 2129
Qy      681  GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGlnSerValSerSerSer 700
Db      2130 GGACTCTCGACGAGCAGACAGAAAGCTTCTCTGACGAGAGAGCTGTCTCTCTTCA 2189

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Qy      701  GlyLeuGlyGlnGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
Db      2190 GGCCTGGGTGAGAGAGAACTCTGCGCTTCTCTCAAGCTCTCTTCTGAGTATGC 2249
Qy      721  LysAlaAspLeuGlyCysArgSerTyrThrAspGlnLeuHisAlaValaPro 738
Db      2250 AAAGCAATCTTGTTGCGCGACACTCACTGATGAATCCACCGGCTGCGCCCT 2303

RESULT 8
US-10-608-449-1
; Sequence 1, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Tsinhua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: 12003269C-US/10/608,449
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-608-449-1

Alignment Scores:
Pred. No.: 0 Length: 4477
Score: 3908.00 Matches: 732
Percent Similarity: 99.5% Conservative: 2
Best Local Similarity: 99.2% Mismatches: 4
Query Match: 99.0% Gaps: 0
DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x US-10-608-449-1 (1-4477)
Qy      1  MetAlaProTPrLeuGlnLeuCysSerValPhePheThrValAsnAlaCysLeuAsnGly 20
Db      90  ATGGCCCGGTGGTGGAGAGCTCTGCTCTTTACGGTCAACCGCTGCTCAACGGC 149
Qy      21  SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTPrGlyValaAspThrCysGly 40
Db      150  TCCAGACTGCTGTGGCCCGCTGCGGCTCGGCGCGCGCGGCGGCCCAACCTGTGCG 209
Qy      41  TPrArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLysTyr 60
Db      210  TGGAGGGAGTGGGGCCAGCCAGCAGAAACAGTGGCTGTACAACTCACTTCAATAT 269
Qy      61  AspAsnCysThrThrTyrLeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsn 80
Db      270  GACAAATTGACCACTTACTTGAATCCAGTGGGAACATGTGATCTGACGCCCAAGAT 329
Qy      81  IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValaThrIleLeuTPrSerPro 100
Db      330  ATCACCATCAGCAGATGCTTCCATGACCAAGTGGAGCTGACCAATCTTGTGTCGCCA 389
Qy      101  GlyAlaLeuGlyIleGluPheLeuLysGlyPheArgValIleLeuGlnGlnLeuLysSer 120
Db      390  GGGGCCCTCGGATCGAAATTCGAAAGATTTCCGGTAAATATCTGAGAGAGCTGAAGTGC 449
Qy      121  GlnGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
Db      450  GAGGAGAGACAGTGGCCCAACACTGATTTCAAGATCCAGAGAGCTCAACATGACTTC 509
Qy      141  LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGlnThrAspTyrPhe 160
Db      510  AAAAGAAGCTGAGATGGAATCTCAACTTCTCTGAATATGAATTTGAAAGGATTAATTC 569
Qy      161  ValLysValValaProPheProSerIleLysAsnGlnSerAsnTyrHisProPhePhe 180
Db      570  GTAAGGTGTCTCTTCTCTTCAATTAATAAGAAAGCAATTAACACCTTCTCTTCTT 629

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Qy 181 ArgThrArgAlaCysAerPLeuLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
Db 630 AGAACCCGAGCCTGTGACCTGTTCTTACAGCCGAGCAATCTAGCTTTAAACCTTTGCG 689
Qy 201 LysProArgAsnLeuAsnLysSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
Db 690 AACCTCGGAACCTGAACTACAGCAGCATGCTCGGACATGACGAGTGTCTTTCGACAC 749
Qy 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisGlyTyrLeuValHisGlyGly 240
Db 750 GACCCGACAACTTCGCGCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 809
Qy 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrThrGlnThrThrSerCysLeuLeu 260
Db 810 CTTTCAAGCGAAGACCTGTGACGAGCAAGCACTACAGAGTACCAAGCTGCTCTTCTTCTT 869
Qy 261 GlnAsnValSerProGlyAspTyrLeuLeuValAspAspThrAsnThrThrArg 280
Db 870 CAATATCTTCTCAGGGGATTAATATTAATGAGCTGATGATGATGATGATGATGATGATGAT 929
Qy 281 LysValMetHisGlyTyrAlaLeuLysProValHisSerProTrpAlaGlyProLeuArg 300
Db 930 AAGGTATGATTAATGCTTAAAGCCAGTGCATCCCGTGGCGCCGATCAGAGCC 989
Qy 301 MetAlaLeuThrValProLeuValValLysSerAlaPheAlaThrLeuPheThrValMet 320
Db 990 GTGGCCATCAAGGCCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1049
Qy 321 CysArgLysLysGlnGlnGlnGlnLysLysSerHisLeuAspGlnGlnSerSerGlnSer 340
Db 1050 TGGCGAAGAGCAAGCAAGAAATATATATTCATCATTAATGAAGAGCTCGAATCTT 1109
Qy 341 SerThrTyrThrAlaAlaLeuProArgGlnArgLeuArgProArgProLysValPheLeu 360
Db 1110 TCCACATATACCTGACAGCTCCCAAGAGAGAGGCTCGCGCGCGCGAGAGTCTTCTTC 1169
Qy 361 CysThrSerSerLysAspGlnGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
Db 1170 TGCATATCCAGTAAAGATGAGCAAGATATCATGATATGCTTCTTCTTCTTCTTCTTCTT 1229
Qy 381 LeuGlnAspPheCysGlyCysGlnValAlaLeuAspLeuTrpGlnAspPheSerLeuCys 400
Db 1230 CTCACAGACCTTGTGTGCTGAGGTGCTGTGACCTGTGGAGAACTTCAGCTCTGTCT 1289
Qy 401 ArgGlnGlyGlnArgGlnTrpValLysGlnLysLysLysSerGlnPheLeuLeuVal 420
Db 1290 AGAAGAGGAGAGAGATGAGTATCCAGAAATCCACAGATCCAGTTCATCATGATGCTG 1349
Qy 421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisGlyGlyGly 440
Db 1350 GTTGTGTTCCAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1409
Qy 441 GlyArgGlySerGlyLysGlyGlnLeuPheLeuValAlaValSerAlaLeuAlaGlnLys 460
Db 1410 GGCCTGAGGCTCGGGAGAAAGAGACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1469
Qy 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheLeuAlaValTyrPhe 480
Db 1470 CTCGCGCAGGCAAGAGATGCTGCTGCGCGCTGCTGCAAGATTATCGCGCTTATCTTT 1529
Qy 481 AspTyrSerCysGlyGlyAspValProGlyLysLeuAspLeuSerThrLysTyrArgLeu 500
Db 1530 GATTATTTCCCGAGGAGAGAGCTCCCGGATCTCTAACTGATGATCAAGTACAGACTC 1589
Qy 501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
Db 1590 ATGAGACATCTTCTCTGCTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1649
Qy 521 ProGlyGlnHisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArg 540
Db 1650 CCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1709
Qy 541 SerLeuTyrValAlaLeuCysAsnMetHisGlnPheLeuAspGlnLysProAspTrpPhe 560

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Db 1710 TCCCTAATGCTCCGCAATTTGCAACATGCAACAGTTATTTACAGAGAGCCGACTGTTTC 1769
Qy 561 GlnLysGlnPheValProPheHisProProProLeuArgTyrArgLysProValLeuGlu 580
Db 1770 GAAAGCAGTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1829
Qy 581 LysPheAspSerGlyLeuValLeuAspAspValMetCysLysProGlyProGlyLysAsp 600
Db 1830 AAATTTGATTCGAGCTTGTGTTTAAATGATGATGATGATGATGATGATGATGATGATGATG 1889
Qy 601 PheCysLeuLysValGlnAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHis 620
Db 1890 TTCTGCTTAAGGTAAAGAGGCGGCTGTTCTTGGGCAACCGGACAGCCGACTCCGACAC 1949
Qy 621 GlnSerGlnHisGlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
Db 1950 GAGAGTCAGATGAGGAGGCTGGAACCAAGCGGAGAGGCGGCGCTTCTTCTTCTTCTTCT 2009
Qy 641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArg 660
Db 2010 GCGCGCTGCAACCCCTGCTGCAACGCTGAAAGCCGAGCCCTTCTGACATGCTGCGG 2069
Qy 661 AspSerGlyLysTyrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGlu 680
Db 2070 GACTCAGCATCTATGATCTGTCTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2129
Qy 681 GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSerSer 700
Db 2130 GAGCTCGACGAGACGACAGCAAGACGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2189
Qy 701 GlyLeuGlyGlnGlnGlnLysProProAlaLeuProSerLysLeuLeuSerSerGlySer 720
Db 2190 GGCCTGCTGAGAGAGAACTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2249
Qy 721 LysAlaAspLeuGlyCysArgSerTyrThrAspGlnLeuHisAlaValAlaPro 738
Db 2250 AAGCAGATCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2303

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RESULT 9

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US-09-912-157-1
; Sequence 1, Application US/0912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(2344)
US-09-912-157-1

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Alignment Scores:

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Pred. No.: 0 Length: 2383
Score: 3901.00 Matches: 734
Percent Similarity: 97.7% Conservative: 1
Best Local Similarity: 97.6% Mismatches: 3
Query Match: 98.8% Indels: 14
DB: 3 Gaps: 1

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US-10-616-788-2 (1-738) x US-09-912-157-1 (1-2383)

Qy 1 MetAlaProTrpLeuGlnLeuCysSerValPhePheThrValAlaAlaCysLeuAsnGly 20

Db 86 ATGGCCCGGCTGGGAGCTCTGCTCGTCTTTTACGGTCAACGCTCTCAAGGC 145
Qy 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTrpGlyValAspThrCysGly 40
Db 146 TCCAGCTGGCTGGCCGCTGGGGGGTCCGGCCGCGGGGCGCCGACCTGTGGC 205
Qy 41 TTPArg-----GlyValGlyPro 46
Db 206 TGGAGGATGAAGCGGCTGCCCAACCCCGCTTGTGTCTTAATGAGGAGTGGGAGCA 265
Qy 47 AlAserArgAnserGlyLeuTyArgnIleThrPheLeuSerThrThrTyr 66
Db 266 GCCAGCAGAAACGTGGCTGTACAAATCCTTCAAAATATGACATTTGTACACACTTAC 325
Qy 67 LeuAnpProValGlyLysHisValIleAlaAspAlaGlnAnilIleThrIleSerGlnTyr 86
Db 326 TTGAATCCAGTGGGGAGACATGTGATTTGTGACGCCCAAGAAATATCACCATCAGCCAGTAT 385
Qy 87 AlaCysHisAspGlnValAlaValIleThrIleLeuThrSerProGlyValAlaGlyIleGlu 106
Db 386 GCTTGCATATACCAAGTGGAGTCACATTTTGTGCCCAAGGGGCCCTGGCATGAA 445
Qy 107 PheLeuLysGlyPheArgValIleLeuGlnGlyLeuLysSerGlyArgGlnCysGln 126
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Qy 127 GlnLeuIleLeuLysAspProLysGlnLeuAnpSerSerPheLysArgThrGlyMetGlu 146
Db 506 CAACGTATCTAAAGATCGGAAGCACTCAACAGTGTCTTCAAAACCTGGAAATGAA 565
Qy 147 SerGlnProPheLeuAnpMetLysPheGluThrAspTyrPheValLysValIleProPhe 166
Db 566 TCTCAACCTTCTCGAAATATGAAATTGAACGGAATATTCGTAAAGTTGTCCTTTT 625
Qy 167 ProSerIleLysAnpGlnSerAsnTyrHisProPhePheArgThrArgAlaCysAsp 186
Db 626 CTTTCCATTAAAAAGAAAGCAATTACCACCTTTCTTTTGAACCCGAGCCTGTGAC 685
Qy 187 LeuLeuLeuGlnProAspAnpLeuAlaCysLysProPheTrpLysProArgAnpLeuAnp 206
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Qy 207 IleSerGlnHisGlySerAspMetGlnValSerPheAspHisAlaProHisAspPheGly 226
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Qy 227 PheArgPhePheTyrLeuHisGlyTyrLysLeuLysHisGlnGlyProPheLysArgLysThr 246
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Qy 327 GlnAnpIleTyrSerHisLeuAspGlnGlnSerSerGlnSerSerThrTyrThrAlaAla 346
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Qy 647 LeuHisThrValLysAlaGlySerProSerAspMetProArgAspSerGlyIleTyrAsp 666
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 ; Sequence 1, Application US/10717282
 ; Publication No. US20040077052A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Kuestner, Rolf E.
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Human Cytokine Receptor
 ; FILE REFERENCE: 00-49
 ; CURRENT APPLICATION NUMBER: US/10/717,282
 ; CURRENT FILING DATE: 2003-11-19
 ; PRIOR APPLICATION NUMBER: US/09/912,157
 ; PRIOR FILING DATE: 2001-07-24
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PasteSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 2383
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; NAME/KEY: CDS
 ; LOCATION: (86) ... (2344)
 ; US-10-717-282-1
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 Score: 3901.00 Matches: 734
 Percent Similarity: 97.7% Conservative: 1
 Best Local Similarity: 97.6% Mismatches: 3
 Query Match: 98.8% Indels: 14
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 Qy 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyValArgAlaTrpGlyValAspThrCyGly 40
 Db 146 TCGCAGCTGCTGCTGCGCGCTGCGGCGTCCGCGCGCGCGCGCACTGTCG 205
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 Qy 87 AlaCyHisAspGlnValAlaValThrIleLeuTrpSerProGlyAlaLeuGlyTlGln 106
 Db 386 GCTTGCATGACCAAGTGGCAGTCAACATTTTGGTCCCAAGGCGCCCTCGGCAATGAA 445
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 Qy 287 LeuYsaProValHisSerProTrrPAlaGlyProIleArgAlaMetAlaIleThrValPro 306
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Db	1646	CTCTGTTCCCACTTGCACTCCCGAGACCAACGCGCTCCCGAGAGCCGGGCGACACACCGGA	1705
QY	527	GINGLYSERARGARGAENTYRPHNARGSERLYSERGLYARGSERLEUTYVALAILE	546
Db	1706	CAGGCGACACAGAGAACTACTCCGGAGAGCAAGTCAGGCGCGGTCCCTTAAGTGGCCATT	1765
QY	547	CYANMETHLEGINPHLEILEAPGILUINUPROABPTPHNGLULYVGINPHVVALPRO	566
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QY	567	PHENILAPROPROLEUARGTYRARGILUPROVALILEUGLULYSPHEAPSERGLYLEU	586
Db	1826	TTCCATCTCTCTCCACTCGCGCTACCGGAGCCAGCTCTTGAGAAATTGATTCCGGGCTTG	1885
QY	587	VALLEUANAAPVALMETCYSLYAPROGILUPROGUSERAAPHECYALEULYVALGLU	606
Db	1886	CTTTAAATGATGATCATGTGCAAAACAGAGGCGTGAGAGTGACTTGCTGCTTAAAGGTAGAG	1945
QY	607	ALAPROVALILEUGLYVALATHRGLYPROALAAPSERGINHLEGLUSERGLNHLEGLYGLY	626
Db	1946	GCGGCTGTCTTCTGGGGCAACCGGACAGCCGACTCCAGCAAGACAGATGAGTGGGGC	2005
QY	627	LEUAPBGILNAPBGILGLUALARPPROALALEUAPBGILYSERALAILEUGLUPROLEU	646
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QY	647	LEUHLSTRVALLYSALAGLYSERPROSERAPMETPROARGAPSERGLYILETYRASP	666
Db	2066	CTGCACACAGGTGAAGCCGGGAGCCCTCGGACATGCCCGGGACTCAGGCATCATATAC	2125
QY	667	SERSERVALPROSERSERGLILEUSERLEUPROLEUMETGLULYLEUSERTHRASPGLN	686
Db	2126	TGCTGTGCGCCCTCAATCCGAGGTGTCTCTGCACTGATGAAAGGACTCTCCACGGAACAG	2185
QY	687	THRGILUINRSESRSELEUTHRGLUSERVALSERSESRSESRGLYLEUGLYGLULUGLU	706
Db	2186	ACAGAAAGCTCTTCCCTACGAGAGCGGTCTCTCTTCAAGGCTGAGGAGGAGGA	2245
QY	707	PROPROALALEUPROSERLYSLEULEUSERSERGISYSECYSLYVALAASPYLEUGLYCY	726
Db	2246	CCTCGTGCCTTTCCTTCCAGCTCCTCTCTTCTGAGGTATGCAAGACAGATCTTGATTGC	2305
QY	727	ARGSERLYTHRASPGLILEUHLISALVALAALAPRO	738
Db	2306	CGCAGCTACACATGATGAATCCACACGCGGTGCGCCCT	2341
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; Sequence 4, Application US/09912157			
; Patent No. US20020165348A1			
; GENERAL INFORMATION:			
; APPLICANT: Piresnell, Scott R.			
; APPLICANT: Kuestner, Rolf E.			
; APPLICANT: Gao, Zeren			
; TITLE OF INVENTION: Human Cytokine Receptor			
; FILE REFERENCE: 00-49			
; CURRENT APPLICATION NUMBER: US/09/912,157			
; CURRENT FILING DATE: 2001-07-23			
; NUMBER OF SEQ ID NOS: 13			
; SOFTWARE: FASTSEQ for Windows Version 3.0			
; SEQ ID NO 4			
; LENGTH: 2383			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (86) ... (2344)			
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Pred. No.:	0	Length:	2383
Score:	3891.00	Matches:	732
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QY	67	LeuAaProValGlyLySerValLLeAlaAraAlaGlnAanLLeThLLeSerGlnTyr	86	
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DB	386	GCTTGCCATGACCAAGTGGCAGTCAACCATCTTGTGTCCCAAGGCGCTCTGGCATGAA	445	
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QY	127	GlnLeuLLeuLyAaProLySerGlnLeuAaSerSerPheLySAArgThGlyMetGly	146	
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QY	147	SerGlnProPheLeuAaMetLyPheGlnThrAArgTyrPheValLyValValProPhe	166	
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DB	626	CCTTCATTTAAAAAGAAAGCAATTTACACCTTTCTTTAGAACCCAGCTGTGAC	685	
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DB	806	TTCCGTTTCTTCTATCTTCACTAACGTCAAGCAACAGCAAGCACTTTCAAGCGAAACCC	865	
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Qy 667 SerSerValProSerSerGluLeuSerLeuProLeuMetGluGlyLeuSerThrAspGln 686
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Db 2186 ACAGAAACGCTTCTCTGACGAGAGCGTGTCTCTCTTCAAGGCTCGGGAGAGAGAA 2245
Qy 707 ProProAlaLeuProSerLysLeuLeuSerSerGlySerCysLysValAspLeuGlyCys 726
Db 2246 CTCCTCGCCCTTCTTCCAAAGCTCTCTCTTGTGGGTCAATGCAAAAGAGATCTTGTTGC 2305
Qy 727 ArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
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RESULT 12
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; Sequence 4, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Pirelli, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTA for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2383
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86) ... (2344)
US-10-717-282-4

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Score: 3891.00 Matches: 732
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Best local Similarity: 97.3% Mismatches: 5
Query Match: 98.6% Indels: 14
DB: 7 Gaps: 1

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Qy 21 SerGlnLeuAlaValAlaAlaGlyLysGlyArgAlaTTrpGlyValAspThrCysGly 40
Db 146 TCGAGCTGCTGTGCGGCTGTGCGGCTCGGCGGCTCGGCGGCGGCGGCACTGTGCGC 205
Qy 41 TrpArg-----GlyValGlyPro 46
Db 206 TGGAGATGAAAGCGGCTGCCGACCCGCGCTTGTGTCTATGAGGAGTGGGCGCA 265
Qy 47 AlaSerArgAsnSerGlyLeuTyrPheIleThrPheLysTyrAspAsnGlyThrThrTyr 66
Db 266 GCGCAGGAAACAGTGGGCTGTACMACATCACTTCAAAATATGACATTTATACCACTTAC 325
Qy 67 LeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsnIleThrIleSerGlnTyr 86
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Qy 87 AlaCysHisAspGlnValAlaValThrIleLeuTTrpSerProGlyAlaLeuGlyLysGlu 106
Db 386 GCTTGCATAGACAAAGGAGTCAACCATCTTGTGTCCTCCAGGGGCGCTCGCATCGAA 445
Qy 107 PheLeuLysGlyPheAlaGlyValIleLeuGlnGluLeuLysSerGluGlyArgGlnCysGln 126

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 Qy 127 GlnleuileuileuysaapprolyglileuanserSerPheylsaargthlymerGlu 146
 Db 506 CAATGATTTCAAAAGATCCGAAACAGCTCAACAGTGGCTTCAAAAGAACTCGAATGAA 565
 Qy 147 SerGlnProPheleuansmetylePhegluthrAspTyPheVallylValProPhe 166
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 Qy 167 ProSerIlelysaenguserAntyThiAProphePheargthraGalaCyasp 186
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 Db 686 CTGTGTGTACGCGGACCAATCTAGCTTGAACCTTCTGAAAGCTCGGAACCTTAAC 745
 Qy 207 IleSerGlnHlsaglSerAspMetGlnValSerPheAspHlsalProHlsAspPheGly 226
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 Qy 227 PheargPhePheTytleuHlsTyTylyleuHlsHlsagllyProPheLyasgLythr 246
 Db 806 TTCGGTTCTTCTATCTTCACTCAACAGCTCAAGCAGGACCTTCAAGCAGAAAGACC 865
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 Qy 307 leuValValIleSerAlaPheAlaThrleuPheThraValMetCyAsaglylylyGlnGln 326
 Db 1046 CTGGTATCATATGGAATTCGACAGCTCTTCACTGAGATGCTCCCAAGAACCAACAA 1105
 Qy 327 GlnuanIleTySerHlsleuAspGlnugluserSerGlnuserSerThraTyThAlaAla 346
 Db 1106 GAAATATATATATCACTTTATGATGAAGAGCTCTGAGCTTCAACATACACTGACGA 1165
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 Db 1166 CTCCTCAAGAGAGGCTCCGGCGCGGCGGAGGCTTCTCTGCTATTCAGATTAAGAT 1225
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 Qy 387 CyseGlnValAlaIleAspLeuTyrgIuAspPheSerleuCyAsargGlnGlnArgGlu 406
 Db 1286 TGTATAGTGGCTCTGACACTGTGGAAACCTTCAAGCTCTTATGAAGAGGACAGAGAA 1345
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 Qy 427 LyAsTyPheValaAspLylylyAspTyTylylyHlslyGlyGlyAlaArgGlySerGlyLy 446
 Db 1406 AAGTACTTGTGCAAGAGAACTACAAACAAAGAGGTGCGCAGGCTCGGAGAA 1465
 Qy 447 GlnGlyleuPheleuValAlaValaSerAlaIleIleGlnlylyleuArgGlnAlaLyGln 466
 Db 1466 GGAAGACTCTTCTGCTGGCGGTGACCAATTCGCAAAAGCTCCGCGACAGGACAG 1525
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Qy 487 AspValProGlyIleleuAspLeuSerThraTyArgleuMetAspAnleuProGln 506
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 Db 1706 CAGGAGCAGCAAGAGAACTATCTCCGAGCAATCAAGCGGTCTCTATACGTGCGCAT 1765
 Qy 547 CyAspMetHlsaglPheIleAspGlnuglProAspTyPheGlnlylyPheValPro 566
 Db 1766 TGCAATGACACAGATTTATGACAGAGAGCCGACCTGTTCAAAAGCACTTCC 1825
 Qy 567 PheHlsProProPheleuArgTyArgGluProValleuGlnlyAspPheAspSerGlyleu 586
 Db 1826 TTCATCTCTCACTGCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGCTTG 1885
 Qy 587 ValleuAspAspValMetCyelysProGlyProGlnuserAspPheCyelyslyValGln 606
 Db 1886 GTTTAAATGATGTCAATGCAAAACAGGCTGAGAGTGAATCTTCCCTAAAGTAAAG 1945
 Qy 607 AlaProValleuGlnlyAlaThrglyProAlaAspSerGlnHlsagluserGlnHlsaglly 626
 Db 1946 GCGGCTGTTCTTGGGCAACCGGACCAAGCCGACTCCCAAGCAGAGTCAAGCTGGGGG 2005
 Qy 627 leuAspGlnaspGlyGlnAlaArgProAlaIleuAspGlySerAlaIleuGlnProleu 646
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 Db 2066 CTGACACAGGTGAACCGGCAAGCCCTCGGACATCCGGGAGCTCAAGCATCTATGAC 2125
 Qy 667 SerSerValProSerSerGlnuserleuProleuMetGlnIleuserThraAspGln 686
 Db 2126 TCGTGTGCTCTCAATCCAGCTGTCTTGCCTATGAGAGACTTCTGACGAGACAG 2185
 Qy 687 ThrGlnThraSerleuThrgluserValSerSerSerSerGlyleuGlnugln 706
 Db 2186 ACAGAAAGCTTCCCTGAGAGAGAGAGGTCTCTCTTCAAGCCGTGGGTGAAGAA 2245
 Qy 707 ProProAlaIleuProSerlyleuLeuuserSerGlySerCyelysAlaAspLeuGlyCy 726
 Db 2246 CTCTGCTGCTCTTCTCAAGCTCTCTCTTCTGAGGTATGCAAGCAGATCTTGTGTC 2305
 Qy 727 ArgSerTyThraAspGlnleuHlsAlaValAlaPro 738
 Db 2306 CGCAGCTACATGATGAATCCACGCGCGGCTCT 2341

RESULT 13
 US-10-343-348-15
 : Sequence 15. Application US/10343348
 : Publication No. US20040038242A1
 : GENERAL INFORMATION:
 : APPLICANT: Edmonds, Brian
 : APPLICANT: Micnovic, Radmila
 : APPLICANT: Ou, Weijia
 : APPLICANT: Su, Eric
 : APPLICANT: Techang, Sheng-Hung
 : APPLICANT: Wang, He
 : TITLE OF INVENTION: No. US20040038242A1 secreted proteins and their uses
 : FILE REFERENCE: X-14001
 : CURRENT APPLICATION NUMBER: US/10/343,348
 : NUMBER OF SEQ ID NOS: 38
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 15
 : LENGTH: 4392
 : TYPE: DNA

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 QY 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTrpGlyValAspThrCysGly 40
 Db TCCAGCTGGCTGTGCGCTGGCGGGTCCGGCCGGCGCGCGGCGGCGGCACTGTAGC 189
 QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyraAsnIleThrPheLeuTyr 60
 Db TGGAGGAGATGGGGGCGAGCGCAGCAAAACAGTGGGCTGTAAACAACATCACTTCAATAT 249
 QY 61 AspAsnCysThrThrThrLeuAsnProValGlyLeuHisValIleAlaAspAlaGlnAsn 80
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 QY 81 IleThrIleSerGlnTyraCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
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 QY 101 GlyAlaLeuGlyIleGlyPheLeuLeuGlyPheArgValIleLeuGlnGlyLeuLeuSer 120
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 QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
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 QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrTyrLeuLeuHisGlyGly 240
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 QY 241 ProPheLysArgLysThrCysLeuGlnGlnThrThrGlnThrThrSerCysLeuLeu 260
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QY 361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
 Db TGTATTTCCAGTAATAATGGCCAGATCACTGAATGTGTCCAGTGTTCGCTACTTC 1206
 QY 381 LeuGlnAspPheCysGlyCysGlyValAlaLeuAspLeuTrpGlnAspPheSerLeuCys 400
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 QY 421 ValCysSerLysGlyMetLysTyrPheValAspLysLeuAsnTyrLysHisLysGlyGly 440
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 QY 521 ProGlyGlnHisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArg 540
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 QY 561 GlnLysGlnPheValProPheHisProProProLeuArgTyrArgGlnProValLeuGln 580
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Search completed: March 1, 2006, 08:12:27
Job time : 1349 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_pzn model

Run on: March 1, 2006, 07:09:05 ; Search time 2424 Seconds
(without alignments) 667.481 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948
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Searched: 7218512 seqs, 1096188070 residues

Total number of hits satisfying chosen parameters: 14437024

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MATEL=2000000000 -HOST=abs806P
-USRR=US10616788 @CCN 1.1 335 @rnuc 28022006.160437.14609 -MCPU=6 -ICPU=3
-NO MMP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC -DEV TIMEOUT=120
-MAIN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA New:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	3706	93.9	2894	9 US-11-072-512-1429	Sequence 1429, Ap
2	325	8.2	612	6 US-09-925-065A-50990	Sequence 50990, A
3	325	8.2	612	6 US-09-925-065A-50991	Sequence 50991, A
4	325	8.2	2387	6 US-09-925-065A-672368	Sequence 672368,

5	254	6.4	539	6 US-09-925-065A-829666	Sequence 829666,
6	225	5.7	1385	8 US-10-750-185-36133	Sequence 36133, A
7	225	5.7	1385	8 US-10-750-623-36133	Sequence 36133, A
8	151.5	3.8	1365	8 US-10-750-185-50374	Sequence 50374, A
9	151.5	3.8	1365	8 US-10-750-623-50374	Sequence 50374, A
10	135.5	3.4	1701	5 US-09-978-360A-33	Sequence 33, Appl
11	135	3.4	1515	7 US-10-063-703-157	Sequence 157, App
12	135	3.4	1515	12 US-11-102-224-157	Sequence 157, App
13	118	3.0	1001	9 US-11-204-311-244	Sequence 244, App
14	116.5	3.0	16382	12 US-11-108-172-1112	Sequence 1112, App
15	116.5	3.0	16382	12 US-11-000-688-239	Sequence 239, App
16	112.5	2.8	3280	8 US-10-821-234-167	Sequence 167, App
17	112	2.8	1001	9 US-11-204-311-245	Sequence 245, App
18	109	2.8	3805	8 US-10-510-524-2	Sequence 2, Appl
19	109	2.8	3805	8 US-10-955-054A-144	Sequence 144, App
20	109	2.8	3805	9 US-11-245-147-170	Sequence 170, App
21	106.5	2.7	1400	12 US-11-136-527-6247	Sequence 6247, Ap
22	106.5	2.7	3807	12 US-11-136-527-2151	Sequence 2151, Ap
23	105	2.7	4768	8 US-10-719-111-1	Sequence 1, Appl
24	104.5	2.6	2714	8 US-10-918-857-1	Sequence 1, Appl
25	104.5	2.6	3227	9 US-11-245-147-112	Sequence 112, App
26	104.5	2.6	4986	9 US-11-245-147-231	Sequence 231, App
27	104	2.6	2389	12 US-11-136-527-504	Sequence 504, App
28	104	2.6	3805	9 US-11-245-147-214	Sequence 214, App
29	104	2.6	4234	8 US-10-955-054A-133	Sequence 133, App
30	104	2.6	88421	12 US-11-205-109-1	Sequence 1, Appl
31	103.5	2.6	2948	7 US-10-918-857-9	Sequence 9, Appl
32	103.5	2.6	3038	7 US-10-922-166-19	Sequence 19, Appl
33	103.5	2.6	3038	8 US-10-918-857-5	Sequence 5, Appl
34	103.5	2.6	6820	7 US-10-922-166-14	Sequence 14, Appl
35	103.5	2.6	116856	12 US-11-143-980-1	Sequence 1, Appl
36	102	2.6	4558	9 US-11-177-894-4	Sequence 4, Appl
37	101	2.6	4400	12 US-11-136-527-1982	Sequence 1982, Ap
38	101	2.6	4767	12 US-11-145-035-23	Sequence 23, Appl
39	101	2.6	5265	12 US-11-122-329-81	Sequence 81, Appl
40	100.5	2.5	2070	9 US-11-040-218-4	Sequence 4, Appl
41	100.5	2.5	2070	9 US-11-040-218-30	Sequence 30, Appl
42	100.5	2.5	2070	9 US-11-040-218-32	Sequence 32, Appl
43	100.5	2.5	3073	12 US-11-113-424-11	Sequence 11, Appl
44	100.5	2.5	4195	9 US-11-075-047A-5	Sequence 5, Appl
45	100.5	2.5	4195	12 US-11-076-427A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-11-072-512-1429
Sequence 1429, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAMI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SERI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OR INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978

PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1429
LENGTH: 2894
TYPE: DNA
ORGANISM: Homo sapiens
US-11-072-512-1429

Alignment Scores:
Pred. No.: 0 Length: 2894
Score: 3706.00 Matches: 694
Percent Similarity: 99.7% Conservative: 2
Best Local Similarity: 99.4% Mismatches: 2
Query Match: 93.9% Indels: 0
DB: Gaps: 0

US-10-616-788-2 (1-738) x US-11-072-512-1429 (1-2894)

QY 41 TTPATGGLYVALGIPROALSERARGANSERGLYEUTYRAENILETHRPHELYTYR 60
DB 210 TGGCAGGAGTGGGGCCAGCCAGCAAGAGTGGCTGTACACATCACCTTCAAAATAT 269
QY 61 AAPAANCYETHRTYRTRLEUAPPROVALGLYVSHLEVALLEALAAPALAGLAPN 80
DB 270 GACATATGACCACTTACTTGAATCCAGTGGGAGGATGTGATGTGAGAGCCCAAAAT 329
QY 81 ILETHRILESERGLNYRALACYNHISAPGLINVALAVALTHRIILEUTRPSERPRO 100
DB 330 ATGACCATGACCCAGCATGTGCTTGCATGACCAAGTGCACATCTTTGCTCCCA 389
QY 101 GLVALALEUGLYLIEGLUPHELEULYEGLYPHEARGVALILEUGLUGLULEULYSE 120
DB 390 GGGGCCCTCGGACATCGAATCTGTAAAGATTTCGGGTAAATACAGAGAGCTGAAGTCG 449
QY 121 GLUGLYARGGLNYGEGINGLILEULYAPPROLYSGLULEUAPNSERSETPHE 140
DB 450 GAGGAGGAGACAGTGCACAACTGATTCTAAAGATCCGAGAGCTGCACAGTAGCTTC 509
QY 141 LYSARGTHRGLYMEGLUSERGLNPROPHLEUAPNMEGLYVPHGLUTHRASPTYPHE 160
DB 510 AAAAGAACTGGAAATGGAATCTCAACCTTCTGAAATATGAATTTGAACGGAATTATTC 569
QY 161 VALLYVALVALPROPHESERILEYVANGLUSERANITYRHSEROPHEPHE 180
DB 570 GTAAAGGTGTCCCTTTTCCATTAATAAAGAAACAAATATACACCTTTCTCTTT 629
QY 181 ARGTHRTGRLACYSAPRPLEULEULGLNPROAPNLEUALACYSLEVPORPHEPTR 200
DB 630 AGAACCAGAGCTGTGACCTGTGTGTACAGCCGGAACAATCTAGCTTTGAAACCTTTGCG 689
QY 201 LYSERPROARGANLEUAPNILESERGLNHISGLYSEAPNMEGLINVALSERPHEAPNHS 220
DB 690 AAGCTCGGAACCTGGAACATGACGCAAGATGGCTCGGACATGACAGGTCTCTTGCACAC 749
QY 221 ALAPROHISAPNPHGLYPHEARGPHEPHEUTYLEULYVLEULYHISGLUGLY 240
DB 750 GCACCGCAACAATCTCGGCTTCGTTTCTTTCTATCTTCACTCAAGCTCAAGCAAGAGGA 809
QY 241 PROPHELYSARGLYPHTNYGLYGLINGLUGLINTHRTHGLUTHRTHSERCYULEULEU 260
DB 810 CTTTTCAGGAGAAAGACTGTGAGCAGAGAGAACTACAGAGATGACCAAGCTGCTCTCTT 869
QY 261 GLNAPNVALSERPROGLYASPTYRILEGLULEUVALAAPAPRTHASNTHTHRARG 280
DB 870 CAAAATTTTCTCCAGGGGATTAATTAATGACCTGTGATGACATTAACACAAAGAGA 929
QY 281 LYSVALMECHISYTRALALEULYAPPROVALHISERPROTPRALAGLYPROLLEARGALA 300
DB 930 AAAGTATGATATATGCTTAAGCCAGTGCATCCCGTGGCGGGCCCATCAGAGGCC 989

QY 301 METALAILETHRYALPROLEUVALILLESERALAPHEALATHRPHETHRYALMEC 320
DB 990 GTGGCCATCACAGTGCACCTGTGATCATATGCGCATTTGGCAGCGCTTCACTGATG 1049
QY 321 CYARGLYLVGGLINGLUAENILEYSEPHILEUAPGLIUSERSERGLUSER 340
DB 1050 TGGCGCAAGAGCAACAAAGAAATATATATTCACATTTAGATGAAAGAGCTCGAGTCT 1109
QY 341 SETTHRTYRTHRALALEUPROARGGLUARGLEUARGPROAPRPROLYSVLAPHELEU 360
DB 1110 TCCACATACCTGCACACATCTCCCAAGAGAGGCTCCGGCCGAGAGGCTTTCTC 1169
QY 361 CYSTYSESERLYSAPRGLINAPNHSMECAPNVALGGLINCYSPEALATYPHE 380
DB 1170 TGCTATTTCCAGTAAGATGGCCAGAAATCAATGATGCTCAGATGTTCCGCTACTTC 1229
QY 381 LEUGLAPRPHECYAGLYCYVGLUVALALEUAPRLEUTRGLIAPRPHESERLEUCY 400
DB 1230 CTCACGAACTTCTGTGGCTGTGAGTGGCTTGGAACCTGTGGAGAACTTCACTCTGT 1289
QY 401 ARGGLUGLYLARGLIUTRVALILEGLINLVSHISGLUSERGLNPHLEILEVAL 420
DB 1290 AGAGAAAGGCGAGAGAAATGGTGCATCCAGAAATCCAGAGTCCAGATTCACTGTG 1349
QY 421 VALCYSESERLYSGLYMEGLYRPHLYPHEVALAPRPLYEAPNTYRSHISLYSGLY 440
DB 1350 GTTTGTTCCAAAGATATGAAGTACTTTGTGGAACAAAGACATCAACAAAGAGAGGT 1409
QY 441 GLYARGGLYSEGLYLYVGLJULEUPHELEUVALALVALSERALAILLEGLULY 460
DB 1410 GGCCGAGGCTCGGGGAAAGAGAGCTTCTGTGGTGGCTGCACATTCGCGAAAG 1469
QY 461 LEUARGGLALAYGLINSESERSERALALAEUSERLYPHELEVALATYPHE 480
DB 1470 CTCGCGCAGGCCAAGAGAGTGTCTCGCGGCGCTCAGCAAGTTATCGCGCTACTTT 1529
QY 481 ASPTYSERCYSGGLUGLYAPRVALPROGLYILEUAPRLEUSERTHRYLYRARGLEU 500
DB 1530 GATTATTTCCGAGGAGGAGACGTCCTCGGATCTGAGCTGATGACCAAGTACAGATCTC 1589
QY 501 METAPRANLEUPROGLINLEUCYSEPHILEUHSERARGAPNHSGLYLEUGLINGLU 520
DB 1590 ATGACAAATCTTCTCAGCTCTGTCCCACTGCCACCTCCGAAACACAGCGCTCCAGAG 1649
QY 521 PROGLYGLNHISHRXARGGLINGLYSERARGARGAPNTYRPHARGSERLYSSERGLYARG 540
DB 1650 CCGGGCAGCAGCAGGAGCAGGCGCAGCAAGAACTACTTCCGAGCAAGTACAGCGCGG 1709
QY 541 SERLEUTYRVALAILLECYAPNMECHISGLNPHILEAPGLUGLUPROAPRTPHE 560
DB 1710 TCCCTATACGTCGCCATTTGCAACATGCAACGATTTATGACAGAGCCGCACTGGTTC 1769
QY 561 GLULYGLINPHEVALPROPHENHSERPROPROLEUARGTYRARGLUPROVALLEUGLU 580
DB 1770 GAAAGAGAGTTCCTTCCCTTCCATCTCTCCCTCAGCTGAGGAGGCGAGCTTGGAG 1829
QY 581 LYSERPHASERGLYLEUVALLEUAPNAPRVALMECYLYSERPROGLYUSERASPR 600
DB 1830 AAATTTGATTCGGGCTTGTTTAAATGATGATGATGCAACCAAGGCTTGAGAGTAC 1889
QY 601 PHECYLEUPLYVALGJUALPROVALLEUGLIALATHRGLYPROLAPASERGLNHIS 620
DB 1890 TTCTGCTTAAGATAGAGGGGCTGTTCTTGGGGCAACCGGACCAAGCTCCAGAC 1949
QY 621 GLUSERGLNHISGLYGLYLEUAPRGLYGLUALAARGPROLALAEUAPGLYSER 640
DB 1950 GAGAGTCAGATGGGGCTGTGACCAAGAGGAGGCGCGCTGCTGACGGTAGC 2009
QY 641 ALALALEUGLINPROLEULEUHSITHRYVALLYVALAGLYSERPROSERAPRMECPROARG 660
DB 2010 GCGGCCCTGCAACCCCTGTGCAACAGGTGAAAGCGGAGCGCTTCGCAATGCGCGG 2069
QY 661 ASPSERGLYLETYRAPHESERVALPROSERSERGLUUSERLEUPROLEUMETGLU 680

Db 311 GAAGACCTTCAAGCAAGACCTGTACGAG 343

RESULT 4
US-09-925-065A-672368
; Sequence 672368, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672368
; LENGTH: 2387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-672368

Alignment Scores:
Pred. No.: 9.21e-20 Length: 2387
Score: 325.00 Matches: 68
Percent Similarity: 55.7% Conservative: 5
Best Local Similarity: 51.9% Mismatches: 5
Query Match: 8.2% Indels: 54
DB: 6 Gaps: 2

US-10-616-788-2 (1-738) x US-09-925-065A-672368 (1-2387)

Qy 153 MetlysphegluThraAspTyrPheValValProPheProSerileYsaEnglu 172
Db 1784 CTAAACCTAAACAAAGTATCTTATCTCTTAATA----- 1819
Qy 173 SerAsnTyrHisProPhePhePheArgThrArgAlaCysAspLeuLeuEngluProAsp 192
Db 1820 -----GCTGTGACCTGTTGTACAGCCGAGC 1846
Qy 193 AsnLeuAlaCysValysProPhe----- 199
Db 1847 AATCTAGCTGTAAACCTCG-TAAGTAATAGTGTCTTATCTATCAAGTTCAAAGTATC 1905
Qy 199 ----- 199
Db 1906 GCCACTATGATGCTGTAGGCTAGCCTCTGCTCTCACTCTGGGCTCTACTTCTTCCA 1965
Qy 200 ---TrrlyspProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPhe 218
Db 1966 GTCGTGAAGCCTCGGAACCTGAACATCAGCCAGCATGCGGACATGCGAGGTCTCTTC 2025
Qy 219 AspHisAlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrTylsLeuLysHis 238
Db 2026 GACCATGACACCGCAACCTTCGCTTCGCTTCCTTCTATCTTCACTCAAGCTCAAGCAC 2085
Qy 239 GluGlyProPheLysArgLysThrCysLysGln 249
Db 2086 GAAGACCTTTCAGCGAAGACCTGTACGAG 2118

RESULT 5
US-09-925-065A-829666
; Sequence 829666, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 829666
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-829666

Alignment Scores:
Pred. No.: 6.4e-14 Length: 599
Score: 254.00 Matches: 56
Percent Similarity: 51.3% Conservative: 5
Best Local Similarity: 47.1% Mismatches: 5
Query Match: 6.4% Indels: 54
DB: 6 Gaps: 2

US-10-616-788-2 (1-738) x US-09-925-065A-829666 (1-599)

Qy 153 MetlysphegluThraAspTyrPheValValProPheProSerileYsaEnglu 172
Db 299 CTAAACCTAAACAAAGTATCTTATCTCTTAATA----- 334
Qy 173 SerAsnTyrHisProPhePhePheArgThrArgAlaCysAspLeuLeuEngluProAsp 192
Db 335 -----GCTGTGACCTGTTGTACAGCCGAGC 361
Qy 193 AsnLeuAlaCysValysProPhe----- 199
Db 362 AATCTAGCTGTAAACCTCG-TAAGTAATAGTGTCTTATCTATCAAGTTCAAAGTATC 420
Qy 199 ----- 199
Db 421 GCCACTATGATGCTGTAGGCTAGCCTCTGCTCTCACTCTGGGCTCTACTTCTTCCA 480
Qy 200 ---TrrlyspProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPhe 218
Db 481 GTCGTGAAGCCTCGGAACCTGAACATCAGCCAGCATGCGGACATGCGAGGTCTCTTC 540
Qy 219 AspHisAlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrTylsLeuLysHis 237
Db 541 GACCATGACACCGCAACCTTCGCTTCGCTTCCTTCTATCTTCACTCAAGCTCAAG 597

RESULT 6
US-10-750-185-36133
; Sequence 36133, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

FILE REFERENCE: MM1100-2
 CURRENT APPLICATION NUMBER: US/10/750,185
 CURRENT FILING DATE: 2003-12-31
 PRIOR APPLICATION NUMBER: US 60/437,482
 PRIOR FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 36133
 LENGTH: 1385
 TYPE: DNA
 ORGANISM: Bovine 19866881362247
 US-10-750-185-36133

Alignment Scores:
 Pred. No.: 9,34e-11 Length: 1385
 Score: 225.00 Matches: 41
 Percent Similarity: 100.0% Conservative: 2
 Best Local Similarity: 95.3% Mismatches: 0
 Query Match: 5.7% Indels: 0
 DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x US-10-750-185-36133 (1-1385)

Qy 62 AsnCyThrThyTyrLeuAspProValGlyHisValIleAlaAspAlaGlnAsnIle 81
 Db 824 GACTGCACCACTTACTTGAATCCAGTGGGAGACATGATGCTGACGCCAGAACATC 883
 Qy 82 ThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrSerProGly 101
 Db 884 ACCATCAGTCAGTATGCTGCGACGACCAAGTGGCTGCACCATCTTGTGTCCTCCGGG 943
 Qy 102 Alaleugly 104
 Db 944 GCCCTCGGT 952

RESULT 7
 US-10-750-623-36133
 Sequence 36133, Application US/10750623
 Publication No. US20050287531A1
 GENERAL INFORMATION:
 APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 FILE REFERENCE: MM1100-1
 CURRENT APPLICATION NUMBER: US/10/750,623
 CURRENT FILING DATE: 2003-12-31
 PRIOR APPLICATION NUMBER: US 60/437,482
 PRIOR FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 36133
 LENGTH: 1385
 TYPE: DNA
 ORGANISM: Bovine 19866881362247
 US-10-750-623-36133

Alignment Scores:
 Pred. No.: 9,34e-11 Length: 1385
 Score: 225.00 Matches: 41
 Percent Similarity: 100.0% Conservative: 2
 Best Local Similarity: 95.3% Mismatches: 0
 Query Match: 5.7% Indels: 0
 DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x US-10-750-623-36133 (1-1385)

Qy 62 AsnCyThrThyTyrLeuAspProValGlyHisValIleAlaAspAlaGlnAsnIle 81
 Db 824 GACTGCACCACTTACTTGAATCCAGTGGGAGACATGATGCTGACGCCAGAACATC 883
 Qy 82 ThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrSerProGly 101
 Db 884 ACCATCAGTCAGTATGCTGCGACGACCAAGTGGCTGCACCATCTTGTGTCCTCCGGG 943
 Qy 102 Alaleugly 104
 Db 944 GCCCTCGGT 952

Db 824 GACTGCACCACTTACTTGAATCCAGTGGGAGACATGATGCTGACGCCAGAACATC 883
 Qy 82 ThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrSerProGly 101
 Db 884 ACCATCAGTCAGTATGCTGCGACGACCAAGTGGCTGCACCATCTTGTGTCCTCCGGG 943
 Qy 102 Alaleugly 104
 Db 944 GCCCTCGGT 952

RESULT 8
 US-10-750-185-50374

Sequence 50374, Application US/10750185
 Publication No. US20050260603A1
 GENERAL INFORMATION:
 APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis
 TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 FILE REFERENCE: MM1100-2
 CURRENT APPLICATION NUMBER: US/10/750,185
 CURRENT FILING DATE: 2003-12-31
 PRIOR APPLICATION NUMBER: US 60/437,482
 PRIOR FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 50374
 LENGTH: 1365
 TYPE: DNA
 ORGANISM: Bovine 19866881634056
 US-10-750-185-50374

Alignment Scores:
 Pred. No.: 0.000636 Length: 1365
 Score: 151.50 Matches: 62
 Percent Similarity: 39.1% Conservative: 42
 Best Local Similarity: 23.3% Mismatches: 119
 Query Match: 3.8% Indels: 43
 DB: 8 Gaps: 9

US-10-616-788-2 (1-738) x US-10-750-185-50374 (1-1365)

Qy 296 GlyProIleArgAlaMetAlaIleThrValProLeuValVal----- 309
 Db 314 GGGATATTTCCTCTGCGAGTAGTAACACTTGTATGCTCAGCCAGCCGCTTGACA 373
 Qy 310 -----IleSerAlaPheAlaThrLeuPheThrValMetCysArgLysGlnGln 326
 Db 374 AGGGGTCATTATCTGCGCATGATGTTGACATGCGGTGAAGCTTACTGCTGCGAGA 433
 Qy 327 GlnAsnIleTyrSerHisLeuAspGlnGlnSerSerGlnSerThrTyrThrAlaAla 346
 Db 434 GATGACATATGCTTCTCTCCGCCACAGAAAGATCAAGAACTTCTCTCAATACC 493
 Qy 347 LeuProArgLysLeuArgProArgProArgProArgProArgProArgProArgPro 366
 Db 494 -----ACGCTACGCGCTCTCCATTAGGCTTGTGTGTTACCTCTGAAATA 541
 Qy 367 GlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPheLeuGlnAspPheCysGly 386
 Db 542 TGGTTCATCATC-----ACAGTTGTACTTACATGATGTTCTTCAAAACGCTGAGA 595
 Qy 387 CysGlnValAlaLeuAspLeuTyrGlnAspPheSerLeuCysArgGlnGlnArgGln 406
 Db 596 AGTGAAGTTATCTCTGGAAGTGGCAGAAAGAAATATCCAGATGAGTCCCGTCAG 655
 Qy 407 TrpValIleGlnLysIleHisGlnSerGlnPheIleIleValValCysSerLysGlnMet 426
 Db 656 TGGCTTACCACTCAGAAAGACGCGATAGGTCACTTCTCTTCCATGATGTAAC 715

QY 427 LyeTyrPheValAspLysLysAsnTyrLysGlyGlyGlyGlySerGlyLys 446
DB 716 ACC-----ACGTGCATGTTACTGTGACGAGAAAGAGGCGCCCTGTGAGACTCC 769
QY 447 GlyLysLeuPheLeuValAlaValSerAlaIleAlaGlyLysLeuArgGlnAlaLysGln 466
DB 770 CGAGACTGTTCCACTCGCTTTTAACTCTTTCGAGTATCTGAG-----817
QY 467 SerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSerCysGlyGly 486
DB 818 ---AGCCAGGCTCATCTGCACAAATACGTGGTGTCTTCACTTCAG-----GAGGGT 865
QY 487 AspValProGly-----IleLeuAspLeuSerThrLysTyrArgLeuMetAspAsn 503
DB 866 GACATCCAGACAGACTACAGGCGACTACGCTTCCCGCCACGTACCGCTTCACAGAGAC 925
QY 504 LeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnIleProGlyGln 523
DB 926 GCTACAGGTTTCTGTGAGAG-----CTCCCTCCGTCGCAAGCAG 964
QY 524 HisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArgSerLeuTyr 543
DB 965 CATGTGTGCGTGGGAGAGAG-----TCACGCACTGTCTCAC 1000
QY 544 ValAlaIleCysAsnMet 549
DB 1001 TACAGCTGCTGCTCCTG 1018

RESULT 9

US-10-750-623-50374
; Sequence 50374, Application US/10750623
; Publication No. US2005028753A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50374
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Bovine 1986681634056
US-10-750-623-50374

Alignment Scores:

Pred. No.: 0.00636 Length: 1365
Score: 151.50 Matches: 62
Percent Similarity: 39.1% Conservative: 42
Best Local Similarity: 23.3% Mismatches: 119
Query Match: 3.8% Indels: 43
DB: 8 Gaps: 9

US-10-616-788-2 (1-738) x US-10-750-623-50374 (1-1365)

QY 296 G1YProIleArgAlaMetAlaIleThrValProLeuValVal-----309
DB 314 CGGATATTTCTCTCGGAGTAGTAACACTTGAATGCTCAGCAGCGCGCTTACGA 373
QY 310 -----115SerAlaPheAlaThrLeuPheThrValMetCysArgGlyLysGln 326
DB 374 AGGGGATATTATCTGCATGATTTGACATGCGCTGAAGCCTTACTGCTGTGAGA 433

QY 327 GluAsnIleTyrSerHisLeuAspGlnGlySerSerGlnSerThrTyrThrAlaAla 346
DB 434 GATGACATATAGTTTCTTCTCCCAAGAAAGATCAAGAAAGCTTCTTCACTACC 493
QY 347 LeuProArgGlnArgLeuArgProArgProGlyValPheLeuCysTyrSerSerLysAsp 366
DB 494 -----ACGTACTGCGCTTCATTAAGGTTCTTGTGTTTACCTTCTGAATA 541
QY 367 GlyLysAsnHisMetAsnValAlaGlnCysPheAlaTyrPheLeuGlnAspPheCysGly 386
DB 542 TGGTTCCATAC-----ACAGTTGTACTTACTGAGATTCTTCAAAACCGCTCAGA 555
QY 387 CysGlnValAlaLeuAspLeuTyrGluAspPheSerLeuCysArgGlnGlyAlaGln 406
DB 596 AGTGAATATCTTGTGAAAGTGCAGAAATAAATGCGAGATGGTCCCGTGCAG 655
QY 407 TyrValIleGlnLysIleHisGlnSerGlnPheIleIleValAlaCysSerLysGlyMet 426
DB 656 TGGCTTACCACTCAGAAAGCAAGCGAGATTAAGTCAATTTCTTCTTCCAAATGGTAA 715
QY 427 LyeTyrPheValAspLysLysAsnTyrLysLysGlyGlyGlyGlySerGlyLys 446
DB 716 ACC-----ACGTGCATGTTACTGTGACGAGAAAGAGGCGCCCTGTGAGACTCC 769
QY 447 GlyLysLeuPheLeuValAlaValSerAlaIleAlaGlyLysLeuArgGlnAlaLysGln 466
DB 770 CGAGACTGTTCCACTCGCTTTTAACTCTTTCGAGTATCTGAG-----817
QY 467 SerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSerCysGlyGly 486
DB 818 ---AGCCAGGCTCATCTGCACAAATACGTGGTGTCTTCACTTCAG-----GAGGGT 865
QY 487 AspValProGly-----IleLeuAspLeuSerThrLysTyrArgLeuMetAspAsn 503
DB 866 GACATCCAGACAGACTACAGGCGACTACGCTTCCCGCCACGTACCGCTTCACAGAGAC 925
QY 504 LeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnIleProGlyGln 523
DB 926 GCTACAGGTTTCTGTGAGAG-----CTCCCTCCGTCGCAAGCAG 964
QY 524 HisThrArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArgSerLeuTyr 543
DB 965 CATGTGTGCGTGGGAGAGAG-----TCACGCACTGTCTCAC 1000
QY 544 ValAlaIleCysAsnMet 549
DB 1001 TACAGCTGCTGCTCCTG 1018

RESULT 10

US-09-978-360A-33
; Sequence 33, Application US/09978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bouqueleref, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: 56.USA.CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273

	TITLE OF INVENTION:	ACIDS ENCODING THE SAME
	FILE REFERENCE:	P323ORIC1
	CURRENT APPLICATION NUMBER:	US/10/063,703
	CURRENT FILING DATE:	2002-05-08
	Prior Application removed - See Palm or File Wrapper	
	NUMBER OF SEQ ID NOS:	170
	SEQ ID NO 157	
	LENGTH:	1515
	TYPE:	DNA
	ORGANISM:	Homo Sapien
	US-10-063-703-157	
	Alignment Scores:	
	Pred. No.:	0.0249
	Score:	135.00
	Percent Similarity:	135.00
	Best Local Similarity:	34.4%
	Query Match:	20.9%
		3.4%
	Gaps:	12
	US-10-616-788-2 (1-738) x US-10-063-703-157 (1-1515)	
Oy	AenleuaenileSerGlnHieglySerAepmetGlnValserPheAepHialAproHis	223
Dd	AAATGAATAATGAAGAAGATGGCCCTTCACATGTCTGTGAATTTCACC---TCAACAGGC	489
Oy	AenPheglipheaArgPhePhetyLeuHiSTyTyLseuLYBHiegLIgLyProPhelye	243
Dd	-----TCCCTAGACACCATATGAATGAATGAATAA	516
Oy	Arglys-----ThCylyBgIngu	250
Dd	AAAAAGTGTCACAGGCCGGAAGCCTGGGATCCGAACATCACTGCTTTGAAGAAGAT	576
Oy	GlnThrThrGluThrTherSerCyLeuLeuglnAenValserProGlyAapTyrl-e-I	270
Dd	GAG-----GAGACAGTAGAAGTA-A-CTTCACAACACTCCCTCGGAAACAGATCAT	629
Oy	eGluLeuValAspaBpThrAantThrThrArgLyvalMethiSTyTyAlaleuLypprova	290
Dd	GGCTCTTATTCACACAGCACACTATC-----ATCGGGTTTTCTCAGGT	671
Oy	HisSerProTrpAlaGlyProIleArgAlaMetAlaIethrValProLeuValAlI	310
Dd	GTTCGAGCCACACCGAAGAAAACAAACCGCAGCTTCAGTGTGATCCAGTACGGGA	731
Oy	eSerAlaPheAlaThrLeu-----	316
Dd	TAGTCAGAGCTGTACGGTCGTCAGCTGACTCCATATTTTCTCTACTTGTGGCAGCAGTGCAT	791
Oy	-----PheThrValMetCyArgLyBelysIngInguAenIleTyYserHI	332
Dd	CCGACATAAAGAACAGTGTGTCTGC-----CCACAAACAGCGCTTCCTCC	842
Oy	sLeuAepgluGlnuserSerGlnuserSerThTyThrAlaAlaleu-----	347
Dd	TCTGTATTAACAACAAACAAACGCGGAGGCTGCTGCTCTCCCTCGCTGTCTGCT	902
Oy	-----ProArgGlyuArgyleuAr	353
Dd	GGTGCCACATGGGCTGTGGTCGGCAGGAGTCTATTAATGTGGAGCGACGAAAGGATCAA	962
Oy	g-----ProArgProLySValIpheluCySTyrSe	363
Dd	GAAAGCTTCCTTTCTACACACACACTACTGCCCCCATTTAAGGTTCTTGIGGTTTACC	1022
Oy	rSerLyAspGlyGlnAenHIsMeCAsnValValGlnCySphenalATyRphenLeuGlnAs	383
Dd	ATCTGAATAATGTTTCCATCAC-----ACATTTGTACTTCACTGAATTTCTTCAAAA	1076
Oy	pHeCyseGlyCySgiValAlalaAeuAepLeuTrpGlnAepHeserLeuCySAArgInGI	403
Dd	CCATTGCGAAGAGTGAGTATCTTTGAAAAGTGGCAAAAAAGAAATATGACAGATGGG	1136

```

OY      403  YGLHARGELVTRVALLILEGLNYLRLHLSGLUSERGINPHLELLELVALVALCYSE 423
DB      1137  TCCAGTGCAGTGGCTTGGCACTCAAAAGAGCGACGACAAAGAGCTCTTCTTCTTTC 1196
OY      423  TLYSGILYMECLVYTYRPhEVALAsPlyVLYsAvNTYrLYsHIELYSGILYGLYLAATGSL 443
DB      1197  CAATACGCTCAACACATGTGTGGATGTGTAACGTGTGGCCAAAGAGGAGGAGGAGTCCCACTGA 1256
OY      443  YSERGILYLYSGILYGLULEuPhELeuVALAlAVALSERAlAlAlAGILYLYLeuATGGI 463
DB      1257  GAACCTCTCAA---GACCTCTTCCCTTCCCTTTTAACTTTTTCGACGATGTTAAGA-- 1311
OY      463  nAlALysGInSerSerSerAlAlALeUSeRLYsPHeILeAlAVALTYrPhEAsPlyrSe 483
DB      1312  -----AGCCAGATTCATCTGCACAAATACGTGGTGCTACTTTCAGAGAT 1358
OY      483  rCYSGILYAsPVALProGlyIleuAsPLeuSeRThLYsTYrArgLeuMeTAsPAs 503
DB      1359  TGATACAAAGACGATTCACATAGCTGTGATGTGTCGCCCAAGTACACCTCATGAAGGA 1418
OY      503  nLeuProGInLeuCYsSerHIELeu 511
DB      1419  TGCACACTGCTTCTGTGCAGAACTT 1443

RESULT 12
US-11-102-240-157
/ Sequence 157, Application US/11102240
/ Publication No. US20050260647A1
/ GENERAL INFORMATION:
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESSI
/ FILE REFERENCE: P3230R1C106C
/ CURRENT APPLICATION NUMBER: US/11/102,240
/ PRIOR FILING DATE: 2005-04-08
/ PRIOR APPLICATION NUMBER: 10/063662
/ PRIOR FILING DATE: 2002-05-07
/ PRIOR APPLICATION NUMBER: 10/006867
/ PRIOR FILING DATE: 2001-12-06
/ PRIOR APPLICATION NUMBER: PCT/US00/23328
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: 60/170262
/ PRIOR FILING DATE: 199-12-09
/ NUMBER OF SEQ ID NOS: 170
/ SEQ ID NO 157
/ LENGTH: 1515
/ TYPE: DNA
/ ORGANISM: Homo Sapien
US-11-102-240-157

Alignment Scores:
Pred. No.: 0.0249 Length: 1515
Score: 135.00 Matches: 77
Percent Similarity: 34.4% Conservative: 50
Best Local Similarity: 20.9% Mismatches: 150
Query Match: 3.4% Indels: 93
DB: 12 Gaps: 12

US-10-616-788-2 (1-738) x US-11-102-240-157 (1-1515)
OY      204  AsnLeuAsnIleSeRGLnHIEGLYSeRAePMeTGLnVALSeRPhEAsPHeILAlAlAProHIS 223
DB      433  AATGCAAAATATGAAAGACATGAGCCCTTCATCATGTCTGTGAATTTACCC--TCACCGAGC 489
OY      224  AsnPhEGLYrPhEAsPHePHeTYrLeuHIErTYrLYLeuLYsHIEGLYGLYProPhELYs 243
DB      490  -----TGCCTACACCAACATATGAATATATMAA 516

```

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Qy 244 Arghys-----ThCySlyeGlnlu 250
Db 517 AAAAGGTGTCAAGGCGGAAGCTGTGGATCCGAACATCATCTGCTTGAAGAGAT 576
Qy 251 GlnThrThrgluthrThSerCySleuGlnluAnValSerProglYAspTyle-I 270
Db 577 GAG-----GAGACAGTGAAGTGA--CTTCAACAACCACTCCCTGGGAAACAGATACAT 629
Qy 270 egluValAspThrAenthThrArglyValMetHsTyrAlaLeuYsProva 290
Db 630 GGCTTATCCACAACAGCACTATC-----ATCGGTTTTCTCAGT 671
Qy 290 lHsSerProtrpAlaglyProileArgAlaMetAlaIleThrValProleuValI 310
Db 672 GTTGAAGCCACACCAAGAAACAAACCGAGCTTCACTGTGATTCAGTACTGGGGA 731
Qy 310 eSerAlaPheAlaThreU-----316
Db 732 TAGTGAAGTGTCTACGGTCACTGACTCATATTTTCTTACTTGTGGCAGCACTGCAT 791
Qy 317 -----PheThrValMetCyBArglyBlyeGlnGlnluAnIleTyrSerH 332
Db 792 CCGACATAAAGAACAGTTGTGCTCTGC-----CCACAAACAGGCTCCCTTCC 842
Qy 332 sLeuAspGluGluSerSerGluSerSerThrTyrThraAlaAlaLeu-----347
Db 843 TCTGGATTAACAACAAAGCAAGCGGAGCTGCTGCTCTCTCTGCTCTGCT 902
Qy 348 -----ProArgGluArgLeu 353
Db 903 GGTGGCCACATGGGTGCTGTGGAGGATCTATCTAATGTGAGGACGAAAGATCAA 962
Qy 353 g-----ProArgProlyValPheLeuCyTyrSe 363
Db 963 GAAGACTCTCTTTCTACACACCACTACTGCCCCCATTTAAGCTTCTGCTGTTTACC 1022
Qy 363 rSerLyAspGlyGlnAnHsMetAnValIleGlnCySphelaTyrPheLeuGln 383
Db 1023 ATCTGAATATGTTTCCATCC-----ACAAATTGTACTTCACTGAATTTCTCAAAA 1076
Qy 383 PheCyGlyGlnValAlaLeuAspLeuTyrGluAspPheSerLeuCyBArgGlu 403
Db 1077 CCATTCGAGAAGTGAAGTCTCATCTTGAAGAGTGCAGAAAAGAAATAGCAGAGATGG 1136
Qy 403 yGlnAspGluTyrValIleGlnLySileHsGluSerGlnPheIleValValCySe 423
Db 1137 TCCAGTGCAGTGGCTTCCACTCAAAAGAGCAGACAGACAAAGTCTCTTCTTCTTTC 1196
Qy 423 fLyBglYMetLyTyrPheValAspLyBlySantYrLyHsIlyBlyGlyGlyArg 443
Db 1197 CAATGACGTCAACAGTGTGCGCATGTGACCTGTGGCAAGAGCGAGCTCCCACTGA 1256
Qy 443 ySerGlyLyGlyGlnLeuPheLeuValAlaValSerAlaIleAlaGluLySleuArg 463
Db 1257 GAAGTCTCAA--GACTCTTCCCTTCCCTTAACTTTTCTGCAAGTATCTAACA-- 1311
Qy 463 nAlaLyGlnSerSerSerAlaAlaLeuSerLySphelIleAlaValTyrPheAspTyrSe 483
Db 1312 -----AGCCAGATTCTATGCAACAATATAGTGTGTCTTACTTATAGAGAT 1358
Qy 483 rCyBgluGlyAspValProglYIleLeuAspLeuSerThlyTyrArgLeuMetAsp 503
Db 1359 TGAATACAAAGACATTAACAATGCTCTCAAGTGTGCCCCAAGTACCACTCAGAAAGA 1418
Qy 503 nLeuProGlnLeuCySerHsLeu 511
Db 1419 TGCCACTGCTTCTCTGCAAGACTT 1443

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RESULT 13
 US-11-204-311-244
 ; Sequence 244, Application US/11204311
 ; Publication No. US20060040304A1
 ; GENERAL INFORMATION:

```

APPLICANT: Blumenfeld, Maria
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueterec, Lydie
APPLICANT: Cohen, Amick
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFERENCE: 62.US4.DIV
CURRENT APPLICATION NUMBER: US/11/204,311
PRIOR FILING DATE: 2005-08-15
PRIOR APPLICATION NUMBER: US/10/294,934
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/671,317
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/131,961
NUMBER OF SEQ ID NOS: 977
SOFTWARE: Patent .pm
SEQ ID NO 244
LENGTH: 1001
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 501
OTHER INFORMATION: 12-192-334 : polymorphic base G or A
FEATURE:
NAME/KEY: misc binding
LOCATION: 481..500
OTHER INFORMATION: 12-192-334.misl, potential
FEATURE:
NAME/KEY: misc binding
LOCATION: 502..521
OTHER INFORMATION: 12-192-334.misl, potential complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 815..834
OTHER INFORMATION: upstream amplification primer, complement
FEATURE:
NAME/KEY: primer bind
LOCATION: 346..365
OTHER INFORMATION: downstream amplification primer
FEATURE:
NAME/KEY: misc binding
LOCATION: 489..513
OTHER INFORMATION: 12-192-334 potential probe
US-11-204-311-244
Alignment Scores:
Pred. No.: 0.562 Length: 1001
Score: 118.00 Matches: 74
Percent Similarity: 37.8% Conservative: 37
Best Local Similarity: 25.2% Mismatches: 117
Query Match: 3.0% Indels: 66
DB: 9 Gaps: 15
US-10-616-788-2 (1-738) x US-11-204-311-244 (1-1001)
Qy 477 AlValTyrPheAspTyrSerCyBgluGlyAspValProglYIle-----491
Db 33 GCATATCCAGCTCCATACAGTCCACGGAGGCTGTGCGGGGTAAAGCGAGAGAGGG 92
Qy 492 -----LeuAspLeuSerThlyTyrArgLeuMetAspAsnLeu 504
Db 93 CCAAGCTATCCCACTGCAGCTGACCTTCACTTCAAAAGACAGTATATGACACAGG 152
Qy 505 ProGlnLeuCySerHsLeuHsSerArgAspHsGlyLeuGlnlu-----ProglY 522
Db 153 CTTAGAGCTGTCTTCAAGTCAACCACTGTGAAAGGACAGACATATATGACACAGG 212

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QY 523 GlnHlethraArgInglYserArgArgAnTyRphaeRserLySerGlyArgSerLeu 542
Db 213 CAGACACTACCC-----CTCAGGATGACTCTCCACATCCAGGAGCTTAAAGCCC--- 263
QY 543 TyValAlaIleCybAenMeHlAgInPheIleApGluInProApRTrpPheGluYs 562
Db 264 -----AGTACGACAACTTT-----CCCTCGTCCACGAGG 296
QY 563 GlnPheValIProPheHls---ProProProLeu----- 572
Db 297 CGAGGGAGGCTTGTGATGCTGCACTCCCTTAAGCTGGGTAACCGGTCACTTTGAA 356
QY 573 -----ArgTyRArgGluProValLeuGluYbPheApSerGlyLeuValLeuAsn 589
Db 357 GACCTGACCGGAGAGAGAGAGCGGCTTCCAGCGCATCAACAGTCAGTCAGGTGAG 416
QY 590 AspValMet-----CysLyPProGlyProGluSerApPheCybLeuYsValGlu 606
Db 417 GACAAAGCCATCTCGACTCGACAGCCTTCAAGGCTTCCAC-----ACTTTGTC 467
QY 607 AlaProValLeuGlyAlaThrGly---ProAlaApSerGlnHlsGluSerGlnHlsGly 625
Db 468 TCACCTGCAACAGGAGCTTCTGCTGCTGCTGCTGCTTCTTAAGCACCCAGT----- 518
QY 626 GlyLeuApGlnApGlyGluAlaArgProAlaLeuApGlySerAlaAlaLeuGlnPro 645
Db 519 ---ATGATGACACAGCAGAGACACACACAGTCCCAACAGCTGCTGGGCTTACGAGCCC 575
QY 646 LeuLeuHlethraValIleValIleGlySerProSerApPheProArgApSerGlyIleTyR 665
Db 576 TTAGCATCTGCT-----GCAAGGGGTCCCTCTACACTCCCATGTCGGGAGAGAGAC 629
QY 666 -ApPserSerValIProSerSerGluLeuSerLeuProLeuMeGluGlyLeuSerThra 685
Db 630 AGACACACAGGAGGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 689
QY 685 pGlnThrgluThrSerSerLeuThrgluSerVal-----SerSerSerSerGly 702
Db 690 CAGAGCTACGCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 749
QY 702 euGlyGluGluInProProAlaLeuProSerLybLeuLeuSerSerGlySerCybLyb 722
Db 750 GCGGGCATGAGAG-----AACAAAGCATGGCACTTCTGCTCTGCTGCTGCTGCTGCTGCT 790
QY 722 laApLeuGlyCybArgSerTyThraApGluLeuHls 734
Db 791 -----AGCTGCCGACGAGGCCCTCCCGCTCCAC 820

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RESULT 14
US-11-108-172-1112
; Sequence 1112, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangechun
; APPLICANT: Lodee, Michael J.
; APPLICANT: Seerleat, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wedvick, Thomas S.
; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15

```

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; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1112
; LENGTH: 16382
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-108-172-1112

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Alignment Scores:
Pred. No.: 27.4 Length: 16382
Score: 116.50 Matches: 156
Percent Similarity: 31.4% Conservative: 99
Best Local Similarity: 19.2% Mismatches: 253
Query Match: 3.0% Indels: 305
DB: 12 Gaps: 39

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US-10-616-788-2 (1-738) x US-11-108-172-1112 (1-16382)
QY 19 AsnGlySerGlnLeuAlaValAlaIleGlySerGlyArgAlaTrpGlyValaPheTr 38
Db 471 AATGTCAAGAGATTGTCGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 530
QY 39 CysGlyTrpArgGlyValGlyProAlaSerArgApSerGlyLeuTyR----- 54
Db 531 -----AAGGGGTCAAGTGAATTCATGCAAGTTCATGCAAGGCGAT 575
QY 55 -----AsnIlethraPheLybTyRArgApCybThrThryrLeuAnProVal----- 70
Db 576 GTCTTAAGATGAGTCTTACAGGCCCTTCAATGTCGAGCCCACTACAGCTGATGATCTC 635
QY 71 ---GlyLybHleValIleAlaApAlaGlnAenIleThrlseGlnTyralaCyb--- 88
Db 636 TCGGGGTCAAGGTCAAGCTAGTACCCCGTGTCTGCTCTGCGCACAGCTGAGG 695
QY 89 -----His-----AspGlnValAlaValThrIleLeuTrpSer 99
Db 696 CAGAAACATACGACTGCAACATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 752
QY 100 ProGlyAlaLeuGlyIleGluPheLeuYsGlyPheArgValIleLeuGluLeuYs 119
Db 753 -----GGCAACCATATATATATATATATATATATATATATATATATATATATATATAT 782
QY 120 SerGluGlyArg-----GlnCybGlnGlnLeuIleu 130
Db 783 TCCCATCTGCGATGATTTGGCTTCTGTTGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 842
QY 131 LybApProLybGlnLeuAnSerSerPheLybArgThryGly-----MetGlu 146
Db 843 AACCATGGGGATATCACTGCTCCCGTGGGCTTCAGCAGGATGATGTGATGATGATGATGATG 902

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; NUMBER OF SEQ ID NOS: 1596
 ; SOFTWARE: Patent version 3.2
 ; SEQ ID NO 239
 ; LENGTH: 16382
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial sequences: primer
 ; NAME/KEY: misc feature
 ; LOCATION: (1..16382)
 ; OTHER INFORMATION: fc fragment of 199 binding protein (FCGBP)
 ; OTHER INFORMATION: gene.
 ; US-11-000-688-239

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	27.4	16382	156	99	253	305
Percent Similarity:	116.50					
Best Local Similarity:	31.4%					
Query Match:	19.2%					
DB:	12					39

US-10-616-788-2 (1-738) x US-11-000-688-239 (1-16382)

Qy 19 AsnGlySerGlnLeuAlaValAlaAlaGlySerGlyValArgAlaTrpGlyValAspThr 38
 Db 471 AATGTCAAGAGAGTTTGGCTGGTGGCCGCGGCGAGGTCTCGGACGTCTACGCTG 530
 Qy 39 CyAGlyTrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTy 54
 Db 531 -----AAGGGTCAGTGACATTCATCAATGCAAGTTCTATCAGCAGCGCAT 575
 Qy 55 -----AsnIleThrPheLeuTyTrpAspCysThrThrTyTrleuAsnProVal----- 70
 Db 576 GTCTAAGAGTGACTCTACAGCCCTCAATGTGGCCAGCTACAGAGCTCAGTGCATCTC 635
 Qy 71 ---GlyHisValIleAlaAspAlaGlnAsnIleThrIleSerGlnTyAlaCys--- 88
 Db 636 TCGGGGTCAAAAGTCAACAGTACAGTACCCCGTGGCTCTCTCTGCGCCACAGCTGGCG 655
 Qy 89 -----His-----AspGlnValAlaValThrIleLeuTrpSer 99
 Db 696 CAGAAACATACGACCTGCACACATGTGTGAGCAGCTGCTACCCAGCTGCTGCTGG--- 752
 Qy 100 ProGlyAlaLeuGlyIleGluPheLeuGlyGlyPheArgValIleLeuGluGluLeuLys 119
 Db 753 -----GGCACCACATATGTATGATCCACAGCTGGCC 782
 Qy 120 SerGluGlyArg-----GlnCysGlnGlnLeuIleLeu 130
 Db 783 TCCCAATCTGCTATGATTTGGCTTGTGTGGCCAGCCAGCCACAAAGCTGACCTTAC 842
 Qy 131 LysAspProLysGlnLeuAsnSerPheLysArgThrGly-----MetGlu 146
 Db 843 AACCATGGGGGTATCACTGGCTCCCGTGGCTCAGGACAGTGTATGTGAGATTGAG 902
 Qy 147 SerGlnProPheLeuAsnMetLysPheGluThrAspTyPheValLysValAlaProPhe 166
 Db 903 GTCCGGCATCTCGCCACACTCTACTCTGTGCAAAATGTGGCATCCAGGTCTCGTTCTTT 962
 Qy 167 -----ProSerIleLysAsnGlnUserAsnTyHisAspPhePheAspGlnArgAla 184
 Db 963 GGACAGGTCCCATAGAGATGATGACATTATGACCCCTTAC----- 1004
 Qy 185 CysAspLeuLeuGlnProAspAsnLeuAlaCysLysPheProPheTrpLysProArgAsn 204
 Db 1005 -----CTGGTCTGATCCAGATGTGTGGCGCTTACGCGCAGGCTATGTGTCAAGAGT 1058
 Qy 205 -----Leu 205
 Db 1059 GTACAGAGCTGTGAGGGCGTGGCCCTGGTAGTGGACAGAGAGCTATCAGCGGGCTG 1118

Qy 206 AsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHisAlaProHisAsnPro 225
 Db 1119 ACCATATGATGGGATGTCAGTGGGGCCAGGCTCACCCTGGAGAGCTGTGCCA----- 1169
 Qy 226 GlyPheArgPhePheTyTrleuHisTyTrLysLeuLysHisGluGlyProPheLysArgLys 245
 Db 1170 GGCAGTGAAGTTCTCGTATCTGAAGTGAAGCTC-----GGC 1205
 Qy 246 ThrCysLeuGlnGluGlnThrThrThrThrThrSerCysLeuLeuGlnAsnValSerPro 265
 Db 1206 ACGAGTACATGATTCACACAGCCGAGGCGCACACCACTT----- 1247
 Qy 266 GlyAspTyTrIleIleGluLeuValAspAspThrAsnThrThrArgLysValMetHisTy 285
 Db 1248 GAGCTGTACCTTGGGGCTGGCC-----AAGGCTATAGGCTTAC 1286
 Qy 286 Ala-----LeuLysProValHisSerProTrpAlaGly 296
 Db 1287 GCACAGCTGTGATTTGGCGCGGAGCTGTATCTCCACAGTGAAGCCCTTGGCAAGGC 1346
 Qy 297 ProIleArgAlaMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeu 316
 Db 1346 ----- 1346
 Qy 317 PheThrValMetCysArgLysLysGlnGlnGlnAsnIleTySerHisLeuAspGluGlu 336
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 Db 1401 GTGGCGAGATTCACAC-----GCTGTGTCGGCGCCGCGGCGGACCCCAT--- 1445
 Qy 357 LysValPheLeuCysTyTrSerSerLysAspGlyGlnAsnHisMetAsnValAlaGlnCys 376
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 Qy 377 PheAlaTyPheLeuGlnAspPheCysGlyCysGluValAlaLeuAspPheTrpGluAsp 396
 Db 1491 -----TCTTACACATGATGTGAGCTGTGCAC-----GAGGAC 1523
 Qy 397 PheSerLeuCysArgGluGluGlnArgGluTrpValIleGlnLysIleHisGluSerGln 416
 Db 1524 GACACCCCTG----- 1532
 Qy 417 PheIleIleValValCysSerLysGlyMetLysTyTrPheValAspLysAsnTyLys 436
 Db 1533 -----CCGCGCTCAGCTGAGGCGCAAGAC---GAG 1562
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 Db 1563 CACCGGGGACGGCGCGGCTCTTACGTTGGGCTGTCACTGTGGCGGCTTACAGCCAC 1622
 Qy 445 -----GlyLysGlyGluLeuPheLeuValAlaValSer----- 455
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 Qy 456 -----AlaIleAlaGluLysLeuArgGlnAlaValGlnSerSerSerAlaAlaLeu 472
 Db 1683 CTGCAGTCTCTCCCTGATGAGGTGCTCGCGTGTATACAGAGCGGACCAAGCGGCGGTG 1742
 Qy 473 SerLysPheIle-----AlaValTyTrPheAspTySerCysGluGlyAspValPro 489
 Db 1743 GTGCAGTGTCTTGGCTGGCTGTGCTCATTTATGATGGAGCTGGCAG----- 1790
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 Db 1791 -----CTGGCATCTCAGCTGCTGTGACCTTCCAAAGACAGGTGTGGCGCTGTGTGGC 1844
 Qy 510 HisLeuHisSerArgAspHisGlyLeuGlnGluProGlyGlnHisThrArgGlnLysSer 529
 Db 1845 AACTATTAAT-----GGTGAAC 1859
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GenCore version 5.1.7
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Run on: March 1, 2006, 06:49:29 ; Search time 344 Seconds
(without alignments)
3813.490 Million cell updates/sec

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Perfect score: 3948
Sequence: 1 MAPWOLCIVFPVNAACNG.....SCKADICRSYDELAAVAP 738

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3690	93.5	2894	3	US-09-747-259-17 1429
3	3248	82.3	3948	3	US-09-789-451-125
4	321.5	8.1	3120	3	US-09-949-002-117
5	321.5	8.1	3120	3	US-09-949-002-117
6	321.5	8.1	3223	2	US-08-620-694A-9
7	321.5	8.1	3223	3	US-08-620-694A-9
8	321.5	8.1	3223	3	US-09-022-255-9
9	321.5	8.1	3223	3	US-09-022-255-9
					Sequence 9, App11
					Sequence 9, App11
					Sequence 3, App11

10	321.5	8.1	3223	3	US-09-022-253-9	Sequence 9, App11
11	321.5	8.1	3223	3	US-09-022-260-9	Sequence 9, App11
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13	321.5	8.1	3223	3	US-09-022-257-9	Sequence 9, App11
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26	145	3.7	23015	3	US-09-949-016-12807	Sequence 12807, A
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28	136	3.4	1810	3	US-09-949-016-5787	Sequence 5787, App
29	136	3.4	2171	3	US-09-976-594-762	Sequence 762, App
30	135.5	3.4	1701	3	US-09-599-360B-56	Sequence 56, App1
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34	126	3.2	5105	3	US-09-919-039-293	Sequence 293, App
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36	121	3.1	23995	3	US-09-949-016-17363	Sequence 17363, A
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38	120	3.0	2165	3	US-09-796-844-17	Sequence 17, App1
39	119.5	3.0	1918	3	US-09-188-930-226	Sequence 226, App
40	119.5	3.0	2165	3	US-09-312-283C-226	Sequence 226, App
41	119.5	3.0	4262	3	US-09-949-016-2134	Sequence 2134, App
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45	118	3.0	1001	3	US-09-671-317-244	Sequence 244, App

ALIGNMENTS

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; Sequence 1429, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length CDNA
; FILE REFERENCES: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1429
; LENGTH: 2894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1429

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Pred. No.: 0
Score: 3706.00
Percent Similarity: 99.7%
Best Local Similarity: 99.4%
Query Match: 93.9%
DB: 3
Length: 2894
Matches: 694
Conservative: 2
Indels: 0
Gaps: 0

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DB 210 TGGCAGGAGATGGGCGCAGCCAGCAGAACAGTGGGCTTACACATCTCAATAT 269

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Db 330 ATCAACATCAAGCCAGATGCTTGCCATGACCAAGTGGCACTGACCAATCTCTTGATGCCCA 369
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QY 201 LysProArgAaPnLeuAaPnIleSerGlnHISGlySerAaPnMetGlnValSerPheAaPn 220
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RESULT 2

US-09-747-259-17
; Sequence 17, Application US/09747259
; Patent No. 656645

GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.

; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth
APPLICANT: Tumas, Daniel
APPLICANT: Vanloekeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Matanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1CPI (US)
CURRENT APPLICATION NUMBER: US/09/747,259
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US 60/175,481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR FILING DATE: 2000-06-22
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PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
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SEQ ID NO 17
LENGTH: 2319
TYPE: DNA
ORGANISM: Homo Sapien
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Score: 3690.00 Matches: 702
Percent Similarity: 96.0% Conservative: 2
Best Local Similarity: 95.8% Mismatches: 11
Query Match: 93.5% Indels: 18
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DB 232 CAGAAATATCCATCCATGCGAGCTGATGCTTGGCAGACCAAGTGGCACTCATTTCTTGG 291
QY SerProGlyValAlaLeuGlyIleGluPheLeuGlyPheArgValIleLeuGluLeu 118
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DB 412 AGCTTCAAAAAGAACTGGAATGGAATCTCAACCTTCTCTGAATATGAATTTGAACGAT 471
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DB 472 TATTTGTAAGGTTGTCCCTTTCTTCATTAAGAAAGAAAGCAATTCACACCTTTC 531
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DB 532 TTCTTTAGAACCGACCGCTGTGACCTGTGTATACCGCGACATCTAGCTGTAAACC 591
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DB 592 TTCTGAAGCTTCGAACTGAACTCAGCCAGCAGATGCGTCCGACATGCAAGTCTCTTC 651
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QY 226 GlyPheArgPhePheTyrrLeuHisTyrrLysLeuHisGluGlyProPheLysArgLys 245
DB 712 GCGCTTCGTTCTTCTTATCTTCACTACAGCTCAGCTCAGCAAGACCTTTCAGCGCAAG 771
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QY 286 AlaLeuLysProValHisSerProTrpAlaGlyProIleArgAlaMetAlaIleThrVal 305
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DB 952 CCACTGTAGTCATATCGCATTCGCGAGCTCTTCACTGTATGTGCGCAAGAGCAA 1011
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QY 346 AlaLeuProArgGluArgLeuArgProArgProLysValPheLeuCytyrrSerSerLys 365
DB 1072 GCATCTCCCAAGAGAGGCTCCGCGCGCGCGCAAGGTCTTCTGCTATTCACATTA 1131
QY 366 AspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrrPheLeuGlnAspPheCys 385
DB 1132 GATGSCAATATCAATGATATGTCAGTGTTCGCTTCTTCCAGAGACTTCTGT 1191
QY 386 GlyCyGlyValAlaLeuAspLeuTrpGluAspPheSerLeuCytyrrGlyGlnArg 405
DB 1192 GCGTGTAGAGTGGCTCTGACCTGTGGGAAGCTTCAAGCTCTGTATGAAAGGCGAGAGA 1251

QY 406 GUTTPVALLIIEGLNLYSLHISGLUSERGILNHEILEILEVALCYSESLYGLY 425
 DB 1252 GAATGGGTCTCCAGAAAGATCCAGAGTCCCAAGTTATCATTTGGTTTTCCTCAAGGT 1311
 QY 426 MELLTYRPHVALLAPLYSLYAAENTYRLYSHISLYGLYGLYATRGILYSEGLY 445
 DB 1312 ATGAAGTACTTTTGGCAAGAAAGAACTCAACAAACAAAGAGGTGGCCGAGCTCGGGG 1371
 QY 446 LYGGLYGLNLEUHELEUVALAVALSERVALLEALGLYLYLEUVALYSGILNALYLS 465
 DB 1372 AAAGAGAGCTCTTCCTGGTGGCGGTGTCAAGCATTCGCAAAAGCTCCCGCAGGCCAAG 1431
 QY 466 GLNSESERVALAALALEUSERLYSPHEILEALVALTYRPHAEPTYRSEYSGILN 485
 DB 1432 CAGAGTTCCGTCGGCGGCTCAGCAAGTTATTCGCCCTCTAATTGATTTCCTGGAG 1491
 QY 486 GLYASPVALPROGLYILEUASPLEUSERTHLYSTYRARGLEUWELAPAEMLLEUPRO 505
 DB 1492 GGAAGAGTCCCGGTATCTTAGACTGATACCAAGTACAGACTCATGACCAATCTTCCT 1551
 QY 506 GLNLEUCYSESLYSLHISLHISERVALYRGAAPHISGLYLEUENGLUPROGLYGLNHLSTHR 525
 DB 1552 CAGCTCTGTTCCCACTGCACTCCCGAGACACGCGCTCCAGAGCGGGCAGCACACG 1611
 QY 526 ARGGLYSEARARGATGANTYRPHAEYRSESLYSESLYARSESLYTYRVALALA 545
 DB 1612 CGACAGGCGACGAGAGAACTACTTCCGAGCAAGTCAAGCCGCTCCCTAATGCTGCC 1671
 QY 546 ILCYAAMNETHISGLNPHETILEAPGLUGLUPROAAPTTPHGLYLYSGILNPHVAL 565
 DB 1672 ATTTGCAACATGACCCAGTTTATGACGAGAGCCGAGCTGTTGAAAAGCAGTTGCTT 1731
 QY 566 PROPHETIAPROPHOPROLEUARGTYRARGLUPROVALLEUGLULYSPHEAPSEGLY 585
 DB 1732 CCTTCATCTCTCCATCGCTGCTGCTACCGGAGCACTTGGAGAAATTTGATTCGGGC 1791
 QY 586 LEUVALLEUAAAPVALMETCYLYSPROGLYPROGLYSEARPHPECYLYLEUVAL 605
 DB 1792 TTGGTTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1851
 QY 606 GLUVALPROVALLEUGLYALATHRGLYPROVALAPSESLYINHLISGLY 625
 DB 1852 GAGCGGCTGTTCTTGGGCGAACCGGACAGCCGAGCTCCAGACGAGAGTCAAGCATGGG 1911
 QY 626 GLYLEUASPGILNAPGLYGLUALARGPROVALALEUAPGLYSESLYALALEUGLUPRO 645
 DB 1912 GGCCTGACCAAGACGGGAGGCGCGCTGCTTGAAGGTAGCGCGCTGCAACCC 1971
 QY 646 LEULEUHIATHRVALLYSLAGLYSERPROSERAPMECPROARGAPSESLYILETYR 665
 DB 1972 CTGCTGACACGGTGAAGGCGGCGAGCCCTCGGACATGCGCGGAGCTCAAGCATTTAT 2031
 QY 666 AAPSESLYVALPROSESLYGLYLEUUSERLEUPROLEUWETGLYLYLEUSERTHRAP 685
 DB 2032 GACTCGCTGCGCTCATCGAGCTGCTCTGCGCACTGATGAGAGACTCTCGACGAGC 2091
 QY 686 GLNTHRGLYTHRSESLYTHRGLYSESLYVALYSESLYSESLYGLYLYLEUGLULY 705
 DB 2092 CAGACAGAAACGCTTCTCGACGAGAGGTGCTCTTCAAGGCGCGGAGGAG 2151
 QY 706 GLUPROVALALEUPROSESLYLYLEUUSERSESLYSESLYCYLYVALAAPLEUGLY 725
 DB 2152 GAACCTCTGCTCTCTTCAAGCTCTCTCTTCTGGTCAATGCAAGCATTTGGT 2211
 QY 726 CYAARGSELYRTHRAPGLYLEUHIATHRVALAVALA 738
 DB 2212 TGCAGAGTACACTGATGAATCCAGCGGCTGCGCTT 2250

; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Aundt, Vinod
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhao, Qing A.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Ma, Yungting
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Wang, Yonghong
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghosh, Reena
 ; APPLICANT: Dimanac, Radoje T.
 ; TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
 ; FILE REFERENCE: 803
 ; CURRENT APPLICATION NUMBER: US/09/799,451
 ; CURRENT FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 948
 ; SOFTWARE: pc FL_genes Version 2.0
 ; SEQ ID NO 125
 ; LENGTH: 3948
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (60) .. (1844)
 US-09-799-451-125
 Alignment Scores:
 Pred. No.: 0 Length: 3948
 Score: 3248.00 Matches: 609
 Percent Similarity: 99.7% Conservative: 1
 Bees Local Similarity: 99.5% Mismatches: 2
 Query Match: 82.3% Indels: 0
 DB: 3 Gaps: 0
 US-10-616-788-2 (1-738) x US-09-799-451-125 (1-3948)
 QY 127 GILNLEUVALLEUVALYAPPROLYSGILNLEUASPSERPHLYSARGTHRGILYMETGLU 146
 DB 6 CAATATTTCTAAAGATCCGAAGAGCTCAACAGATGCTTCAAAAGATGGAATGGA 65
 QY 147 SERGLNPROPHETIAPROPHOPROLEUARGTYRPHAEPTYRSESLYVALAVALA 166
 DB 66 TCTCAACCTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 125
 QY 167 PROSESLYLYSESLYSESLYSESLYSESLYSESLYSESLYSESLYSESLYSESLY 186
 DB 126 CTTTCATTAATAAAGCAAGCAATTAACACCTTCTCTTGAACCCGAGCTGTGAC 185
 QY 187 LEULEUENGLUPROAAPTTPHGLYLYSGILNPHVAL 206
 DB 186 CTGTTTGTACAGCGGACATCTAGCTTGAACCTTCTGGAAGCTCGGAACCTGAC 245
 QY 207 ILESERGLNHLISGLYSEARAPMECPROVALYSESLYSESLYSESLYSESLYSESLY 226
 DB 246 ATGAGCAGAGATGCTCGGACATGAGAGGTGCTTGGACAGCAGCAGCAGCAGCAGCAG 305
 QY 227 PHAARGPHETIAPROPHOPROLEUARGTYRPHAEPTYRSESLYVALAVALA 246
 DB 306 TTCCGTTCTCTCATCTTCACTCAAGCTCAAGCAGCAAGCAAGCAAGCAAGCAAGCA 365
 QY 247 CYLYSGILNGLNTHRGLYTHRGLYSESLYSESLYSESLYSESLYSESLYSESLYSE 266
 DB 366 TGTAGCAGAGAGAACTACAGAGATGACAGTGCCTCTTCAAAATGTTTCTCAAGG 425
 QY 267 APTYRILEILEGLNLEUVALAAPAEPTTPHAEPTTPHAEPTTPHAEPTTPHAEPTTPH 286

RESULT 3
 US-09-799-451-125
 ; Sequence 125, Application US/09799451
 ; Patent No. 6783969
 ; GENERAL INFORMATION:

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Db 426 GATTATTAATGACCTGCTGATGACCTAACACACAAAGATGATCATTTATGCC 485
Qy 287 LeuIysProValHisSerProTIPAlaGlyProIleArgAlaMetAlaIleThrValPro 306
Db 486 TTAAAGCAGAGCACTCCCGTGGGCGGCGCCCATCAGAGCGGGCCATCATAGTGCCA 545
Qy 307 LeuValValIleSerAlaPheAlaThrLeuPheThrValMetCysArgLysLysGlnGln 326
Db 546 CTGGTAGCATATGCGCATTCGACGCTCTTCACTGATGATGTCGCCGAAGACACAA 605
Qy 327 GluAsnIleTyrSerHisLeuAspGluGluSerSerGluSerSerThrTyrThrAlaAla 346
Db 606 GAAATATATATTTACATTTAGATGAAGAGCTCTGAGCTTTCCACATACATCGACCA 665
Qy 347 LeuProArgGluArgLeuArgProArgProLysValPheLeuCysTyrSerSerLysAsp 366
Db 666 CTCCCAAGAGAGAGGCTCCGCGCGGCGGCGAAGGCTTTCTCTGCTATTCAGTAAAGAT 725
Qy 367 GlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPheLeuGlnAspPheCysGly 386
Db 726 GGCAGAGATCATGAATGTCGTCAAGTTCGCTACCTTCACAGGACTTCGTGGC 785
Qy 387 CysGluValAlaLeuAspLeuTyrGluAspPheSerLeuCysArgGluGluArgGlu 406
Db 786 TGTAGAGTGGCTCTGACCTGTGGAGAGACTTCAGCTCTTGAAGAGAGGCGACAGAGA 845
Qy 407 TrrValIleGlnLysIleHisGluSerGlnPheIleIleValAlaCysSerLysGlyMet 426
Db 846 TGGGTATCCAGAGATCCAGATCCAGTCCAGTTCATGTCGTTGTTGTTCCAAAGATAG 905
Qy 427 LysTyrPheValAspLysLysAsnTyrLysHisLysGlyGlyArgGlySerGlyLys 446
Db 906 AAGACTTGTGGCAAGAGAACTACAAACAAAGAGGTGGCGCGAGCTCCGGGAAA 965
Qy 447 GlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLysLeuArgGlnAlaLysGln 466
Db 966 GAGAGCTCTTCGTCGGTGGCGGTCTCAGCACTCCGAAAGCTCCGCGACGCAAGAG 1025
Qy 467 SerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSerCysGluGly 486
Db 1026 AGTTCGTCGCGGCGCTCAGCAAGTTATCCCGCTACTTGTATTTATTCCTGGAGGGA 1085
Qy 487 AspValProGlyIleLeuAspLeuSerThrLysTyrArgLysMetAspAsnLeuProGln 506
Db 1086 GACCTCCCGGCTATCTAGACTGATGATCAAGACTCAAGCAATCTTCCTCAG 1145
Qy 507 LeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGluProGlyGlnHisThrArg 526
Db 1146 CTCTGTTCCCACTGCACTCCGAGACCAAGCGCTCCGAGGCGCGGCGACACACGCGA 1205
Qy 527 GlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArgSerLeuTyrValAlaIle 546
Db 1206 CAGGCGCAGCAAGAACTACTTCCGAGCAAGTCAAGCCCGCTCCCTATAGTGGCAATT 1265
Qy 547 CysAsnMetHisGlnPheIleAspGluGluProAspTyrPheGluLysGlnPheValPro 566
Db 1266 TGCACAATGACACAGTTATTTAGACGAGGAGCCGACGTGGTTCGAAAAGCACTTCGTTCC 1325
Qy 567 PheHisProProProLysArgTyrArgGluProValLeuGluLysPheAspSerGlyLeu 586
Db 1326 TTCATCTCTCTCCACGCGCTACCGGAGCCAGCTTGGAGAAATTTGATTTCCGGCTTG 1385
Qy 587 ValLeuAsnAspValMetCysLysProGlyProGluSerAspPheCysLeuValGlu 606
Db 1386 GTTTTAAATATATGATGATGTGCAACGAGGCGCTGAGATGACTTCTGCTTAAAGTAGAG 1445
Qy 607 AlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHisGluSerGlnHisGly 626
Db 1446 GCGGCTGTTCTTGGGGCAACGAGCAAGCGACTCCGACGAGAGTCAACATGGGGGC 1505
Qy 627 LeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySerAlaAlaLeuGlnProLeu 646

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Db 1506 CTGAGCAAGACGGGAGGCGCCGCGCTTGACGCTGAGCGCGCGCTGCAACCCCTG 1565
Qy 647 LeuHisThrValIleValAlaGlySerProSerAspMetProArgAspSerGlyIleTyrAsp 666
Db 1566 CTGACACGCGTGAAGCGGAGCGGCGGCTCGACATGCGGGGAGCTCAGCATCTATGAC 1625
Qy 667 SerSerValProSerSerGluLeuSerLeuProLeuMetGluGlyLeuSerThrAspGln 686
Db 1626 TGTCTGTGCTTCATTCAGAGCTGTCTCTCTCCACTGATGAGAGACTCTGACGAGACAG 1685
Qy 687 ThrGluThrSerSerLeuThrGluSerValSerSerSerSerGlyLeuGluGluGln 706
Db 1686 ACAGAAAGCTTCTCCGACGAGAGCGTTCCTCTTCAAGCGCGGAGAGAGAA 1745
Qy 707 ProProAlaLeuProSerLysLysLeuLeuSerSerGlySerGlyValAlaAspLeuGly 726
Db 1746 CTTCTGCTCCCTCTCTTCCAAAGCTCTCTCTGCGGTCAAGCAAGAGATCTTGTGTC 1805
Qy 727 ArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
Db 1806 CGCAGTACACTGATGAATCTCAGCGGCTGCGCT 1841

RESULT 4
US-09-949-002-117
: Sequence 117, Application US/09949002
: Patent No. 690016
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: C1000790
: CURRENT APPLICATION NUMBER: US/09/949,002
: PRIOR FILING DATE: 2000-01-28
: PRIOR APPLICATION NUMBER: 60/231,401
: NUMBER OF SEQ. ID NOS: 10823
: SOFTWARE: FASTSEQ For Windows Version 4.0
: SEQ ID NO 117
: LENGTH: 3120
: TYPE: DNA
: ORGANISM: Human
US-09-949-002-117

Alignment Scores:
Pred. No.: 1.38e-24 Length: 3120
Score: 321.50 Matches: 183
Percent Similarity: 35.9% Conservative: 106
Best Local Similarity: 22.7% Mismatches: 357
Query Match: 8.1% Indels: 161
DB: Gaps: 34

US-10-616-788-2 (1-738) x US-09-949-002-117 (1-3120)
Qy 31 GlyArgAlaTrrGlyValAspThrCysGlyTrrArgGlyValGlyProAlaSerArgAsn 50
Db 70 GCGCCCTGCGGGGCTGCTCTGCTGCTCTGCGCGTG-CTGGCGCGGCTGGCGGCTCC 128
Qy 51 SerGlyLeu-----TyrAsnIleThrPhe 58
Db 129 CTGCGACTCTCGACCAACCGGCGGCTGCTCTCCACCGCGGAGCTGAACCTGACGCTC 188
Qy 59 LysTyrAspAsnCys-----ThrThrTyrLeuAsnProValGlyHisValIleAla 76
Db 189 AAGAAATGTCCTGCGCGATGACAGCTGATTCACCT----- 227
Qy 77 AspAlaGlnAsnIleThr-----IleSerGlnTyrAlaCys 88
Db 228 -----CGAAACCTGACCCCTCTCCCAAGAGACTGAGATCCAGCTGACCTTGGC 281
Qy 89 HisAspGln-----ValAlaValThrIleLeuThrPheSer---ProGlyAla 102
Db 282 CACACCAGCAAGAGACCTGTTCCCGTGGCTCAGCATGAGACATGACATGACAGAC 341

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QY 103 LeuGlyTLeuGluPheLeuYsGlyPheArgValIleLeuGluGluLeuYsSerGluGly 122
 DB 342 GCCAGCATCTGTAAGGAGGTCAGAGATTAATCTGCTGCAAGCAACCAATGAA 401
 QY 123 ArgGlnCyseGlnGlnLeuIleLeuYsAerProLyseGlnLeuYsSerSerPheYsArg 142
 DB 402 CGTTGGGCGCTCAGG-----TTTGAAGTTCTGTCCAAACTGAGGCACTACCAACAGCGG 455
 QY 143 ThrGlyMetGluSerGlnProPheLeuYsMetLeuYsPheGluThrArgIleValLeu 162
 DB 456 TGGCGTTTACCTTACGCCACTTGTG---GTTGACCTTCGACCAAGAAATGAGTGACC 512
 QY 163 ValI-----ValProPheProSerIleLeuYsAerGluSerAntYrHisProPhePhe 180
 DB 513 GTTCACCACTGCGCAAGCCATCCCTGATGAGGACCAACCAACCACTGCAAGAAATTC 572
 QY 181 ArgThrArgIleCyseAerPheLeuLeuGluProAerAerLeuIleCylys----- 197
 DB 573 CTGTGCTGTAAGTGAAGCAAGCAGAGATGAAGTAAACCAAGCATGACAGCTCAGGC 632
 QY 198 ProPheTrpYsProAerAerLeu----- 205
 DB 633 AGCCTGAGGAGCC---AACATCACCGTGAAGACCTTGAAGGCCACACAGCTGCTGTG 689
 QY 206 -----AenIleSerGlnHisGlySerAerMetGlnValSerPheAerHis 220
 DB 690 AGCTTACCTGCGAAGCAATTAACCCATTAACCATTAACCATTAACCATTAACCATTAAC 749
 QY 221 AlaProHisAerPheGlyPheAerGlyPheAerGlyPheAerGlyPheAerGlyPheAer 240
 DB 750 ATGAGAGAACCAAGTGTCTTGAAGCAATGAC---CACATACCTGCGCCCAAGCAAGAA 806
 QY 241 ProPheYsArgIleYsThrCylysGlnGluGlnThrThrGluThrThrSerCylysLeu 260
 DB 807 GAGTTCACCAAGGATCAACGATCACTACATCACTACCAACCTTAAAGGCTGTGCGC 866
 QY 261 GlnAerValSerProGluAerProIleIleGlnLeuValAerAerHis-----Aer 277
 DB 867 CACCAAGTGAAGTCAAGCCCTTCTTCAAGCAAGCTGCTCAATGACCTGCTCAAGCACTCC 926
 QY 278 ThrThrArgIleValMetHisIleValLeuYsAerProValHisSerProTrpAlaGlyPro 297
 DB 927 GCGATCTTCCCTGCGCAAGAAATGCCAGACATCTCAACCAATCCGACATACATGCC 986
 QY 298 IleArgIleMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPhe 317
 DB 987 CTGTGGGTGTAAGTCACTACAGGAGCATCTCAATCTGCTGAGGCTGCTGATCTCTG 1046
 QY 318 ThrValMetCyseArgIleYsGlnGlnGlnLeuAerIleYsSerHisLeuAerGluGluSer 337
 DB 1047 CTATCTGCTGCAATGACCTGAGGCTGAGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1097
 QY 338 SerGluSerSerThrIleValAlaLeuProArgGluArgLeuAerProAerPro--- 356
 DB 1098 AGTGATACACCAATTAACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1157
 QY 357 -----LysValPheLeuCyseYsSerSerIleYsAerGluGlnAerHisMetAerVal 373
 DB 1158 AACCCAGAGAGGCTGATCACTACTACAGCC---GACCAACCCCTCACTGAGTGAAGCTG 1214
 QY 374 ValGlnCysePheAlaIleYsPheLeuGlnAerPheCyseGluValAlaLeuAerLeu 393
 DB 1215 GTCTGAATTAATGCGCCAGTCTGCTGCAAGCTGCGGCAAGGAGTGGCCCTGAGACTG 1274
 QY 394 TrpGluAerPheSerLeuCyseArgGluGlyGlnArgIleTrpVal-----Ile 409
 DB 1275 CTGGAAGAGAGGCACTGCGAGGAGCAAGTAACTGAGCTGGTGGGCGCTGAGAAAGCAG 1334
 QY 410 GlnYsIleHisGluSerGlnPheIleIleValValCyseSerIleYsMetLeuYsTrpPhe 429
 DB 1335 GAGATGTGTGAGAGCACTCAAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1388

QY 430 ValAerPheYsAerValIleYsGlnGluGly----- 441
 DB 1389 -----GCCAAGTGGAGAGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1442
 QY 442 ArgGlySerGlyValGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluYsLeu 461
 DB 1443 CAGGGAAGCCCGTGGGAGGAGCTGTCATGCAAGCCATGAACATGATCTCTCCCGAGCTTC 1502
 QY 462 ArgGlnAlaYsGlnSerSerSerIleAlaLeuSerIlePheIleAlaValIleYsPhe----- 480
 DB 1503 AAGAGG-----CCAGCTGCTGTGCGCAAGCTTACGATCTGCTGCTGCTGCTGCTGCTG 1547
 QY 481 AerYsSerCyseGluGlyAerValProGlyIleLeuAerPheLeuSerThrIleYsTrpAerLeu 500
 DB 1548 GAGTGAAGCTGTAAGCGGCAAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 1607
 QY 501 MetAerAerLeuProGlnLeuCyseSerHisIleAerAerAerHisIleAerGluGlnGlu 520
 DB 1608 ATGACAGAGTTGAGAGAGTG-----TACTTCCGATCCAGAGCTTGAAGATGTTCCAG 1661
 QY 521 ProGlyGlnHisThrArgGlnGly-----SerArgAerAerThrPheArgSerLeuYsSer 538
 DB 1662 CCGGCGCGATGACCGCGTGAAGGAGCTGTGAGGAGCAACTACCTGCGAGCCCGGCGC 1721
 QY 539 GlyArgSerLeuTrpValAlaIleCyseAerMetHisGlnPheIleAerGluGluProAer 558
 DB 1722 GCGAGGCACTCCG 1781
 QY 559 TrpPheGlu-----LysGlnPheValProPheHisProPro 570
 DB 1782 TGGTTGAAATGAGAACTTACTACAGAGATGACAGAGATGAGCCCTGCTGCGAGAA 1841
 QY 571 ProLeuAerGlyThrArgIleProValLeuGluYsPheAerSerGlyLeuValLeuAerAer 590
 DB 1842 GAGGTG---TTTGAAGAGCACTGCTGCTCCG---GAAACCGGCACTGTAAGCGGCGG 1895
 QY 591 ValMetCyseAerProGlyProGluSerAerPheCyseLeuValGluAlaProValLeu 610
 DB 1896 CCCCTGTGCGGAG---CTGCTCCAGAGCGCTGCTGCGCATTAAC---CGCTGCTGTC 1949
 QY 611 GlyAlaThrGlyProAlaAerSerGlnHisGluSerGlnHis----- 624
 DB 1950 GGGGAGAGAGAGACAGACAGATGAGCAAGCTGAACTCACTGAGCCCGCGGCTCAG 2009
 QY 624 ----- 624
 DB 2010 CCAAGCGCGAGCCCTTCAACCTGCTGCTGCGCGAGAGAGGAGGCGCTGCTGCGCC 2069
 QY 625 -----GlyGlyLeuAerGlnAerGlyGluAlaArgProAlaLeuAerGlySer 640
 DB 2070 GCGGTGAAGCTGAGCGCTGCTGCTGAGCGGCGAGTCCGCTGCACTGCGCGGAGAG 2129
 QY 641 AlaAlaLeuGlnProLeuLeuHisThrValIleValIleGlySerProSerAerMetProArg 660
 DB 2130 GGGGAGGCTGCGCGCTGCTGAGGAGCGGCGGCTGAGG-----CGA 2171
 QY 661 AerpSerGlyIleYsAerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680
 DB 2172 AATAGGTCTCTTCTC-----CTCCCTGAGACCCGAGAGCTGCGCCCTT----- 2216
 QY 681 GlyLeuSerThrAerPheGlnThrGluThrSerSerLeuThrGlySerValSerSerSer 700
 DB 2217 GGCAGAGACCCCAATGAGCTGCTGATCTCTTCCAGAGAGACTGAGG----- 2267
 QY 701 GlyLeuGlyGluGluProProAlaLeuProSerLeuYsLeuLeuSerSerGlySerCyse 720
 DB 2268 -----GAGCACTCGAAGGCTTGAATGCTCTGCTTGAAGAGAGTCTGAGCTGCTC 2318
 QY 721 LysAlaAerPheGlyCyse 726
 DB 2319 CAGGCCAGAGGCGCTGC 2336

RESULT 5

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US-09-949-002-126
; Sequence 126, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 3120
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-126

Alignment Scores:
Pred. No.: 1,38e-24 Length: 3120
Score: 321.50 Matches: 183
Percent Similarity: 36.0% Conservative: 107
Best Local Similarity: 22.7% Mismatches: 356
Query Match: 8.1% Indels: 161
Gaps: 34

US-10-616-788-2 (1-738) x US-09-949-002-126 (1-3120)
QY 31 G1AARGAATATGATGValaAspThrCysGlyTTPArglyValGlyProAlaSerArgAsn 50
Db 70 GGGCCCTGCTGGGGCTGCTCTCTGCTCTGCTGGGCGTG-CTGGCCCGGGTGGCGCTCC 188
QY 51 SerGlyLeu-----TyrAsnIleThrPhe 58
Db 129 CTGGAGATCTCTGAGACACCGGGGCTGTCTGCTCCAGCGGGGCTTAACCTGACGGTCC 188
QY 59 LysTyrAspAsnCys-----ThrTyrLeuAsnProValGlyValIleAla 76
Db 189 AAGAATAGTACCTGGCTGATGACAGTGATTCACCT----- 227
QY 77 AspAlaGlnAsnIleThr-----IleSerGlnTyrAlaCys 88
Db 228 -----CGAATCTGACCCCTCTCTCCCAAGAGCCTGACGATCCAGCTGCACTTGGC 281
QY 89 HisAspGln-----ValAlaValThrIleLeuTyrPse-----ProGlyAla 102
Db 282 CACACCCACAGAGAGACCTGTCCCGGTGGCTCACTCAATGATGACATGACAGACAGAC 341
QY 103 LeuGlyIleGluPheLeuLysGlyPheArgValIleLeuGluGluLeuLysSerGly 122
Db 342 GCCAGATCTCTGATCTCGAGGCTGACAGATTAATCTCTCTGACGCTGAACACCAAGAA 401
QY 123 ArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPheLysArg 142
Db 402 CGTTTGGCTGACG-----TTTGAAGTTTCTGTCCAACTGAGGACATCACACAGCGCG 455
QY 143 ThrGlyMetCysLeuSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPheVal 162
Db 456 TGGCGTTTACCTTACGCCACTTGTG--GTTGACCTTACCGAAGAAATGAGGTACC 512
QY 163 Val-----ValProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhe 180
Db 513 GTTTCACACAGTGGCCAGACCATCCCGATGCGGAGACCAACACACAGCTCCAGAAATTC 572
QY 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLys----- 197
Db 573 CTGTGCTGCTGATGTCGACAGCGCAGGATGAAGGTAAACAGCGCATGATGAGCTCAGGC 632
QY 198 ProPheThrLysProArgAsnLeu----- 205

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Db 633 AGCGTGGGAGCCCC--AAATCATCCGTGAGAGACCTGTGAGGCCACAGCTGCGTGTG 689
QY 206 -----AsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
Db 690 AGCTTCAACCTGTGGAACGAACTATACCATTCAGATCTCTGCTGACCAATTTTCCGAC 749
QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLeuValIleGly 240
Db 750 ATGAGAAACACAGTGTCTTGAGCACATGAC--CACTATCTCGGCCCAACACAGAA 806
QY 241 ProPheLysArgLysThrCysLysGlnGluGlnThrThrGluThrThrSerCysLeuLeu 260
Db 807 GAGTTCACAGGAGATCAACAGTCACTCACTACGCAACCTTAAGAGTGTGTGCGC 866
QY 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThr-----Asn 277
Db 867 CACCAAGTGCAGATCCAGCCCTTCTTACAGAGCTGCTCAATGACCTGCTCAGACCTCC 926
QY 278 ThrThrArgLysValMetHisTyrAlaLeuLysProValHisSerProTyrAlaGlyPro 297
Db 927 GCGACTGTTTCTGCCAAGAAATGCCAGACATCTCAAGTGTCTACCGAGACTATACGCC 986
QY 298 IleArgAlaMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPhe 317
Db 987 CTGTGGGTGATCTGTTTACATCAGGGGATCTCCATCTGTGTGTGGCTCTCGTATCTGTG 1046
QY 318 ThrValMetCysArgLysLysGlnGlnAsnIleTyrSerHisLeuAspGluGluSer 337
Db 1047 CTGATGCTGTGATGACCTGAGAGCTGAGTGTGGCTGGAAGT-----GAAATATAC 1097
QY 338 SerGluSerSerThrTyrThrAlaIleLeuProArgGluLysArgLeuArgPro-- 356
Db 1098 AGTAAATACCAAAATACCGATGCGCTGCGGCTGACCTGATCCCTCCACCGCTG 1157
QY 357 -----LysValPheLeuCysTyrSerSerLysAspGlyGlnAsnHisMetAsnVal 373
Db 1158 AAGCCAGAAAGCTCTGAACTATCTACAGCC--GACCAACCCCTTAACGTGAGACTG 1214
QY 374 ValGlnCysPheAlaTyrPheLeuGlnAspPheCysGlyCysGluValAlaLeuAspLeu 393
Db 1215 GTCCTGAATATTCGCCAGATCTCTGTCACCGCTGCGGCAAGAGTGGCTGAGCTG 1274
QY 394 TrpGluAspPheSerLeuCysArgGluGlnArgGluTyrVal-----Ile 409
Db 1275 CTGAAGAGAGAGCACTCTCGAGGAGAGATGATGACCTGTGGTGGCTGTCAAGAGCAG 1334
QY 410 GlnLysIleHisLeuSerGlnPheIleIleValAlaCysSerLysGlyMetLysTyrPhe 429
Db 1335 GAGATGTGAGAGCACTTAAGTATCTGTCTGTCTCTCCGCGGACAGCGC----- 1388
QY 430 ValAspLysLysAsnTyrLysHisLysGlyGly----- 441
Db 1389 -----GCCAAGTGGAGAGGCTCTGGGCGGGGGGCGCTGTGGCGGCTGCGTGAC 1442
QY 442 ArgGlySerGlyLysGlyLeuPheLeuValAlaValSerAlaIleAlaGluLysLeu 461
Db 1443 CACGGAAAGCCCTGGGGGAGACTGTTCATCTGACAGCAATGATCTCCCGGACTTC 1502
QY 462 ArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe-- 480
Db 1503 AAGAGG-----CAAGCTGTGTTGGGACCTTACGTAAGTCTGTCTTCTTACG 1547
QY 481 AspTyrSerCysGluGlyAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeu 500
Db 1548 GAGTCAAGCTGATGACGGCGAGCGTCCCGACCTGTGTGGCGGGCGCGCGGTACCGGCTC 1607
QY 501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
Db 1608 ATGACAGGTTTCAGAGAGGTG-----TACTTCGCGATCCAGGACCTTGAGAGTTTCCAG 1661
QY 521 ProGlyLysHisThrArgGlnGly-----SerArgArgAsnTyrPheArgSerLysSer 538
Db 1662 CCGGGCCGATGACCGCGTGAAGGAGCTGTGCGGGGAGAACTACTCTCGGAGCCCGGGGC 1721

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QY 539 G|A|V|A|S|e|r|e|u|t|y|r|v|a|l|a|l|e|c|y|a|s|e|n|e|h|i|e|g|i|n|h|e|l|e|a|r|g|i|u|g|i|p|r|o|a|r|p| 558
 D| 1722 G|G|G|A|G|G|A|G|C|T|C|C|C|C|C|C|C|T|G|A|G|G|T|C|G|G|A|G|C|T|G|G|G|A|G|C|C|C|C|C|G|G|A|C| 1781
 QY 559 T|T|P|h|e|G|l|u|-----L|y|e|G|i|n|h|e|V|a|l|P|r|o|h|e|i|s|P|r|o|h|e|i| 570
 D| 1782 T|G|G|T|G|A|A|T|G|T|G|A|A|C|C|T|A|C|T|A|C|G|A|T|A|C|G|A|T|G|C|C|G|C|C|T|G|G|A|C|G|A| 1841
 QY 571 P|r|o|h|e|i|a|r|g|t|y|r|a|r|g|i|u|p|r|o|v|a|l|e|u|g|i|u|b|r|h|e|a|r|p|e|r|g|i|y|l|e|u|V|a|l|l|e|u|a|r|a|r|p| 590
 D| 1842 G|A|G|T|G|-----T|T|T|A|G|G|G|C|C|A|C|T|G|C|T|G|C|C|G|-----G|A|A|C|C|G|G|C|A|T|C|T|G|A|A|C|G|G|G|C|G| 1895
 QY 591 V|a|l|e|c|y|a|s|e|u|r|p|r|o|g|i|u|p|r|o|g|i|u|s|e|r|a|r|p|h|e|c|y|a|s|e|u|r|y|v|a|l|g|i|u|a|l|P|r|o|v|a|l|e|u| 610
 D| 1896 C|C|C|C|T|G|T|G|C|G|A|G|-----C|C|T|G|G|T|C|C|C|A|G|C|C|T|G|C|C|G|C|C|A|T|A|G|C|-----C|G|C|T|G|G|T|C| 1949
 QY 611 G|l|y|a|l|a|t|h|r|g|i|y|P|r|o|a|l|a|r|p|e|r|g|i|n|h|i|e|g|i|u|s|e|r|g|i|n|h|i|s|----- 624
 D| 1950 G|G|G|A|G|G|A|G|A|G|A|G|A|G|A|G|A|G|T|G|G|A|A|A|C|T|G|G|A|A|C|C|T|G|A|C|C|T|G|A|C|C|C|G|G|G|T|G|A|G| 2009
 QY 624 ----- 624
 D| 2010 C|A|G|C|C|G|C|G|A|G|C|C|C|C|T|C|A|C|A|C|C|T|G|T|G|T|G|T|G|C|G|C|G|C|G|A|G|A|G|G|G|G|C|C|T|G|T|G|G|C|C| 2069
 QY 625 -----G|l|y|g|i|l|e|u|a|r|p|i|n|a|r|p|g|i|y|g|i|u|a|l|a|r|p|r|o|a|l|a|e|u|a|r|p|g|i|y|s|e|r| 640
 D| 2070 G|C|C|G|T|G|A|G|C|C|T|G|G|C|C|C|C|T|G|G|A|G|C|G|T|G|G|C|C|G|C|C|G|C|C|G|C|C|G|G|G|G|G|A|G| 2129
 QY 641 A|l|a|l|a|l|e|u|g|i|n|h|P|r|o|h|e|i|u|e|h|i|s|t|h|r|v|a|l|y|e|a|g|i|y|s|e|r|P|r|o|h|e|i|a|r|p|e|r|P|r|o|h|e|i| 660
 D| 2130 G|G|G|A|G|G|C|C|C|C|G|C|T|G|G|G|G|A|G|C|C|G|G|G|G|G|C|T|G|G|-----C|G|A| 2171
 QY 661 A|r|p|S|e|r|g|i|y|l|e|r|y|r|a|r|p|e|r|S|e|r|V|a|l|P|r|o|h|e|i|S|e|r|g|i|u|e|r|S|e|r|u|e|r|P|r|o|h|e|i|u|e|r|P|r|o|h|e|i|u|e|r| 680
 D| 2172 A|A|T|A|G|G|C|T|C|T|C|T|T|C|-----C|T|C|C|C|G|T|G|A|C|C|C|G|A|G|A|C|T|G|C|C|C|C|T|T|----- 2216
 QY 681 G|l|y|e|r|S|e|r|h|r|a|r|p|i|n|h|r|g|i|u|h|h|e|r|S|e|r|S|e|r|u|e|r|h|u|g|i|u|s|e|r|V|a|l|S|e|r|S|e|r|S|e|r| 700
 D| 2217 G|G|A|G|A|G|C|A|C|C|C|C|A|T|G|G|G|T|C|T|G|A|C|C|T|C|T|C|A|G|A|G|A|C|G|G|A|G|----- 2267
 QY 701 G|l|y|e|u|g|i|y|g|i|u|g|i|u|p|r|o|a|l|e|u|P|r|o|h|e|i|S|e|r|S|e|r|u|e|r|S|e|r|g|i|y|S|e|r|y| 720
 D| 2268 -----G|A|G|A|C|C|T|G|A|A|G|G|T|T|G|A|T|C|T|C|G|T|T|C|A|G|A|C|A|G|A|T|C|G|A|G|C|T|G|C| 2218
 QY 721 L|y|e|A|l|a|a|r|p|e|u|g|i|y|y| 726
 D| 2319 C|A|G|G|C|C|A|G|G|G|G|G|G|C|T|G|C| 2336
 RESULT 6
 US-08-620-694A-9
 ; Sequence 9, Application US/08620694A
 ; Patent No. 5869286
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Panlow, William
 ; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/620,694A

; FILING DATE: 21 MARCH 1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/538,765
 ; FILING DATE: 7 AUGUST 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/410,535
 ; FILING DATE: 23 MARCH 1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,695
 ; REFERENCE/DOCKET NUMBER: 2617-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3223 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Human
 ; STRAIN: IL-17 R (IL17A8 receptor)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 93..2693
 ; US-08-620-694A-9
 Alignment Scores:
 Pred. No.: 1,466-24 Length: 3223
 Score: 321.50 Matches: 183
 Percent Similarity: 35.9% Conservative: 106
 Best Local Similarity: 22.7% Mismatches: 357
 Query Match: 8.1% Indels: 161
 DB: 2 Gaps: 34
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 D| 130 G|G|C|C|C|T|G|C|T|G|G|G|G|C|T|G|C|T|G|C|T|G|C|T|G|G|G|C|T|G|-----C|T|G|G|C|C|C|G|G|G|G|C|C|C|T|C| 188
 QY 51 S|e|r|g|i|y|l|e|u|-----T|y|r|a|n|i|l|e|h|r|h|e| 58
 D| 189 C|T|G|G|A|C|T|C|T|G|A|C|A|C|G|G|G|G|C|T|G|T|G|T|C|C|A|G|C|G|G|G|G|C|T|A|A|A|C|T|G|A|C|G|G|T|C| 248
 QY 59 L|y|e|r|y|r|a|r|p|a|r|n|C|y|s|-----T|h|r|h|r|y|r|e|u|a|r|p|r|o|v|a|l|g|i|y|h|i|s|v|a|i|l|e|a|l|a| 76
 D| 249 A|A|A|A|T|A|G|T|A|C|C|T|G|C|T|G|A|T|G|A|C|A|C|T|G|A|T|T|C|A|C|C|T|----- 287
 QY 77 A|s|p|a|l|g|i|n|h|a|n|i|l|e|h|r|-----I|l|e|r|S|e|r|g|i|n|h|r|a|c|y|s| 88
 D| 288 -----G|A|A|A|C|T|G|A|C|C|C|C|C|C|T|C|T|C|C|C|A|A|A|G|A|C|T|G|A|A|T|T|C|A|G|C|T|T|G|C|C| 341
 QY 89 H|i|s|p|g|i|n|-----V|a|l|a|V|a|l|h|r|i|l|e|u|r|p|r|e|r|-----P|r|o|g|i|y|a|l|a| 102
 D| 342 C|A|C|A|C|C|A|C|A|G|A|G|A|C|C|T|T|C|C|C|C|G|G|G|C|C|A|C|A|T|G|A|T|G|A|C|A|C|T|G|A|C|G|A|C|A|G|A|C| 401
 QY 103 L|e|u|g|i|y|l|e|g|i|u|h|e|u|l|e|u|y|s|g|i|y|p|h|e|r|g|v|a|i|l|e|u|g|i|u|l|e|u|l|e|u|y|S|e|r|g|i|u|g|i|y| 122
 D| 402 G|C|A|G|A|T|C|T|G|A|C|T|C|A|G|G|G|T|G|C|A|G|A|G|T|A|T|C|T|G|C|C|T|G|C|C|G|A|C|C|T|G|A|A|C|C|A|T|G|A| 461
 QY 123 A|r|g|i|n|C|y|e|g|i|n|h|e|u|l|e|u|l|e|u|y|s|a|r|p|r|o|l|y|g|i|u|e|u|a|r|S|e|r|S|e|r|P|h|e|r|y|a|r|g| 142
 D| 462 C|G|T|T|T|G|G|T|G|C|G|-----T|T|T|A|G|T|T|T|G|T|C|C|A|A|C|T|G|G|G|A|T|C|A|C|A|G|G|C|G| 515
 QY 143 T|h|r|g|i|y|e|r|S|e|r|g|i|n|h|P|r|o|h|e|i|a|r|p|e|r|h|i|s|v|a|i|l|e|a|l|a| 162

Db 516 TGGGTTTACCTTACAGCACTTGTG---CTTACCCCTGACCGAATATGAGTACC 572
 Qy 163 Val-----ValProPheProSerIleValAsnGlnSerAntyThiProPhePhe 180
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 Qy 181 ArgThrArgIaCyAspLeuLeuLeuGlnProAspAsnLeuIaCyValS----- 197
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 Qy 198 ProPheTrpIysProAsnLeu----- 205
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 Qy 206 -----AsnIleSerGlnIleGlySerAspMetGlnIleSerPheAspHis 220
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 Qy 221 AlaProIlaAsnPheGlyPheArgPhePheTrpIleuHisTrpIleuValHisGlnGly 240
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 Qy 298 IleArgIaMetAlaIleThrValProLeuValIleSerAlaPheAlaThrLeuPhe 317
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 Qy 338 SerGlnSerSerThrTrpIaAlaLeuProArgIleuArgIleuArgProArgPro--- 356
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 Qy 374 ValGlnCyAspPheAlaTrpPheLeuGlnAspPheCyAspGlyCyValValAlaLeuAspLeu 393
 Db 1275 GTCTGTAATTTCCGCAAGTCTGCTCAACGCGCTGCGGCAAGAGTGGCTTGAAGCTG 1334
 Qy 394 TrpGlnAspPheSerLeuCyValArgIyGlnArgIleuTrpVal-----Ile 409
 Db 1335 CTGGAAGACGAGGCTATCTGAGGAGCATGATCATGCTGGGTGGCGCTCAGAAACAG 1394
 Qy 410 GlnIleIleIleIleGlnSerGlnPheIleIleValValCySerSerIysGlyMetIysTrpPhe 429
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 Qy 442 ArgGlySerIyGlyGlyLeuPheLeuValAlaValSerAlaIleAlaGlnIyLeu 461
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Db 1563 AAGAG-----CCAGCCTGCTGGGACCTTACGATGCTGCTACTTACG 1607
 Qy 481 AspTrpSerCyValGlnIyAspValProGlyIleLeuAspLeuSerThrIyTrpArgLeu 500
 Db 1608 GAGTCACTGTATACCGCCAGCGTCCGACCTTTCGCGCGCGCGCGCTGACCGCTC 1667
 Qy 501 MetAspAsnLeuProGlnIleuCySerHisLeuHisSerArgAspHisGlyLeuGlnIy 520
 Db 1668 ATGACAGGTTCCAGAGAGT-----TACTTCCGATCCAGACCTCGAGATGTTCCAG 1721
 Qy 521 ProGlyGlnHisThrArgGlnIy-----SerArgArgAntyTrpPheArgSerIysSer 538
 Db 1722 CCGGCGCATGACCGCGTGAAGGAGCTGTCCGGGAGCAATCACTTACCTGCGGACCGCGC 1781
 Qy 539 GlyArgSerLeuTrpValAlaIleCyValMetHisGlnPheIleAspGlnIyProAsp 558
 Db 1782 GCGAGGAGCTCCCGCGCTGAGACAGGTTCCGGGACTGAGAGTCCGCTGTCCGAC 1841
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 Db 1842 TGGTGAATGTGAAGAACTTACTACAGACATGACCAAGATGCCCGCTTCCAGACAA 1901
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 Db 1902 GAGGTG---TTTGAAGAGCCACTGTGCTGCC---GAACCGGATCTGTGAAGCGGCGC 1955
 Qy 591 ValMetCyValysProGlyProGlnSerAspPheCyValLeuIyValGlnAlaProValLeu 610
 Db 1956 CCCCTGTGCGCAG---CCTGCTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2009
 Qy 611 GlyAlaThrGlyProAlaAspSerGlnHisGlnSerGlnHis----- 624
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 Db 2070 CAGCGCGGAGCCCTCCACACCTGTGCTGCGCGCAGAGAGGCGCGCTGTGCGC 2129
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 Qy 641 AlaAlaLeuGlnProLeuHisIleThrValIyAlaGlySerProSerAspMetProArg 660
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 Qy 661 AspSerGlyIleTrpAspSerSerValProSerSerGlyLeuSerLeuProLeuMetGlu 680
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 Qy 681 GlyLeuSerThrAspGlnThrGlnTrpSerSerLeuThrGlnSerValSerSerSerSer 700
 Db 2277 GCGAGAGACACCCCAATGGGCTCTGACCTCTTCCAGAGAGACGTGAGG----- 2327
 Qy 701 GlyLeuGlyGlnIyGlnIyProProAlaLeuProSerIyLeuLeuSerSerGlySerCy 720
 Db 2328 -----GAGCACTCGAAGCTTGAATGCTCTGCTTTCAGAGAGACTGAGCTGC 2378
 Qy 721 LysAlaAspLeuGlyCy 726
 Db 2379 CAGGCCAGGGGGGCTGC 2396

RESULT 7
 US-09-022-255-9
 ; Sequence 9, Application US/09022255
 ; Patent No. 6072033
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Farnlow, William
 ; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:

[illegible]

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DB      2379 CAGGCCCAGGGGCGCTGC 2396  
RESULT 8  
US-09-022-696-9  
Sequence 9, Application US/09022696  
Patent No. 6072037  
GENERAL INFORMATION:  
APPLICANT: Yao, Zhengbin  
APPLICANT: Spriggs, Melanie  
APPLICANT: Fanslow, William  
TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Apple, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,696  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3223 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Human  
STRAIN: IL-17 R (hCTL8 receptor)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 93..2693  
US-09-022-696-9  
  
Alignment Scores:  
Pred. No.: 1.46e-24 Length: 3223  
Score: 321.50 Matches: 153  
Percent Similarity: 35.9% Conservative: 106  
Best Local Similarity: 22.7% Mismatches: 357  
Query Match: 8.1% Indels: 161  
DB: 3 Gaps: 34  
  
US-10-616-788-2 (1-736) x US-09-022-696-9 (1-3223)  
QY 31 GtAgaatattggtlvalasphrtycglYTtpagtglyValdIyProalaserayden 50  
Db 130 GCCCCCTCTGGGCGTGTCTGTCCTGTCCTGCGCGTG-CAGCCCCCGATGGCCCTCC 188
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QY 51 SerGlyLeu-----TyrAniIleThrPhe 58
 DB 189 CTGGAGCTCTGGAGACACGGGGCGCTGCTGCTCCAGCCGGGGGCTAAACCTGACGGTC 248
 QY 59 LysTyrAspArgCys-----ThrThrTyrLeuAsnProValGlyLysHsValIleAla 76
 DB 249 AAGAAATAGTACTGCTGGATGACAGCTGGATTCACTT-----287
 QY 77 AspAlaGlnAsnIleThr-----IleSerGlnTyrAlaCys 88
 DB 288 -----CGAAACCTGACCTCTCTCCCAAGGACCTGACATCAGCTGCACTTTGCC 341
 QY 89 HisAspGln-----ValAlaValThrIleLeuTyrSer-----ProGlyAla 102
 DB 342 CACACCCAAACAAAGAGACCTGTTCCCGTGGCTACATTCGAATGACATCGACAGAC 401
 QY 103 LeuGlyIleGluPheLeuGlyPheArgValIleLeuGluGluLeuLysSerGluGly 122
 DB 402 GCCAGCATCTGTACTCGAGGGTGCAAGTTATCTGCTCGACGCTGAACACCAATGAA 461
 QY 123 ArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPheLysArg 142
 DB 462 CGTTTGCGCTCAAG-----TTTGAGTTTCTGTCCAACTGAGGACATCAACAGCGCG 515
 QY 143 ThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPheValLys 162
 DB 516 TGGCGTTTACCTTCAGCCACTTTGTG-----GTTACCTTCGACAGGAATTTAGGTAC 572
 QY 163 Val-----ValProPheProSerIleLysAsnGlnSerAsnTyrHisProPhePhe 180
 DB 573 GTTCACACACCTGGCCAGCCCATCTCGATGGGGACCAACCAACGATCGCAAGAAATTTC 632
 QY 181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLys-----197
 DB 633 CTGTGCTGTACTGTGAGCAACCGAGATGAAGTAAACAACCCATCATGAGCTCAGGC 692
 QY 198 ProPheTyrLysProAspAsnLeu-----205
 DB 693 AGCCTGTGGACCCC-----AACATACCCCTGGAGACCCCTGAGGCCCCACAGCTCGGTG 749
 QY 206 -----AsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
 DB 750 AGCTTACCCCTGGAAAGCATATCAACCATTCACAGATCCGCTGACCAAGTTTTCGGCAC 809
 QY 221 AlaProHisAsnPheGlyPheAspPhePheTyrLeuHisTyrLysLysLeuLysGluGly 240
 DB 810 ATGGAGAACCAAGTTGCTTGGACACATGCAC-----CACATACCTGCGCCAGACAGAA 866
 QY 241 ProPheLysArgLysThrCysLysGlnGluGlnThrThrGluThrThrSerCysLeuLeu 260
 DB 867 GAGTTTCAACAGGACATCAACAGTCACTACCTACGCAACCTTAAAGGTGTGTGCC 926
 QY 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThr-----Asn 277
 DB 927 CACCAATGAGATTCAGACCTTCTTACAGACGTCGCTCAATGATGCTGCTACAGACTCC 986
 QY 278 ThrThrArgLysValMetHisTyrAlaLeuLysProValHisSerProThrAlaGlyPro 297
 DB 987 GCGCACTTTTCTCCGCCAAGATGCCAGACATCCAGAACCAATTCGCGACTACATCC 1046
 QY 298 IleArgIleMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPhe 317
 DB 1047 CTGTGGGTGTACTGTTCAATCAACGGGCAATCTCACTGCTGTGGCTCCGATCATCTG 1106
 QY 318 ThrValMetCysArgLysLysGlnGlnGluAsnIleTyrSerHisLeuAspGlnGluSer 337
 DB 1107 CTGATCTCTGCAGACTGAGGCTAGCTGGGCTGTGAAGT-----GAAAAATAC 1157
 QY 338 SerGlySerSerThrTyrThrAlaAlaLeuProArgGluLysArgProArgPro--356
 DB 1158 AGTGATGACACCAAAATACACAGATGAGCTGCTGCGGTGACCTGATCCCCCAGCTG 1217

QY 357 -----LysValPheLeuCysTyrSerSerLysAspGlyGlnAsnHisMetAsnVal 373
 DB 1218 AAGCCAGGAAGGTTCTGATCATCTACTACAGCC-----GACCAACCCCTTACATGGAGCTG 1274
 QY 374 ValGlnCysPheAlaTyrPheLeuGlnAspPheCysGlyCysGlyValAlaLeuAspLeu 393
 DB 1275 GTCTGAAATTCCTCCAGTTCTGCTGCTACCCGCTGGGACCGGAAGTGGCCCTGACCTG 1334
 QY 394 TrpGluAspPheSerLeuCysArgGluGlyGlnArgGluThrVal-----Ile 409
 DB 1335 CTGGAAAGACAGGCACTTCGGAGGAGAGATGATCACTGGGTGGCCGCTCAAGAGCAG 1394
 QY 410 GlnLysIleHisGluSerGlnPheIleIleValAlaCysSerLysGlyMetLysTyrPhe 429
 DB 1395 GAGATGTGGAGAGCAACTTAAGATCATCGTCTGTGCTCCCGGCGACAGCC-----1448
 QY 430 ValAspLysLysAsnTyrLysHisLysGlyGlyLys-----441
 DB 1449 -----GCCAAGTGGACAGCGCTCTGGGCGGGGGGCGCTGTGCGCTGCGCTGCGAC 1502
 QY 442 ArgGlySerGlyLysGluPheLeuValAlaValSerAlaIleAlaGluLysLeu 461
 DB 1503 CACGGAAGCCGCTGGGGGACCTGTTCATCTGACAGCCATGATACATCTCCCGGACTTC 1562
 QY 462 ArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe--480
 DB 1563 AAGAGG-----CCAGCTGTGCTGGACCGCTAGCTGCTACTTCAAG 1607
 QY 481 AspTyrSerCysGluGluLysAspValProGlyLysLeuAspLeuSerThrTyrTyrArgLeu 500
 DB 1608 GAGCTGAGCTGTGACCGGCGACGTCGCCGACCTGTGGGCGGCGCGGCTACCGGCTC 1667
 QY 501 MetAspAsnLeuProGlnLeuCysSerHisLysHisSerArgAspHisGlyLysGlnGly 520
 DB 1668 ATGACAGGTTGACAGAGGTG-----TACTTCGCAATCCAGACCTGAGATGTTCCAG 1721
 QY 521 ProGlyGlnHisThrArgGlnGly-----SerArgArgAsnTyrPheArgSerLys 538
 DB 1722 CCGGGCGCATGACCGCGTAAAGGAGAGCTGTGGGGGACAACTACCTGGGAGCCGGGGC 1781
 QY 539 GlyArgSerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGluProAsp 558
 DB 1782 GGCAGGCAAGTCCGCGCCGCTGACAGGTTCCGGAGCTGGAGGCTGCTGCTCCGAC 1841
 QY 559 TrpPheGlu-----LysGlnPheValProPheHisProPro 570
 DB 1842 TGGTGAATGTGAGAACTTACTACAGATGACACAGATGCCCCGCTCTGGACAGAA 1901
 QY 571 ProLeuArgTyrArgGluProValLeuGluLysPheAspSerGlyLeuValLeuAsnAsp 590
 DB 1902 GAGGTG-----TTTGAGAGAGCACTGTGCTCGC-----GAAACCGGATCGTGAAGCGGGCG 1955
 QY 591 ValMetCysLysProGlyProGluSerAspPheCysLeuLysValAlaLeuAspLeu 610
 DB 1956 CCCCTGTGGCGAG-----CCTGTGCTCCAGGCTGCTGCTGCTGCTGCTGCTGCTG 2009
 QY 611 GlyAlaThrGlyProAlaAspSerGlnHisGlnSerGlnHis-----624
 DB 2010 GGGGAGAGAGAGAGACAGAGTGGAGAGCTGGAACCTTCACTGAGCCCGGGGCTCAG 2069
 QY 624 -----624
 DB 2070 CAGAGCCCGAGCCCTCCACACCTGTGTCTGCGCGAGAGAGGGGCGCTGTGGCC 2129
 QY 625 -----GlyLysLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySer 640
 DB 2130 GCGGTGAGGCTGGGCGCTGCTGACAGGCGCGAGCTCGGCTGACATCGCGGGGAG 2189
 QY 641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArg 660
 DB 2190 GCGGAGGCTGCGCTGCTGGGAGCCCGGAGCTGGG-----CGA 2231
 QY 661 AspSerGlyLysTyrAspSerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680

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Db      2232 AATAGCGCTCTTC-----CTCCCCGAGACCCCGAGACTGCCCTT----- 2276
Qy      681 GlysSerThrAspGlnThrGluThrSerSerLeuThrGlnSerValSerSerSer 700
Db      2277 GGCAGCAGCACCCCATGCGCTCTCTGACCTCTTCAGAGAGACTGAG----- 2327
Qy      701 GlyLeuGlyGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySer 720
Db      2328 -----GAGCACTCGAAGGCTTATGCTCTGCTTCAGACAGACTGAGCTGC 2378
Qy      721 LysAlaLeuLeuGlyCys 726
Db      2379 CAGGCCACGGGGGCTGC 2396

RESULT 9
US-08-978-773-3
Sequence 3, Application US/08978773
Patent No. 6083906
GENERAL INFORMATION:
APPLICANT: Trout, Anthony
TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple PowerMacintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978, 773
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/052, 525
FILING DATE: 27 NOVEMBER 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2623-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
CLONE: IL-17R
FEATURE:
NAME/KEY: CDS
LOCATION: 93..2690
US-08-978-773-3

Alignment Scores:
Pred. No.: 1,46e-24 Length: 3223
Score: 321.50 Matches: 183
Percent Similarity: 35.98 Conservative: 106
Best Local Similarity: 22.74 Mismatches: 357

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Query Match:	8.1%	Indel:	161
DB:	3	Gaps:	34
US-10-616-798-2 (1-738) x US-08-978-773-3 (1-3223)			
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DB	130 GGGCCCTGCTGGGGCTGCTCTGCTGCTCTGGGGGCTG-CTGGCCCGGGTGGCCCTTC	188	
QY	51 SerGlyLeu-----TyrAsn1LeThrPhe	58	
DB	189 CTGGAGCTCCGAGCAACCGGGCGCTGGTCTCCAGCGGGGGCTAAATCGACGGCTC	248	
QY	59 LysTyrAspAnCys-----ThrThryTLeuAnProValGlyLysHisVal1Lea1a	76	
DB	249 AAGATATGACTCTGCTGGATGATGACGCTGATTCACCT-----	287	
QY	77 AspAlaGlnAsn1LeThr-----HisSerGlnTyrAlaCys	88	
DB	288 -----CGAAACCTGACCCCTCTCTCCCAAGACCTGCAGATTCAGCTCATTTGCC	341	
QY	89 HisArgIn-----ValAlaVal1Thr1LeuTyrSer---ProGlyAla	102	
DB	342 CACACCCACAGAGAGACTTTCCTCCCTGGCTCATCGAATGACACTGCACAGAC	401	
QY	103 LeuGly1Leu1PheLeuLysGly1PheArgVal1LeuGlnGluLeuLysSerGlnGly	122	
DB	402 GCCAGCATCCGTGACTCTGAGGGTGACAGATTATCTGCTCGCAGCTGAACCAATGAA	461	
QY	123 ArgGlnCysGlnGlnLeu1LeuLysAspProLysGlnLeuAnSerPheLysArg	142	
DB	462 CGTTTGGCCGTCAG-----TTTGAAGTTCTGTCCAAACCTGAGCATCACACAGCGG	515	
QY	143 ThrGlyMetGInSerGlnProPheLeuAnMetLysPheGlnTyrAspTyrPheValLys	162	
DB	516 TGGCGTTTACCTTCAGGCACATTGTG---GTGACCTTGACAGAAATATGAGTACC	572	
QY	163 Val1-----Val1ProPheProSer1LeLysAnGlnSerAnTyrHisProPhePhe	180	
DB	573 GTTACACACCTGCGCCAGCCAGCCATCTCGATGGGACCCAAACACACAGTCCAGAAATTTC	632	
QY	181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAnLeuAlaCysLys-----	197	
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QY	198 ProPheTPrLysProArgAnLeu-----	205	
DB	693 AGCCTGTGGACCCC---AACATCACCGTGGAGACCTTGAGGGCCACACAGTGGCTG	749	
QY	206 -----Asn1LeSerGlnHisGlySerAspMetGlnValSerPheAspHis	220	
DB	750 AGCTTCACCGCTGGGAAAGATACCACTTACCAAGATCTCGTGCAGACAGATTTCCGAC	809	
QY	221 AlaProHisAnPheGlyPheAspArgPhePheTyrLeuHisTyrTyrLysLeuLysHisGlnGly	240	
DB	810 ATGAGAAACACACAGTCTTGGACACATGAC---CACATACCTGGCGCCAGACCAAGA	866	
QY	241 ProPheLysArgLysThrCysLysGlnGlnGlnThrThrGlnTyrThrSerCysLeuLeu	260	
DB	867 GAGTTTCACACGAGCATTCACGTCACTCACTCAAGCACTTAAAGGTGCTGTCCG	926	
QY	261 GlnAsnValSerProGlyAspTyr1Le1GlnLeuValAspArgThr-----Asn	277	
DB	927 CACCAAGTGCAGATTCACGCTCTTTCAGACAGCTGCTCAATGACTGCTCGACAGACTCC	986	
QY	278 ThrThrArgLysValMetHisTyrTyrAlaLeuLysProValHisSerProTPrAlaGlyPro	297	
DB	987 GCGACTGTCTTCTCCCAAGAAATCCAGACATCCAGAAACCAATTCGGGACTACATGCC	1046	
QY	298 IleArgAlaMetAla1LeThrValProLeuValVal1LeSerAlaPheAlaThrLeuPhe	317	
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/ HYPOTHETICAL: NO
 / ANTI-SENSE: NO
 / ORIGINAL SOURCE:
 / ORGANISM: Human
 / STRAIN: IL-17 R (hCTLA8 receptor)
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 93..2693
 / US-09-022-253-9

 Alignment Scores:
 Pred. No.: 1,46e-24 Length: 3223
 Score: 321.50 Matches: 183
 Percent Similarity: 35.9% Conservative: 106
 Best Local Similarity: 22.7% Mismatches: 357
 Query Match: 8.1% Indels: 161
 Gaps: 34
 DB: 3
 US-10-616-788-2 (1-738) x US-09-022-253-9 (1-3223)

QY 31 GlyAlaAlaTrrGlyValAlaAspThrCysGlyTrrArgGlyValGlyProAlaSerArgAsn 50
 DB 130 GGCCCTGCTGGGGCTGCTCTGCTGCTCTGGGCGTG-CTGGCCCGGGTGGGCGCTCC 188
 QY 51 SerGlyLeu-----TyrAsnIleThrPhe 58
 DB 189 CTGCGACTCTCGACCAACCGGGCGGTGCTGCTCCAGCCGGGGCTAACTGCACGGTC 248
 QY 59 LysTyrAspAsnCys-----ThrThrTyrLeuAsnProValGlyLysHleValIleAla 76
 DB 249 AAGAAATGTAACCTGCGCTGGATGACGTGATTCACCT----- 287
 QY 77 AspAlaGlnAsnIleThr-----IleSerGlnTyrAlaCys 88
 DB 288 -----CGAAACCTGACCCCTCTCTCCCAAGAGACTGACATCCAGCTGCACTTGGCC 341
 QY 89 HisAspGln-----ValAlaValIleThrIleLeuTrrSer-----ProGlyAla 102
 DB 342 CACACCCACAGAGAGACCTGTTCCCGGTGCTCACATCGAATGAGACATGCAAGACAGAC 401
 QY 103 LeuGlyIleGluPheLeuLysGlyPheArgValIleLeuGlnGluLeuLysSerGlnGly 122
 DB 402 GCCAGCATCTCTGTAACCTCGAGGGTGCAGAGTTATCTCTCGACAGCTGAACACCAAGAA 461
 QY 123 ArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPheLysArg 142
 DB 462 CGTTTGCGCTGACG-----TTTGAGTTCTGTCCAACTGAGGGCATCACACAGCGCG 515
 QY 143 ThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspIleTrrPheValLys 162
 DB 516 TGGCGGTTTACCTTCAGCCACTTGTG---GTTGACCTTCAGCAAGAAATGAGGTGACC 572
 QY 163 Val-----ValProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhe 180
 DB 573 GTTCACCACTGCGCAAGCCATCCCTGATGGGAGCCAAACCACTCAAGTCAAGATTTC 632
 QY 181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLys----- 197
 DB 633 CTGTGCTGCTGATGAGCAGCGCAGAGTAGAGTAAACAGGCATGATGAGTCAAGC 692
 QY 198 ProPheTrrLysProArgAsnLeu----- 205
 DB 693 AGCCTGGGACCC---AACATCAACCGTGAGACCTTGAGGCCCAACAGCTGCGTGTG 749
 QY 206 -----AsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
 DB 750 AGCTTACACCTGCGAAGCAATCTACCATTAACAGATCTCTGACAGCAATTTCCGCAC 809
 QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTrrLysLeuLysHleGlnGly 240
 DB 810 ATGAGAGAACCAAGTTGCTTGGACATGACAC---CACATACCTGCGCCAGACAGAA 866
 QY 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrThrGlnThrThrSerCysLeuLeu 260

DB 867 GAATTCACCAAGGATTCACAGCTCACTCAACGAACCTTAAAGGTCTGTGCGC 926
 QY 261 GlnAsnValSerProGlyAspTrrIleGluLeuValAspAspThr-----Asn 277
 DB 927 CACCAAGTGCAATCCAGCCCTTCTTACAGAGCTGCTCAATGACATGCTCCAGACACTCC 986
 QY 278 ThrThrArgLysValMetHisTrrLysAlaLeuLysProValHisSerProTrrAlaGlyPro 297
 DB 987 GCGACTGTTCTCGCCAGAAATGCCAGACACTCCAGAAACCAATTCGACATCAATGCC 1046
 QY 298 IleArgAlaMetAlaIleThrValProLeuValIleIleSerAlaPheAlaThrLeuPhe 317
 DB 1047 CTGTGGGTGATCGTTCATCAACGGCATCTTCATCTGCTGTGGGTCCGCTCATCTCG 1106
 QY 318 ThrValMetCysArgLysLysGlnGlnGlnAsnIleTrrSerHisLeuAspGlnGluSer 337
 DB 1107 CTGATGCTGATGACCTGAGGCTGAGCTGAGGCTGAGAGT-----GAAAAATAC 1157
 QY 338 SerGluSerSerThrTrrThrAlaAlaLeuProArgGluLysLeuArgProArgPro-- 356
 DB 1158 AGTGATGACACCAAAATACACAGATGCGCTGCGCTGACCTGATCCCAACCGCTG 1217
 QY 357 -----LysValPheLeuCysTrrSerSerLysAspGlyGlnAsnHisMetAsnVal 373
 DB 1218 AAGCCAGAGAGGTCTGATCATCTACTACGCC---GACCAACCCCTTACGTGACGTG 1274
 QY 374 ValGlnCysPheAlaTrrPheLeuGlnAspPheCysGlyCysGlyValAlaLeuAspLeu 393
 DB 1275 GTCTGAAATTTGCCAGTTTCTGTCACGCGCTGGGACGGAATGGGCGCTGACCTG 1334
 QY 394 TrrGluAspPheSerLeuCysArgGlnGlyGlnAsnGlnTrrVal-----Ile 409
 DB 1335 CTGGAAGACAGCGCCATCTCGAGAGGACATGATACCTGGGTGGCGCTGAGAGCAG 1394
 QY 410 GlnLysIleHisGluSerGlnPheIleIleValIleCysSerLysGlyMetLysTrrPhe 429
 DB 1395 GAGATGTGAGAGCACTCTTAAGATCATGTCTTGTCTTCCGCGACAGCGCC----- 1448
 QY 430 ValAspLysLysAsnTrrLysHisLysGlyGlyGly----- 441
 DB 1449 -----GCCAAGTGGAGGCGCTCGTGGCGGGGCGCTGTGGCGGTGCGTGCAGAC 1502
 QY 442 ArgGlySerGlyLysGlyLeuPheLeuValAlaValSerAlaIleAlaGlyLysLeu 461
 DB 1503 CACGGAAGCCCGCTGGGGACCTGTTCATCTGACAGCCATGAACATGATCCCTCCGCACTTC 1562
 QY 462 ArgGlnAlaLysGlnSerSerAlaAlaLeuSerLysPheIleAlaValTrrPhe--- 480
 DB 1563 AAGAGG-----CCAGCTGTCTTGGGACCTTACGTACTGTCTTACAGC 1607
 QY 481 AspTrrSerCysGlnGlyAspValProGlyIleLeuAspLeuSerThrLysTrrArgLeu 500
 DB 1608 GAGGTACGCTGACCGGACAGTCCCGGACCTTTGGCGCGCGCGCGCGCTCCCGCTC 1667
 QY 501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGly 520
 DB 1668 ATGACAGAGTTCCAGAGAGGTG-----TACTTCCGATCAGAGACCTGAGATGTTCCAG 1721
 QY 521 ProGlyGlnHisThrArgGlnGly-----SerArgAsnTrrPheArgSerLysSer 538
 DB 1722 CCGAGCGGATGACACCGCTGAGGGAGCTGTGGGAGAACATCTGTGGAGGCCCGGGCC 1781
 QY 539 GlyArgSerLeuTrrValAlaIleCysAsnMetHisGlnPheIleAspGlnGluProAsp 558
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 QY 559 TrrPheGln-----LysGlnPheValProPheHisProPro 570
 DB 1842 TGGTTCGAATGTGAGAACTTACTACAGAGATGACACAGATGCCCCGCTCCGTGACGAA 1901
 QY 571 ProLeuArgTrrArgGluProValLeuGlnLysPheAspSerGlyLeuValLeuAsnAsp 590

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Db      1902 GAGGCG---TTTAGAGGACCACTGCTGCTCG---GGAACCGGATCTGTAAGCGGGCG 1955
Qy      591 ValMetCyLysProGluProGluSerAspPheCyLeuLysValGlnAlaProValLeu 610
      :::
      1956 CCCCTGGTGGCCGAG---CTTGACTCCAGGACCTGCTGGCCATAGAC---CCGCTGGTC 2009
Qy      611 GlyAlaThrProAlaAspSerGlnHisGluSerGlnHis----- 624
      |||
      2010 GGGGAGGAAGAGGACAGCAGTGGCAAGCTGGAACCTCACCTGACAGCCCCGGGGTCAG 2069
Qy      624 ----- 624
Db      2070 CCAAGCGCGGAGCCCTTCACACCTGTGTCTGCGCGGAGGAGGGGGCCCTGTGTGCC 2129
Qy      625 -----GlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
      |||
      2130 GCGGTGAGAGCTGTGGGCCCCCTGAGCGGTGACGATGCCGACGTCCGACCTGGCGGGGAG 2189
Qy      641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerAspMetProArg 660
      |||
      2190 GGGGAGGCTGTCCCGCTGTGGGACGCCGGGGCGCTGGG-----CGA 2231
Qy      661 AspSerGlyIleTyAspSerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680
      |||
      2232 AATAGCGTCTCTTC-----CTCCCCGTGGACCCCGAGAGACTGCCCCCTT----- 2276
Db      681 GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGlnSerValSerSerSer 700
      |||
      2277 GGCAGACACACCCCATGCGCTCTCTGACTGCTTCCAGAGGAGCTGAG----- 2327
Qy      701 GlyLeuGlyGlnGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySer 720
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      2328 -----GAGCACCTCGAAGGCTTATGCTCTGCTCTTCCAGACAGATCTGAGCTGC 2378
Qy      721 LysAlaAspLeuGlyCys 726
      |||
      2379 CAGGCCACGAGGGGCGCTGC 2396
Db

RESULT 11
US-09-022-260-9
; Sequence 9, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022.260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

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: NAME: Perkins, Patricia Anne
: REGISTRATION NUMBER: 34,695
: REFERENCE/DOCKET NUMBER: 2617-B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206)587-0430
: TELEFAX: (206)
: INFORMATION FOR SEO ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3223 base pairs
: type: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Human
: STRAIN: IL-17 R (hCTL48 receptor)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 93..2693
: US-09-022-260-9

Alignment Scores:
Pred. No.: 1,466-24 Length: 3223
Score: 321.50 Matches: 183
Percent Similarity: 35.9% Conserved: 106
Best Local Similarity: 22.7% Mismatches: 357
Query Match: 8.1% Indels: 161
DB: 3 Gaps: 34

US-10-616-788-2 (1-738) x US-09-022-260-9 (1-3223)
QY 31 G1YARGALATRPolyValAspPhxCysGlyTTPArgGlyValGlyProAlaSerArgAsn 50
Db 130 GGGCCCGCGGGGGGCGTCTGCTGCTGCTGCTGCGGGGCGTGG-CTGGCCCGGGGGGGCGCTCC 188
QY 51 SerGlyLeu-----TyrAsn11eThrPhe 58
Db 189 CTGCGACTCTGTGGACCAACCGGCGCTGCTGCTCCAGCCGGGGCTTAACTGCACGCTC 248
QY 59 LyeTyrAspAsnCys-----ThrThrTyrLeuAsnProValGlyVal11eAla 76
Db 249 AAGAAATGATGACTCGCTCGGTGATGACAGCTGANTTACCTC----- 287
QY 77 AspAlaGlnAsn11eThr-----11eSerGlnTyrAlaCys 88
Db 288 -----GAAACTGTACCCCTCCCTCCCAAGACCTGCAGATTCACGCTGACTTTGCC 341
QY 89 HisAspGln-----Val11eVal11Thr11eLeuTTPSer---ProGlyAla 102
Db 342 CACACCCCAACAAGAGACCTGTTCCCGTGGCTCAATCGAATGACACATGACAGAC 401
QY 103 LeuGly11eGluPheLeuYsglyPheArgVal11eLeuGluGluLeuYsSerGluGly 122
Db 402 GCCAGACTCTGTGACTCGAGGGGTACAGATTATCTGCTGCAGCTGAACACCAATGAA 461
QY 123 ArgGlnCysGlnGlnLeu11eLeuYsAspProYsglnLeuAsnSerSerPheYsArg 142
Db 462 CGTTTGTGCTCAG-----TTTGAAGTTCTGTCCAAACAGAGGATCAACCAACAGCGG 515
QY 143 ThrGlyMetGlnSerGlnProPheLeuAsnMetCysPheGluThrAspTyrPheVal11e 162
Db 516 TGGCGTTTAACTTCAGCACCTTGTG---GTGACCTCTGACACGAGAAATGAGGTGACC 572
QY 163 Val1-----ValProPheProSer11eYsAsnGlnSerAsnTyr11eProPhePhe 180
Db 573 GTTCAACCATCTGGCCCAAGCCATCTCCCTGATGGGAGCCCAACCAACACAGTCCAAAGATTTC 632
QY 181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAla11eCys11e 197
Db 633 CTGTGCTGTGACTGTGTAGCACCGCCAGATGAAGGTAAACCAACGCAATGATGAGCTCAGGC 652

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3223 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
STRAIN: IL-17 R (hCTLA8 receptor)
FEATURE:
NAME/KEY: CDS
LOCATION: 93..2693
US-09-022-259-9

Alignment Scores:
Pred. No.: 1,46e-24 Length: 3223
Score: 321.50 Matches: 183
Percent Similarity: 35.9% Conservative: 106
Best Local Similarity: 22.7% Mismatches: 357
Query Match: 8.1% Indels: 161
DB: 3 Gaps: 34

US-10-616-788-2 (1-738) x US-09-022-259-9 (1-3223)
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D 130 GGGCCCTGGCTGGGCTGCTCTGCTGCTCTGCTGGCGTG-CTGGCCCGGGTGGCGCTCC 188
QY 51 SerGlyLeu-----TyrAsnIleThrPhe 58
D 189 CTGGCACTCTCGACCAACCGGCGCTGGTCTGCCAGCCGGGCTAAACTGCACGGTC 248
QY 59 LysTyrAspAsnCyse-----ThrThrTyrIleuAsnProValG1yLysIleValIleAla 76
D 249 AAGAAATGACTACTGCTCGATGACAGCTGATTAACCT-----287
QY 77 AspAlaGlnAsnIleThr-----IleSerGlnTyrAlaCys 88
D 288 -----GGAACCTGACCCCTCTCCCAAGACCTGCAGATGCAGCTGCATTGGCC 341
QY 89 HisAspGln-----ValAlaValThrIleLeuTrrpSer---ProG1ValA 102
D 342 CACACCCCAAGAGAGACTGTCCCGTGGCTCACTGAAATGACACTGCAGACAGAC 401
QY 103 LeuG1yIleGluPheLeuG1yPheArgValIleLeuGluGluLeuLysSerG1uG1y 122
D 402 GCCAGCATCTCTGACTCGAGGGTGCAAGTTACTGTCTGCAAGCTGAACACCAAGAA 461
QY 123 ArgGlnCyseGlnGluLeuIleLeuLysAspProLysGlnLeuAsnSerSerPheLysArg 142
D 462 CGTTTGCGCGTCAAG-----TTTGAGTTTCTGTCCAAACTGAGGATCAACCAAGGCGG 515

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QY 143 ThrG1yMetG1uSerGlnProPheLeuAsnMetLysPheG1uThrAspTyrPheValLys 162
D 516 TGGCGTTTAACCTTCAGCCACTTGTG---GTAGACCCCTGACCAAGAAATGAGTGAC 572
QY 163 Val-----ValProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhe 180
D 573 GTTCACCACTGCTCCCAAGCCATCCCTGATGGGAGCCCAACCAAGTCCAAAGAAATTTC 632
QY 181 ArgThrArgAlaCyseAspLeuLeuGlnProAspAsnLeuAlaLysLys-----197
D 633 CTGTGCTGACTGTAGACCGCCAGATGAAGTAACCAACCCAGTGCATGACTGAGGC 692
QY 198 ProPheTrrpAspProArgAsnLeu-----205
D 693 AGCCTGTGGAGCC---AACATCACCCGTGAGAACCCCTGAGGCCAAGCTGCGCTG 749
QY 206 -----AsnIleSerGlnHisG1ySerAspMetGlnValSerPheAsnHis 220
D 750 AGCTTCAACCCCTGGAAACGAACTTACCAATTAACCAATCTGCTGACAGTTTCCGCAC 809
QY 221 AlaProHisAsnPheG1yPheArgPhePheTyrLeuHisTyrLysLeuLysGluG1y 240
D 810 ATGAGAACCAACAGTTCCTTGAAGCAATGCAC--CAATACCTGCGCCCAAGACAA 866
QY 241 ProPheLysArgLysThrCyseLysGlnGluInThrThrG1uThrThrSerCyseLeu 260
D 867 GAGTTCCACCAAGCATTCACACGTCACATCTGACCACTTAAAGGCTCTGCGC 926
QY 261 GlnAsnValSerProG1yAspTyrIleIleGluLeuValAspAspThr-----Asn 277
D 927 CACCAAGTGACATTCAGCCCTTCTTCAGAGCTGCTCAATGACCTGACACTCC 986
QY 278 ThrThrArgLysValMetHisTyrAlaLeuLysProValHisSerProTrrpAlaG1yPro 297
D 987 GCGACTGTTCTCTGCCAAGAAATGCCAGACACTGCCAAGAACAAATTCGGAATGATGCC 1046
QY 298 IleArgAlaMetAlaIleThrValProLeuValIleSerAlaPheAlaThrLeuPhe 317
D 1047 CTGTGGGTGACTGCTGATTCACAGGGCATCTCATCTGCTGCGGCTCCGCTCATCTG 1106
QY 318 ThrValMetCyseArgLysLysGlnGluAsnIleTyrSerHisLeuAspGluLysSer 337
D 1107 CTCATGCTGTCAGTACCTGAGCTGAGCTGAGCTGGAAGT-----GAAATAATAC 1157
QY 338 SerGluSerSerThrTyrThrAlaAlaLeuProArgGluArgLeuArgProArgPro---356
D 1158 AGTGATGACACCAAAATACACGATGCGCTGCGGCTGACCTGATCCGCCACGCTG 1217
QY 357 -----LysValPheLeuCyseTyrSerSerLysAspG1yGlnAsnHisMetAsnVal 373
D 1218 AACCCAGAAAGGCTCGATCATCTACTAGCC---GACCAACCCCTGATCGTGACGTG 1274
QY 374 ValGlnCysePheAlaTyrPheLeuGlnAspPheCyseG1yCyseG1uValAlaLeuAspLeu 393
D 1275 GTCTGAATTTGCCAGTCTGCTGACCGGCTGCGGAGCGGACAGAGTGGCCCTGACCTG 1334
QY 394 TrrpGluAspPheSerLeuCyseArgGluG1yGlnArgIleTrrpVal-----Ile 409
D 1335 CTGAAAGACGAGCCATCTCGAGGAGGAGCATGATGACCTGGGTGGGCGCTCAAGACAG 1394
QY 410 GlnLysIleHisGluSerGlnPheIleIleValAlaCyseSerLysG1yMetLysTyrPhe 429
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D 1449 -----GCCAAGTGGAGGCGGCTCGGGCGGGGAGCGCTGCGGCGCTGCGCTGAC 1502
QY 442 ArgG1ySerG1yLysG1yLeuPheLeuValAlaValSerAlaIleAlaGluLysLeu 461
D 1503 CACGAAAGCCCGTGGGGGACCTGTTCATGCACTGACCATGAACATGATCTCCCGGACTTC 1562

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 Qy 103 LeuglylleglupheleuylsglyPheArgVallleuglucgluleuylsersglu 122
 Db 402 GCCAGCATCTCTGATCTCGAGGCTGACAGATTAATCTCTCTGACGCTGAACCAATGAA 461
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 Db 462 CGTTTGCGCTGACG-----TTTGAGTTTCTGTCCAACTGAGCGATGCACCAAGCGCG 515
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 Qy 163 Val-----ValProPheProserlleuylsAnsluSerAntyrhlisProPhePhe 180
 Db 573 GTTCACACCTGCGCCCAAGCCCATTCCTGATGGGAGCCCAACCAACAGTCCAAATTC 632
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 Db 693 AGCCTGTGGAGCCCC---AACATCACCTGAGAGACCTGAGAGCCCAACAGCTGCGTGTG 749
 Qy 206 -----AanlleserGlnhleglyserArpmetGlnAlaSerPheArphts 220
 Db 750 AGCTTCAACCTGTGGAACGAAATCAACCATTAACAGATCTGCTGACCAAGTTTCCGCAC 809
 Qy 221 AlaProhlsanPheglupheArgPheArpPheylsleuylsArgly 240
 Db 810 ATGAGAGAACCAAGTTGCTTGAACACATGCAC---CACATACCTGCGCCCAAGCAGAA 866
 Qy 241 ProPheylsArglyserThrCylysGlnleuGlnThrThrGlnThrThrSerCylysleu 260
 Db 867 GAGTTCACACGAGCATCCAAAGCTCACACTCACTTAAAGGCTGTCTGCGC 926
 Qy 261 GlnaAnylserProGlyArpTrllegluleuValAspArpThr-----Asn 277
 Db 927 CACCAAGTCAAGATCCAGCCCTTTCAGCAGCTGCTCAATGACTGCTCAAGACATCC 986
 Qy 278 ThrThrArglyValMethtylzAlaLeuylsProValhlsersProTrpAlaGlyPro 297
 Db 987 GCGACTGTTCCTGCGCAAAATGCAAGACACTCCAAACCAATTCGCGACTACATGCC 1046
 Qy 298 IleArgAlaMetAlaIethrValProleuValVallleserAlaPheAlaThrleuPhe 317
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 Qy 318 ThrValmetCyseArglylysGlnGlnGlnAlaAnllyserhlsleuArpGlnGlnSer 337
 Db 1107 CTGATCTCTGCACTGAGCTGAGGCTAGCTGGGCTGGAGT-----GAAATATAC 1157
 Qy 338 SerGlnuSerThrTrpThrAlaAlaLeuProArgGlnArglyleuArgProArgPro 356
 Db 1158 AGTATATACACCAAAATACAGAGATGCGCTGCTGCGGTGACATGATCCCGCCAGCTG 1217
 Qy 357 -----lybValPheleuCyseTyrSerSerlyAspGlyGlnaAnhlsmetAnyl 373
 Db 1218 AAGCCAGAGAAAGTCTGATCTACTACTAGCC---GACCAACCCCTCTCTGTGAGAGTG 1274
 Qy 374 ValGlnCysePheAlaTrpPheleuGlnArpPheCyseGlyCyseGlnValAlaLeuArpLeu 393
 Db 1275 GTCTCTGAAATTCGCGCAATTCCTCTCAACCGCTGCGGACAGAAAGGAGCCCTGAGACTG 1334
 Qy 394 TrpGlnuArpPheSerleuCyseArgGlnGlyGlnArgGlnTrpVal-----Ile 409
 Db 1335 CTGGAAAGAGAGGCGCATCTGTGGAAGCAGAGATCATGACCTGTGGGTGGCGCGTCAGAAAGCAG 1394

Qy 410 GlnlyeIlehlleglupheleuylleleValIleCyseSerlysglyMetlyeTrpPhe 429
 Db 1395 GAGATGTGAGAGAGCACTTAAGATCATCTGTCTGTCTCCGCGCAGCGCC----- 1448
 Qy 430 ValAspLylybAnylTrpLyblysglyGly----- 441
 Db 1449 -----GCCAAGTGGCAGCGCTCTGGGCGGGGCGCCCTGTGCGCTGCGCTGAGC 1502
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 Db 1503 CAGGAAAGCCCTGTGGGAGCTGTTCACATGACAGCATAAACATGATCTCCCGGACTTC 1562
 Qy 462 ArgGlnAlaIleGlnSerSerSerAlaAlaLeuSerlybPheleAlaValTrpPhe--- 480
 Db 1563 AAGAGC-----CAGCTGTCTTGGAGCACTTACTATCTGTCTTCAAGC 1607
 Qy 481 ArpTrpSerCyseGlnGlyArpValProGlyIleleuArpLeuSerThrlyeTrpArgleu 500
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 Db 1668 ATGAGACAGGTTCCAGAGAGTG-----TACTTCCGATCCAGGACCTTGAGATGTTCCAG 1721
 Qy 521 ProGlyGlnhlsThrArgGlnGly-----SerArgArpAntyrPheArpSerlyser 538
 Db 1722 CCGGCGCGCATGACCGCGTGAAGAGCTGTGCGGAGACATCACTCCGCGAGCCCGGCG 1781
 Qy 539 GlyArgSerleuTrpValAlaIleCyseAnMethtleuPheleArpGlnGlnProArp 558
 Db 1782 GCGAGCAGCTCGCGCGCGCTGAGAGATTCGCGGACTGCGAGTCCGCTGCCGAC 1841
 Qy 559 TrpPheGln-----lybGlnPheValProPhehlsProPro 570
 Db 1842 TGTGTGAAATGTGAGAACTTAATCAGAGATGACAGAGATGCCCGCTCTGAGAGAA 1901
 Qy 571 ProleuArgTrpArgGlnProValleuGlnlybPheArpSerGlyleuValleuAnArp 590
 Db 1902 GAGGTG---TTTAGAGAGCACTGTCTCTCCG---GAAACCGCATCTGTGAAGCGGGCG 1955
 Qy 591 ValMetCyseylsArpProGlyProGlyuSerArpPheCyseylsleuValGlnAlaProValleu 610
 Db 1956 CCGCTGTGTGGCAG---CCTGCTCCAGCGCTGTGCTGAGCAATAGAC---CGCTGTGTC 2009
 Qy 611 GlyAlaThrGlyProAlaArpSerGlnhlsleuSerGlnhls----- 624
 Db 2010 GCGAGAGAAAGAGAGACAGCATGCGAAGCTGAACTTCACTGAGCCCGCGGCTCAG 2069
 Qy 624 ----- 624
 Db 2070 CAGAGCCCGAGCGCTCCACACCTGTGTGCTGCGCGCAGAGAGGGGCGCTGTGCGC 2129
 Qy 625 -----GlyGlyleuArpGlnArpGlyGlnAlaArgProAlaLeuArpGlySer 640
 Db 2130 GCGGTGAGCGTGGCGCTGTGACGCGTGCAGAGTCCGAGTCCGAGTCACTGCGGAGGAG 2189
 Qy 641 AlaAlaLeuGlnProleuileuHlsThrValylsArglySerProserArpMetProArg 660
 Db 2190 GCGGAGCGCTGCGCGTGTGGGAGCCGCGGCGCTGG-----CGA 2231
 Qy 661 ArpSerGlyIleThrArpSerSerValProserSerGlyleuSerleuProleuMetGln 680
 Db 2232 AATAGGCTCTTCTC-----CTCCCTGTGAGCCCGAGAGATCGGCTTT----- 2276
 Qy 681 GlyleuSerThrArpGlnThrGlnThrSerSerleuThrGlnSerValleuSerSerSer 700
 Db 2277 GCGAGAGAGACCCCGATGGGTCTCTGACCTCTTCCAGAGAGACGAGAG----- 2327
 Qy 701 GlyleuGlyGlnGlnGlnProProAlaLeuProSerlyblyleuLeuSerSerGlySerCyb 720
 Db 2328 -----GAGCACTCGAAGGCTTGAATGCTGTCTGCTTTCAGAGAGATCTGAGACTGC 2378

Qy 721 LysAlaAspLeuGlyCys 726
 Db 2379 CAGCCCAAGGGGGCTGC 2396

RESULT 14
 US-09-549-679-9
 ; Sequence 9, Application US/09549679
 ; Patent No. 6680057
 GENERAL INFORMATION:
 APPLICANT: Yao, Zhengbin
 Spriggs, Melanie
 Panelow, William
 TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Power Macintosh
 OPERATING SYSTEM: Apple Operating System 7.5.5
 SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/549,679
 FILING DATE: 14-Apr-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE: <Unknown>
 APPLICATION NUMBER: USSN 08/410,535
 FILING DATE: 23 MARCH 1995

ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3223 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Human
 STRAIN: IL-17 R (hCTLA8 receptor)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 93..2693
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-09-549-679-9

Alignment Scores:
 Pred. No.: 1,46e-24 Length: 3223
 Score: 321.50 Matches: 183
 Percent Similarity: 35.9% Conserved: 106
 Best Local Similarity: 22.7% Mismatches: 357
 Query Match: 8.1% Indels: 161
 DB: 3 Gaps: 34

US-10-616-788-2 (1-738) x US-09-549-679-9 (1-3223)
 Qy 31 G1AArgAlaTrpGlyValAspThrCysGlyTrpArgGlyValGlyProAlaSerArgAsn 50
 Db 130 GGGCCCTGCTGGGGCTGCTCTGCTGCTCTGCTGGGCGTG-CTGGCCCGGGGTGGGCTCTCC 188

Qy 51 SerGlyLeu-----TyrAsnIleThrPhe 58
 Db 189 CTGGAGATCTGTGACCAACCGGGCGTGTCTCTCCACCGGGGGCTAAACTGTGACGCTC 248

Qy 59 LysTyrAspAsnCys-----ThrThrTyrLeuAsnProValGlyHisValIleAla 76
 Db 249 AAGATAGTACTCTGCTGATGATGACGTGATTCACCT----- 287

Qy 77 AspAlaGlnAsnIleThr-----IleSerGlnTyrAlaCys 88
 Db 288 -----CGAAACCTGACCCCTCTCTCCCAAGACCTGACATCCAGCTGTGCTTGGC 341

Qy 89 HisAspGln-----ValAlaValThrIleLeuThrSer-----ProGlyAla 102
 Db 342 CACACCCACAGAGAGACTGTTCCTCCGCTGCTACATTCAGATGACATGACATGACAGAC 401

Qy 103 LeuGly11LeuIleuLeuLysGlyPheArgValIleLeuGlnIleuLysSerGluGly 122
 Db 402 GCCAGATCTGTACTGAGGCTGAGAGTATGCTGCTGACGATGAAACCAATGAA 461

Qy 123 ArgGlnCysGlnGlnIleuLysAspProLysGlnLeuAsnSerPheLysArg 142
 Db 462 CGTTTGCGCTCAG-----TTTGAGTTTCTGTCCAAATGAGGATCACCACAGCGCG 515

Qy 143 ThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPheValLys 162
 Db 516 TGGCGTTTACCTTACGCCACTTGTG-----GTGACCTGACCAAGAAATGAGTGAC 572

Qy 163 Val-----ValProPheProSerIleLysAsnGluSerAsnTyrHisProPhePhe 180
 Db 573 GTTCACCACTGCTGCCAAGCCATCTCGATGGGAGCCAAACACAGCTCAAGAAATTTC 632

Qy 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLys----- 197
 Db 633 CTGTGCTGACTGTAGACAGCCAGAGTAAGTAACAGCCATGATGATGACTCAGGC 692

Qy 198 ProPheTrpLysProArgAsnLeu----- 205
 Db 693 AGCCTGTGGACCC-----AACATCACCGTGAGACCTGAGGCCACCGCTGCTGTG 749

Qy 206 -----AsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
 Db 750 AGCTTACCTGTGAGAACATCTACCATTCACATCTGCTGACAGATTTCCGAC 809

Qy 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLysValGluGly 240
 Db 810 ATGAGAACACAGTGTGCTTGTGACATGAC-----CACATACCTGGGCCAGACAGAA 866

Qy 241 ProPheLysArgLysThrCysLysGlnGlnIleThrThrGluThrThrSerCysLeuLeu 260
 Db 867 GAGTTCACCAAGGATCAACGTCACATCTACGCAACCTTAAAGGCTGTGCG 926

Qy 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThr-----Asn 277
 Db 927 CACCAAGTCAATTCAGAGCTTCTTCCAGAGCTGCTCAATATCTGCTCAAGACTCC 966

Qy 278 ThrThrArgLysValMetHisTyrAlaLeuLysProValHisSerProThrAlaGlyPro 297
 Db 987 GCGACTGTTTCCGCCCAAGAAATGCCAGACATCTCCAGAACATTCGCGATCATGCCC 1046

Qy 298 IleArgAlaMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPhe 317
 Db 1047 CTGTGGGTGTAAGTGTTCATCAGGCGCATCTCATCTGCTGTGGGCTCTCCATCTCG 1106

Qy 318 ThrValMetCysArgLysLysGlnGlnIleAsnIleTyrSerHisLeuAspGluGluSer 337
 Db 1107 CTCATGCTGCTGACCTGAGAGCTGAGGCTGAGCTGAGCTGAGAGT-----GAAATATAC 1157

Qy 338 SerGluSerSerThrTyrThrAlaAlaLeuProArgGluLysArgProArgPro--- 356
 Db 1158 AGTGAATGACCAAAATKACCAATGAGTGCCTGCGGGCTGACCTGATCCCAACGCGCTG 1217

OY	357	-----lyvValPheLeuCySerSerlyuAspGlygluInanhiMeAsnVal	373
Db	1218	AAGCCAGGAAGGTCGTGATCTATCTACAGCC---GACCAACCCCTCTACGTGACGTG	1274
OY	374	ValGlnCyPheAlaTyPheLeuGlnAAspPheCyGlyCyGluValAlaLeuAspLeu	393
Db	1275	GTCCTGAATTCGCCCACTTCTCTGTACACCGCTCCGGACAGAAAGTGGCCCTGGACCTG	1334
OY	394	TrpGluAAspPheSerLeuCyAspGlygluYgluArgGluTrpVal-----Ile	409
Db	1335	CTGGAAAGCAGCGCCATCTCGAGGACAGAGATGACCTGGGTGGCCGTACAGAACAG	1394
OY	410	GlnuylIlehiAsgluSerGlnPheIleIleValValCySerSerlyGlyMetlyeTyPhe	429
Db	1395	GAGATGTGGAGAGACACTTAAGATGATCGTCTGTCTCCCGGACACCGC-----	1448
OY	430	ValAspLylyAsnTyIlehiVlyAsglGlyGly-----	441
Db	1449	-----GCCAATGGCAGCGCCTCTGGGCGGGGGGGCGCCTGTGGCGCTCCGTCCAC	1502
OY	442	ArgGlySerGlyLylyGlygluLeuPheLeuValAlaValSerAlaIleAlaGluLyLeu	461
Db	1503	CACGGAAGCCCGGTGGGGACCTGTTCACGTGACGACATGAATGATCTCCCGGACCTTC	1562
OY	462	ArgGlnAlaIlyGlnSerSerSerAlaAlaLeuSerLylyPheIleAlaValTyPhe---	480
Db	1563	AAGAG-----CCACCTCGCTTCGGCACCTGATGTCGTCTACTTCACG	1607
OY	481	AspTySerCyGluGluGlyAspValProGlyIleLeuAspLeuSerThyTyArgLeu	500
Db	1608	GAGCTCACTGTGTGACGGACGCTCCCGACCTGTTCGGCGGGCGCCGGGTACCGCTTC	1667
OY	501	MetAspAsnLeuProGlnLeuCySerSerhiVleuhiAserTyAspPheIleGluGlnGlu	520
Db	1668	ATGACAGATTCGAGAGAGGTG-----TACTTCGCGATCCAGACCTGGAATGTTCCAG	1721
OY	521	ProGlygluInhiSerhiArgGlnGly-----SerAlaGluAsnTyTyPheArgSerLySer	538
Db	1722	CCGGGCGCCGATGACACCGGTGGAGAGGTGTCCGGGGAACAATCACTTCGAGCGCCGGC	1781
OY	539	GlyAspSerLeuTyTyValAlaIleCyAsnMetHiAsglPheIleAspGluGluProAsp	558
Db	1782	GAGACGACGCTTCGGCGCGCCTGGACAGGTTCCGGGACTGGACAGTCCGCTGTCCGAC	1841
OY	559	TrpPheGlu-----LyGlnPheValProPhehiAspPro	570
Db	1842	TGGTTTCGATGTGAGAACTCTACTCAGACAGATGACAGAGATGCCCGTCCGTGACGAA	1901
OY	571	ProLeuAspTyTyArgGluProValLeuGluLylyPheAspSerGlyLeuValLeuAspAsp	590
Db	1902	GAGGTG---TTTGAGAGACCACTGCTGCTCCG---GGAACCGCATGTGAAGCGGCGC	1955
OY	591	ValMetCylyAspProGlyProGluSerAspPheCyLeuLylyValGlnAlaProValLeu	610
Db	1956	CCCCGTGGTCGGAG---CTGGCTCCAGGCTCTCTGGCCCATGAC---CCGCTGGTTC	2009
OY	611	GlyAlaThrGlyProAlaAspSerGlnhiAsgluSerGlnhiS-----	624
Db	2010	GGGGAGGAAGAGAGAGACAGTGGCAAACTGAACTCACTGACACCCCGGGGTACG	2069
OY	624	-----	624
Db	2070	CCAGCGCCGAGCCCTCCACACCTGTGTGTCCGCGAGAGAGGGGCGCTGTGGTCC	2129
OY	625	-----GlyGlyLeuAspGlnAspGlygluAlaArgProAlaLeuAspGlySer	640
Db	2130	GCGGTGAGCTGGGCGCCCTGTGTCGACGATGCCGACATGCCGTGGCTGGACCTGGCGGGAG	2189
OY	641	AlaAlaLeuGlnProLeuLeuhiSerhiValLylyAlaGlySerProSerAspMetProArg	660
Db	2190	GCGAGAGGCTGCGCGCTGTGGGACGCCCGGCGGTGG-----CGA	2231
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RESULT 15
US-08-620-694A-1
Sequence 1, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanelow, William
TITLE OF INVENTION: NO. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3288 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOCHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Mouse
ORGANISM: HVS13 receptor
FEATURE:
NAME/KEY: CDS
LOCATION: 121..2715
US-08-620-694A-1

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Alignment Scores:

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Best Local Similarity:	23.24	Mismatches:	321
Query Match:	7.64	Indels:	183
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US-10-616-788-2 (1-738) x US-08-620-694A-1 (1-3288)

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Qy 98 TrpSer---ProGlyAlaIleuGlyIleGluPheleuYsgIYpHeArgValIleGluGlu 116
Db 412 TGGACCTCGCAGACAGATGCCAGCATCTGTACTTCAGAGGCTGACAGCTGCCGTCTG 471
Qy 117 GluLeuYsSerGluIglYArgGlnCyvGlnGln-----LeuIleuYs 131
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Db 1290 CCCCCTATGTGAGGTGTGTCTTAAGTTGCGCCAGTCTCTATCACTGCTGTGGCAC 1349
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Run on: March 1, 2006, 06:07:49 ; Search time 9954 Seconds
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4214.433 Million cell updates/sec

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Fgapop 6.0, Fgapext 7.0
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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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17	3690	93.5	2319	6 AR338364	AR338364 Sequence
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ALIGNMENTS

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LOCUS AX251723 3083 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 1 from Patent WO0168859.
ACCESSION AX251723
VERSION AX251723.1 GI:15985081
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.

REFERENCE
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Jing, S.
11-17 receptor like molecules and uses thereof
Patent: WO 0168859-A 1 20-SEP-2001;
Amgen Inc. (US)

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DHAHPNMFPRFYLTKLKHGPPKRTCKQEQOTTETTSCLONVSPBDITIELVDIT
NTRKVMHVALKPVHSPWAPIRAMAVLVLVISAFLPTMCKRQOENIYSHLD
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ORIGIN

Alignment Scores:

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US-10-616-788-2 (1-738) x AX251723 (1-3083)

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QY	41	TPraGlyValGlyProAlaSerAraGanSerGlyLeuTyraenIleThrPheIleTy	60
DB	142	TGCAAGGGAGTGGGGCCAGCCAGCAAGAGTGGGCTGTACAACATCACTTCAATAT	201
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DB	1642	TCCCTATACGTGCGCAATTTGCAACATGCAACAGTTTATTTGAGAGAGGCCCACTG	1701
QY	561	GluTyraGlnPheValProPheHisProProProLeuAraGlyTyraGluProValLeuGlu	580
DB	1702	GAAAGCAAGTGTGTTCCCTTCACTCTCTCCATGCGCTACCGGAGGCACTGTGAG	1761
QY	581	LysPheAaPserGlyLeuValLeuAanAraValMetCysLysProGlyProGlnLysAaP	600
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LOCUS      Sequence 7 from Patent WO0208259.
ACCESSION      AX364576
VERSION      AX364576.1 GI:18696536
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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REFERENCE
AUTHORS      Presnell,S.R., Kuestner,R.E. and Gao,Z.
TITLE      Human cytokine receptor
JOURNAL      Patent: WO 0208259-A 7 31-JAN-2002;
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Score:      3918.00      Matches:      734
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ACCESSION AP458067
VERSION AP458067.1 GI:2179862
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1. (bases 1 to 2724)
AUTHORS Gilbert,J.M. and Gorman,D.M.
TITLE Identification of novel IL-17 related receptors
JOURNAL Unpublished
REFERENCE
2. (bases 1 to 2724)
AUTHORS Gilbert,J.M. and Gorman,D.M.
TITLE Direct Submision
JOURNAL Submitted (13-DEC-2001) Genomics, DNAX Research Inc., 901
California Ave., Palo Alto, CA 94304, USA

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 LOCUS
 DEFINITION Homo sapiens interleukin 17 receptor-like protein long form
 (IL17RLM) mRNA, complete cds; alternatively spliced.
 ACCESSION AF494208

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VERSION      AF94208.1 GI:21667503
KEYWORDS
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Homiidae; Homo.
REFERENCE    1 (bases 1 to 4477)
AUTHORS      Xiong, S., Zhao, Q., Rong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S.,
             Liu, L., and Chang, Z.
TITLE        hSeI Inhibits PC-12 Cell Differentiation by Interfering with
             Ras-Mitogen-activated Protein Kinase MAPK Signaling
JOURNAL      J. Biol. Chem. 278 (50), 50273-50282 (2003)
PUBMED       12958313
REFERENCES   2 (bases 1 to 4477)
AUTHORS      Xiong, S.O., Huang, G.R., Zhao, Q.H., Chen, P.L., Rong, Z.L., Ye, X.Y.,
             Chen, Y., Liu, L., Fu, X.Y., and Chang, Z.Z.
TITLE        Direct Submision
JOURNAL      Submitted (22-MAR-2002) Tsinghua Institute of Genome Research,
             Department of Biological Sciences and Biotechnology, and School of
             Medicine, Tsinghua University, Beijing 100084, P.R. China
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Percent Similarity: 99.5%      Conservative: 2
Beet Local Similarity: 99.2%      Mismatches: 4
Query Match:    99.0%      Indels:      0
DB:             8      Gaps:      0

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QY      21 SerGlnLeuAlaValAlaAgIyGlySerGlyAlaArgAlaTrpGlyValAlaPheThrCySerGly 40
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LOCUS      AX364570
DEFINITION      Sequence 1 from Patent WO208259.
ACCESSION      AX364570
VERSION      AX364570.1 GI:18696530

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KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS      Presnell, S. R., Kuestner, R. E. and Gao, Z.
TITLE      Human cytokine receptor
JOURNAL      Patent: WO 0208259-A 1 31-JAN-2002;
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Percent Similarity: 97.7%      Conservative: 1
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RESULT 6
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 VERSION AX364573.1 GI:18696533
 KEYWORDS
 SOURCE
 ORGANISM
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 1 Presnell,S.R., Kuestner,R.E. and Gao,Z.
 AUTORS Human cytokine receptor
 TITLE Patent: WO 0208259-A 4 31-JAN-2002;
 JOURNAL ZymoGenetics, Inc. (US)
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ORIGIN

Alignment Scores:

Pred. No.:	4,35e-298	Length:	2383
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Query Match:	98.6%	Indels:	14
DB:	6	Gaps:	1

US-10-616-788-2 (1-738) x AX364573 (1-2383)

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QY 41 TrpArg-----GlyValGlyPro 46
DB 206 TGGAGATGAAAGCGGCTGCCGCAACCCGCTTGTGTTGCTATGAGGAGTGGGAGCA 265
QY 47 AlaSerArgAsnSerGlyLeuTyraAsnIleThrPheLeuValAspAsnCySerThrTy 66
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QY 67 LeuAsnProValGlyValIleValIleAspAlaGlnAsnIleThrIleSerGlnTy 86
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QY 87 AlaCysIleAspGlnAlaValIleThrIleLeuTyrSerProGlyValIleGlnGly 106
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QY 107 PheLeuGlyGlyPheArgValIleLeuGlnGlnLeuLeuSerGlnGlyArgGlnCysGln 126
DB 446 TTCCTGAAAGGATTTCCGGGTAAATCTGAGAGACTGAAGTCCGAGGAGAAACAGTCCAA 505
QY 127 GlnLeuIleLeuValAspProGlyGlnLeuAsnSerSerPheLeuValArgThrGlyMetGln 146
DB 506 CAACGATTTCTAAGATCCGAAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGGA 565
QY 147 SerGlnProPheLeuAsnMetLeuValPheGlnThrAspThrPheValIleValProPhe 166
DB 566 TCTCAACCTTCTCTGAATATGAAATTTGAAACGATTAATTTCTAAAGGTGTCCCTTT 625
QY 167 ProSerIleLeuAsnGlnSerAsnTyraIleProPhePhePheArgThrArgAlaCysAsp 186
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DB 1646 CTCTGTTCCCACTGCACTCCGAGACCAAGCCCTCCAGAGACCGGGGAGACAGCGCA 1705
QY 527 GlnGlySerArgArgAsnTyrPheArgSerIleSerGlyValArgSerIleuTyraIle 546
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Qy 647 LeuH1aThrValLysAlaGlySerProSerAspMetProArgAspSerGlyIleTyrAsp 666
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RESULT 7
CS083243 4392 bp DNA linear PAT 18-MAY-2005
LOCUS CS083243
DEFINITION Sequence 15 from Patent EP1529843.
ACCESSION CS083243
VERSION CS083243.1 GI:66349785
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1
Edmonds, B.T., Micanovic, R., Ou, W., Su, E.W., Tschang, S.H. and
Wang, H.
Novel secreted proteins and their uses
Patent: EP 1529843-A 15 11-MAY-2005;
Eli Lilly & Company (US)
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ORIGIN
Alignment Scores:
Pred. No.: 4,87e-295 Length: 4392
Score: 3857.00 Matches: 732
Percent Similarity: 98.8% Conservative: 1
Best Local Similarity: 98.7% Mismatches: 5
Query Match: 97.7% Indels: 4
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Qy 41 TPrArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLysTyr 60
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Qy      341 SerThrTyThrAlaAlaLeuProArgGluArgLeuArgProArgProArgValAlaPheLeu 360
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Qy      599 rAspPheCysLeuValValGlnAlaProValLeuGlyAlaThyGlyProAlaAspSerG 619
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RESULT 8
AX392973
LOCUS AX392973 4392 bp DNA linear PART 23-MAR-2002
DEFINITION Sequence 15 from Patent WO0214358.
ACCESSION AX392973
VERSION AX392973.1 GI:19701020
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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            Homidae; Homo.
REFERENCE 1
AUTHORS Edmonds,B.T., Micanovic,R., Ou,W., Su,E.W., Tschang,S.H. and
            Wang,H.
            Novel secreted proteins and their uses
            Patent: WO 0214358-A 15 21-FEB-2002;
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Pred. No.: 4,87e-295 Length: 4392
Score: 3857.00 Matches: 732
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Best Local Similarity: 98.7% Mismatches: 5
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DB: 6 Gaps: 0

US-10-616-788-2 (1-738). x AX392973 (1-4392)
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CS135272
LOCUS CS135272 2786 bp DNA linear PAT 09-AUG-2005
DEFINITION Sequence 9 from Patent WO2005065711.
ACCESSION CS135272
VERSION CS135272.1 GI:72067723
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Gorman, D.M.
TITLE Mammalian receptor proteins; related reagents and methods
JOURNAL Patent: WO 2005065711-A 9 21-JUL-2005;
Schering Corporation (US)
FEATURES
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Best Local Similarity: 97.8% Mismatches: 12
Query Match: 97.2% Indels: 1
Gaps: 1
US-10-616-788-2 (1-738) x CS135272 (1-2786)

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COMMENT Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.ncl.nih.gov
Contact: MGC help desk
Email: cgaabs-remail.nih.gov
Tissue Procurement: Niklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NMGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
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Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnarsson, P.H., Garcia, A.M., Lu, X., Huiyk, S.W., Loulsesed, H.,
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QY	341	SetThrTyrThrAlaAlaLeuProArgGlnArgLeuArgProArgProIleValPheLeu	360
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QY	361	CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe	380
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QY	401	ArgGlnGlyGlnArgGlnTrrValIleGlnIleLysIleHisGlnSerGlnPheIleIleVal	420
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Db	1552	GATATATCTCGAGAGGAGAGAGTCCCGGTATCTTAGACCTAGATACCAAGTACAGACTC	1611
QY	501	MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu	520
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TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
JOURNAL	Hominidae; Homo		
PUBMED	1 (bases 1 to 2364)		
AUTHORS	Pregger, E., Ziv, I., Shabtay, A., Sher, I., Tsang, M., David, I. B.,		
TITLE	Altuvia, Y. and Ron, D.		
JOURNAL	Alternative splicing generates an isoform of the human Sef gene		
PUBMED	with altered subcellular localization and specificity		
AUTHORS	Proc. Natl. Acad. Sci. U.S.A. 101 (5), 1229-1234 (2004)		
TITLE	14742870		
JOURNAL	2 (bases 1 to 2364)		
PUBMED	Ron, D.		
AUTHORS	Direct Submission		
TITLE	Submitted (27-NOV-2003) Biology, Technion, Israel Institute of		
JOURNAL	Technology, Haifa 32000, Israel		
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 ORGANISM Homo sapiens
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 REFERENCE
 1
 Isegai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S.,
 Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
 Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
 Masuko, Y.
 TITLE
 JOURNAL Full-length cDNA sequences
 Patent: EP 1308459-A 1429 07-MAY-2003;
 Helix Research Institute (JP) ; Research Association for
 Biotechnology (JP)
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 QY 201 LYSPPROATASPLEUAENIIESERGINIIEGLISERASPMERGIVAIISER 220
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS 1
Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R.,
Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H.,
Sekine, M., Ohtsuka, M., Nishi, T., Shibahara, T., Tanaka, T.,
Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y.,
Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M.,
Shiratori, A., Sudoh, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,
Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T.,
Kikawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, S., Sato, K.,
Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H.,
Murakawa, K., Fujimori, K., Tanai, H., Kimura, M., Watanabe, M.,
Hiraoaka, S., Chiba, Y., Ishida, S., Oono, Y., Takiguchi, S., Watanabe, S.,
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Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R.,
Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Oshima, A.,
Sasaki, N., Aotake, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T.,
Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S.,
Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H.,
Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T.,
Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K.,
Kumagai, A., Itakura, S., Fukumoto, Y., Fujimori, Y., Komiyama, M.,
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Ozaki, K., Hiroo, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
Inagaki, H., Ikema, Y., Okamoto, S., Ohtani, R., Kawakami, T.,
Nojima, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
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Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuno, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T., and Sugano, S.
TITLE Complete sequencing and characterization of 21,243 full-length
human cDNAs
JOURNAL Nat. Genet. 36 (1), 40-45 (2004)

PUBLISHED 14702039
REFERENCE
AUTHORS 2
Ohtsuka, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K.,
Arita, M., Musashino, K., Yuki, H., Hara, H., Sugiyama, T., Irie, R.,
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsumura, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B.,
Suzuki, Y., Sugano, S., Nagahari, K., Masuno, Y., Nagai, K. and
Isogai, T.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 2894)
AUTHORS Isogai, T. and Yamamoto, J.
TITLE Direct Substitution
JOURNAL Submitted (04-JUN-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kametani, Kisekazu, Chiba 292-0812, Japan
(E-mail: genomics@rri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB) (supported by Japan
Key Technology Center etc.); 5' - & 3' -end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
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 (IL17RLM) mRNA, complete cds; alternatively spliced.
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 VERSION AF94211.1 GI:21667509
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 4478)
 AUTHORS Xiong,S., Zhao,Q., Rong,Z., Huang,G., Huang,Y., Chen,P., Zhang,S.,
 Liu,L., Fu,X. and Chang,Z.
 TITLE hsf inhibits PC-12 Cell Differentiation by Interfering with
 Ras-Mitogen-activated Protein Kinase MAPK Signaling
 JOURNAL J. Biol. Chem. 278 (50), 50273-50282 (2003)
 PUBMED 12958313
 REFERENCE 2 (bases 1 to 4478)
 AUTHORS Xiong,S., Zhao,Q., Huang,G., Chen,P., Rong,Z., Ye,X., Chen,Y.,
 Liu,L., Fu,X. and Chang,Z.
 TITLE Direct Submision
 JOURNAL Submitted (22-MAR-2002) Tsinghua Institute of Genome Research,
 Department of Biological Sciences and Biotechnology, and School of
 Medicine, Tsinghua University, Beijing 100084, P.R. China
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ORIGIN

Alignment Scores:

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 Best Local Similarity: 99.4% Mismatches: 2
 Query Match: 93.9% Indels: 0
 DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x AF494211 (1-4478)

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 QY 161 VALLYVALVALPROPHESERILELYASAENGLUSERANTYRHSIPROPHEPHE 180
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 QY 201 LYSPROARGASMLEUANLIESERGLNHLISGLYSETHSPMETGLNVALSERPHEAPHIS 220
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Qy      641 AlaAlaLeuGlnProLeuLeuHisThrValIysAlaGlySerProSerAspMetProArg 660
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Qy      661 AspSerGlyIleIysAspSerSerValProSerSerGlyLeuSerLeuProLeuMetGlu 680
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Qy      681 GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSerSer 700
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Qy      701 GlyLeuGlyGluGluProProAlaLeuProSerIysLeuLeuSerSerGlySerCys 720
Db      2191 GGCCTGGGTAGAGGAACTCTGCTCTTCCAAAGCTCTCTCTTGGGTATGC 2250
Qy      721 LysAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
Db      2251 AAAGCAATCTTGGTTCGCGAGCTAGTGAATGAACTCCACGCGGTGCGCCCT 2304

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Search completed: March 1, 2006, 10:38:01.
Job time : 10040 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 06:07:20 ; Search time 973 Seconds

(Without alignments)
5055.023 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948
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Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 333346308 residues

Total number of hits satisfying chosen parameters: 999394

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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Database :

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2: geneseg1990s:
3: geneseg2000s:
4: geneseg2001as:
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8: geneseg2003as:
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10: geneseg2003cs:
11: geneseg2003ds:
12: geneseg2004as:
13: geneseg2004bs:
14: geneseg2005s:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3948	100.0	3083	4	AA815346 DNA encod
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3	3918	99.2	2341	6	ABA95035 Human CYC
4	3908	99.0	4477	13	ADU69241 Human SEF

5	3908	99.0	4477	13	ADW23599 Human IL-
6	3901	98.8	2383	6	ABA95031 Human CYC
7	3891	98.6	2383	6	ABA95033 Human CYC
8	3857	97.7	4392	6	ABK62082 Human CDN
9	3835.5	97.2	2786	6	AA818134 Human DNA
10	3835.5	97.2	2786	14	ABE55653 Human DCS
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18	3690	93.5	2319	9	ADA49781 Human int
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20	3690	93.5	2319	10	ADB66908 DNA enco
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22	3690	93.5	2319	10	ADG87392 Human PRO
23	3690	93.5	2319	10	ADL16688 Human enco
24	3690	93.5	2319	12	ADL16649 Human enco
25	3690	93.5	2319	12	ADL71309 Human IL-
26	3594	91.0	4450	8	AA851235 Human REM
27	3382	85.7	2443	6	ABA95037 House mou
28	3345	84.7	2224	13	ADW76587 House mou
29	3248	82.3	3948	6	ABZ11243 Human pol
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31	3085	78.1	2217	6	ABA95036 Human Zcy
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33	3059	77.5	2259	6	ABA95034 Human CYC
34	3009.5	76.2	2214	6	AA818135 Human DCR
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36	2649	67.1	2217	6	ABA95038 Human cy
37	1595.5	40.4	1620	13	ADK01629 Murine int
38	1329	33.7	960	4	AA816201 5' portio
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41	321.5	8.1	3120	10	ADD25545 Binding d
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ALIGNMENTS

RESULT 1	AA815346 standard; cDNA; 3083 BP.
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AC	AA815346;
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DT	13-FEB-2002 (first entry)
XX	DNA encoding human Interleukin 17 (IL-17) receptor like protein.
DE	DNA encoding human Interleukin 17 (IL-17) receptor like protein.
XX	Interleukin 17; IL-17 receptor like protein; immunomodulatory;
KW	anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW	hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW	anti-coagulant; anti-asthmatic; dermatological; renal; osteopathic;
KW	vascular; cytostatic; anti-leukaemic; anti-fertility; ophthalmological;
KW	hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW	bone disease; vascular disorder; eye disorder; cancer; human; ss.
XX	Homo sapiens.
OS	Homo sapiens.
XX	
XX	
FT	Key
FT	CDS
FT	Location/Qualifiers
FT	22..2235
FT	/tag a
FT	/product "Interleukin 17 (IL-17) receptor like protein"
FT	/partial
XX	/note "No stop codon given"
PN	WO200168859-A2.

XX 20-SEP-2001.
XX 15-MAR-2001; 2001KO-US008678.
XX 16-MAR-2000; 2000US-0189816P.
XX 28-NOV-2000; 2000US-00724460.
XX (AMGE-) AMGEN INC.
XX JING S;
XX MPI; 2001-611392/70.
XX P-PSDB; AAU09904.
XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
XX for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
XX psoriasis and glaucoma.
XX Claim 1; Page 147-148,150-151; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17
XX receptor like polypeptides useful as vaccines and in gene therapy. These
XX have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
XX immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
XX osteopathic, vascular, cytoskeletal, anti-leukemic, anti-infertility and
XX ophthalmological activities. The IL-17 receptor like nucleic acids and
XX proteins may be used to prevent and treat diseases associated with
XX inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
XX include, for example immune disorders (e.g. inflammation, diabetes and
XX transplant rejection), infections (e.g. hepatitis and septicemia),
XX weight disorders (e.g. anorexia, cachexia and obesity), neuronal
XX dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
XX lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin diseases
XX (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
XX bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
XX (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
XX breast cancer), reproductive disorders (e.g. infertility and
XX miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
XX DNA and its complements may also be used as diagnostic probes to detect and
XX quantitate the presence of similar nucleic acids in samples and identify
XX patients needing restorative therapy. The IL17rlp may also be used as
XX antigens in the production of antibodies against the proteins and in
XX assays to identify modulators of expression and activity. The anti-
XX IL17rlp antibodies and antagonists may also be used to down regulate
XX expression and activity. This sequence encodes the human interleukin 17
XX (IL-17) receptor like protein described in the method of the invention

SO Sequence 3083 BP; 782 A; 807 C; 767 G; 727 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:	3083
Score: 3948.00	Matches: 738	
Percent Similarity: 100.0%	Conservative: 0	
Best Local Similarity: 100.0%	Mismatches: 0	
Query Match: 100.0%	Indels: 0	
DB: 4	Gaps: 0	

US-10-616-788-2 (1-738) x AAS15346 (1-3083)

QY 1 MetAlaProThrLeuGlnLeuCySerValPhePheThrValAsnAlaCysLeuAsnGly 20
Db 22 ATGGCCCCGGGCGTGGCTGCTGCTCTCTTTACGGGCAACGGCTCCCTCAAGGCG 81
QY 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyValArgAlaTrpGlyValAspThrCysGly 40
Db 82 TCGCAGCTGGCTGGCGCGCTGGCGGCTCCGGCCGCGCGCGCGCGCGACACTGGCGC 141
QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuValTrpAsnIleThrPheLeuTyr 60
Db 142 TGGAGGGGAGTGGGGCGACGCCAGCAAAACAGTGGGCTGTAAACATCACTTCAATAT 201

QY 61 AspAsnCySerThrThrTyrLeuAsnProValGlyLysHisValIleAlaAspAlaGlnAsn 80
Db 202 GACAAATTGTACACCACTTGAATCCAGTGGGGAACATGTATTCCTACCGCCAGAAAT 261
QY 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
Db 262 ATCACCATCAGCCAGCATGATCTTCCATGACCAAGTGGCAGTCCACTTCTGGTCCCCA 321
QY 101 GlyAlaLeuGlyTlIleGluPheLeuLysGlyPheArgValIleLeuGlnGluLeuLysSer 120
Db 322 GGGGCCCCCTGGCATTCGAATTCCTGAAAGGAATTTGGGTAATCTGGAGAGCGTGAAGTGG 381
QY 121 GluGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
Db 382 GAGGGAAGACAGTGGCCACACATGATCTTAAGAGATCCGAAGAGCTCAACAGTACTTC 441
QY 141 LysArgThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPhe 160
Db 442 AAAAGAACTGGAAATGAAATCTCAACCTTCTGAAATATGAAATTTGAAACGGATATTTTC 501
QY 161 ValLysValValProPheProSerIleLysAsnGluSerAsnTyrThrIleProPhePhe 180
Db 502 GTAAAGTGTGCTCTTTCTTCCATTAAACGAAGCAATTAACCACTTCTTCTTT 561
QY 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
Db 562 AGAACCCGAGCGGTGATCCTGTTTACAGCCGGAACATAGCTTGTAACCCCTCTGG 621
QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnLysSerPheAspHis 220
Db 622 AAGCCCGGAACCTGAACATCAGCCAGCATGCTCGCAATCAGCTGCTTCGACAC 681
QY 221 AlaProHisAsnPheLysPheArgPhePheTyrLeuHisTyrLysLeuLysHisGly 240
Db 682 GCACTGCACAACTTCGCTTCGCTTCCTTCTTCACTTCACTACAGCTCAAGCAAGGA 741
QY 241 ProPheLysArgGlyThrCysLysGlnGlnGlnThrThrGluThrThrSerCysLeuLeu 260
Db 742 CTTTACAGCGAAAGCTGTAAAGCAGAGCAACATCAGACACACAGCTCCCTCTT 801
QY 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrArg 280
Db 802 CAAGAATTTCTCCAGGGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 861
QY 281 LysValMetHisTyrTrpAlaLeuLysProValHisSerProTrpAlaGlyProIleArg 300
Db 862 AAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 921
QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
Db 922 ATGGCCATCAGTGGCCATCTGTAGTCAATTCGCACTTCGCACTGTGATG 981
QY 321 CysArgLysLysGlnGlnGlnLeuAsnIleTyrSerHisLeuAspGlnGlnSerSerGlySer 340
Db 982 TGGCGCAAGACGAAACAAATAATATATATTAATTAATTAATTAATTAATTAATTAATTA 1041
QY 341 SerThrTyrThrAlaAlaLeuProArgGlyLysArgGlyProArgProLysValPheLeu 360
Db 1042 TCCACATACCTGCACACCTCCCAAGAGAGAGCTCGGCGCGGAGAGGCTTTTCTC 1101
QY 361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
Db 1102 TGGTATTTCCAGTAATATGGCCAGATTCATGAATGTGTGTCAGTGTTCGCTACTTC 1161
QY 381 LeuGlnAspPheCysGlyCysGlyValAlaLeuAspLeuTrpGlnAspSerLeuCys 400
Db 1162 CTCACAGACTTCGTGGCTGTAGAGTGGCTCGAAGCTGTGGGAGACCTTCAAGCTCTGT 1221
QY 401 ArgGlnGlyGlnArgGluTrpValIleGlnLysIleHisGluSerGlnIleIleVal 420
Db 1222 AGAGAAAGGAGAGAAATGGGTCAATCCAGAAAGTCCAGAGAGTCCAGATTCATCATTTGG 1281
QY 421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisLysGly 440

QY 21 SerGlnLeuAlaValAlaIleAglySerGlyValArgAlaTrpGlyValAspThrCysGly 40
 DB 82 TCCGAGGTGGCTGTGGCGCTGGGGGCTCCGGCCGGCGGTGGGGCGTGCACACTGTGGC 141
 QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyzAsnIleThrPheIleTyz 60
 DB 142 TGGAGGGAGTGGGGCCAGCAGCAAGACGTGGGCTGTACAAACATCACCTTCAATAT 201
 QY 61 AspAsnCySerThrTrpThrLeuAsnProValGlyIleValIleAlaAspAlaGlnAsn 80
 DB 202 GACATTTGTACCACTTCTTGATCTCAGTGGGAAAGCATGTGATGCTTGACGCCCAAT 261
 QY 81 IleThrIleSerGlnTyzAlaCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
 DB 262 ATCACCATCAGCCAGTATGGCTTGCATGACCAAGTGCAGTCCATCTTTGGTCCCA 321
 QY 101 GlyAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGluGluLeuLeuSer 120
 DB 322 GGGGCTCCGCGCATCGAATTCTGMAAGATTCTGGGTAAATACCTGGAGAGCTGAAGTCC 381
 QY 121 GluGlyValArgGlnCysGlnGlnIleLeuIleValAspProIleValAsnSerSerPhe 140
 DB 382 GAGGAAAGACAGTGCACAACTGATTTCAAAGATCCGAAGCAGCTCAACAGTACCTTC 441
 QY 141 LysArgThrGlyMetGluSerGlnProPheLeuAsnMetLysPheGluThrAspTyzPhe 160
 DB 442 AAAAGAACTGGAAATGGAATCTCAACCTTCTGATATGAAATTGAAAGGATTAATTC 501
 QY 161 ValLysValValProPheProSerIleLysAsnGluSerAsnTyzHisProPhePhe 180
 DB 502 GTAAAGGTTGTCCCTTTCTTCATTAATAACGAAGCAATTACCCCTTTCTCTTT 561
 QY 181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
 DB 562 AGAACCAGACCTGTGACCTGTGTGTACAGCCGACATCTAGCTGTAAACCTTTGG 621
 QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValIleSerPheAspHis 220
 DB 622 AACCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGCAAGTGTCTTCAGACAC 681
 QY 221 AlaProHisAsnPheGlyPheArgPheArgPheTyzLeuHisGlyIleValLeuIleVal 240
 DB 682 GCACCGCAAACTTCGGCTTCCTGTCTCATCTTCAACAGCTCAAGCAGCAAGGAGA 741
 QY 241 ProPheLysArgLysThrCysLysGlnGluGlnThrThrGluThrThrSerCysLeuLeu 260
 DB 742 CTTTCAAGGAAAGACCTGTAGCAGAGCAAACTACAGAGCAGCACTGCTCTT 801
 QY 261 GlnAsnValSerProGlyAspTyzIleIleGluLeuValAspAspThrAsnThrArg 280
 DB 802 CAATAATGTTCTCCAGGGAGTTATATATATGAGCTGGTGGATGACATTAACAACAAGA 861
 QY 281 LysValMetHisGlyTyrAlaLeuLysProValHisSerProTrpAlaGlyProIleArgAla 300
 DB 862 AAAGTATGCAATTATGCTTAAAGCCAGTCACTCCCGTGGCGGCCCATCAGAGCC 921
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 DB 922 ATGGCCATCAAGGCACTGTGATGATATGCGCATTCGAGAGCTTTCACATGTGATG 981
 QY 321 CysArgLysLysGlnGlnIleAsnIleTyzSerHisLeuAspGluGluSerSerGluSer 340
 DB 982 TGGCGAGAAAGCAACAAGAAATATATATTCACATTTAGATGAAGAGACTCGAGTCT 1041
 QY 341 SerThrTyzThrAlaAlaLeuProArgGluArgLeuArgProArgProLysValPheLeu 360
 DB 1042 TCCACATACACTGCACTGCCCAAGAGAGAGGCTCCGGCCGCGCGCAAGGCTTTCTC 1101
 QY 361 CysTyzSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyzPhe 380
 DB 1102 TGGCTATTCCAGTAAAGATGGCCAGAAATCACTGATATGTCTGCTCCAGTATTCCTTCC 1161
 QY 381 LeuGlnAspPheCysGlyCysGluValAlaLeuAspLeuTrpGluAspPheSerLeuCys 400

DB 1162 CTCACAGACTTCTGTGGCTGTGAGGAGTGGCTGGACCTGTGGGAAAGACTTCAAGCTCTGT 1221
 QY 401 ArgGluGlyAlaArgGluTrpValIleGlnLysIleHisGluSerGlnPheIleIleVal 420
 DB 1222 AGAAGAGGCAAGAAATGGGTCAATCCAGAAATCCAGAGTCCAGATTCATCATTTGG 1281
 QY 421 ValCysSerLysGlyMetLysTyzPheValAspLysLysAsnTyzHisGlyGly 440
 DB 1282 GTTTGTTCCAAAGATATGAAGTACTTTGTGACAGAGAAATCAACAACAAGAGAGGT 1341
 QY 441 GlyArgGlySerGlyLysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGlyLys 460
 DB 1342 GGGCGAGGCTCGGGGAAAGAGAGCTTCTGTGGTGGCGGTGTCAAGCTCCGCAAAAG 1401
 QY 461 LeuArgGlnAlaLysGlnSerSerAlaAlaLeuSerLysPheIleAlaValTyzPhe 480
 DB 1402 CTCCGCAAGCCAAAGAGATTCGTCCGGGCGCTCAAGAGTTATTCGCGCTATCTTT 1461
 QY 481 AspTyzSerCysGluGlyAspValProGlyIleLeuAspLeuSerThrLysTyzArgLeu 500
 DB 1462 GATTAATTCCTGGAGGAGACGTCCCGGTATCTAGACTGATACCAAGTACAGACTTC 1521
 QY 501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
 DB 1522 ATGACAAATCTTCTCAGCTGTGTCCACCTGCAGCTCCGAGACCAAGCGCTCCAGAG 1581
 QY 521 ProGlyGlnHisThrArgGlnGlySerArgArgAsnTyzPheArgSerLysSerGlyArg 540
 DB 1582 CCGGGGCAACACCGGACAGAGGAGCAAGAAAGAACTTCCGAGCAAGTCAAGGCCG 1641
 QY 541 SerLeuTyzValAlaIleCysAsnMetHisGlnPheIleAspGluGluProAspTrpPhe 560
 DB 1642 TCCCTATAGCTGCCATTTGCAACATGACACAGTTATTTGACAGAGAGCCGATGTTTC 1701
 QY 561 GluLysGlnPheValProPheHisProProProLeuArgTyzArgGluProValLeuGlu 580
 DB 1702 GAAAGCAGTTCGTTCCCTTCCATCTCTCCACCTGCGCTACCGGAGCCAGTCTTGAG 1761
 QY 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysProGlyProGluSerAsp 600
 DB 1762 AAATTTGATTCGGCTTGGTTTAAATGATGTCAATGTGAACCAAGGGCTTAGATGAC 1821
 QY 601 PheCysLeuLysValGlyAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHis 620
 DB 1822 TTCTGCTTAAAGGTAGAGCGCTGTCTTGGGGCAACGGACACAGCCATCCAGCAC 1881
 QY 621 GluSerGlnHisGlyLysLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySer 640
 DB 1882 GAGAGTCAGCATGGGGGCTGGACCAAGACGGGAGGGCCGGCTGCTGACGGTAGC 1941
 QY 641 AlaAlaLeuGlnProLeuLeuHisGlyThrValLysAlaGlySerProSerAspMetProArg 660
 DB 1942 GCGGCCCTTCACACCTTGTGACACAGGTGAAGCGGGAGGCCCTCGGACATGCGCGG 2001
 QY 661 AspSerGlyIleTyzAspSerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680
 DB 2002 GACTCAGGATCTATATCTGTCTGTGCGCTCATCCGACTGTCTTGCCACTGAGAGAA 2061
 QY 681 GlyLeuSerThrAspGlnThrGluThrSerSerLeuThrGluSerValSerSerSerSer 700
 DB 2062 GAGCTCTCAGCGGACAGACAGAAAGCTTCCCTGACAGGAGCGTGTCTCTTCA 2121
 QY 701 GlyLeuGlyGluGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
 DB 2122 GGCCTGGGTGAAGAGAACTTCCTGCTCTTCTTCCAAAGCTCTCTTCTTGGGTATGC 2181
 QY 721 LysAlaAspLeuGlyCysArgSerTyzThrAspGluLeuHisAlaValAlaPro 738
 DB 2182 AAAGCAAGTCTTGGTGGCCGACCTACATGATGAATCCACAGCGGTCCGCTT 2235
 RESULT 3
 ABA95035

ID ABA95035 standard; DNA; 2341 BP.
 XX
 AC ABA95035;
 XX
 DT 20-MAY-2002 (first entry)
 XX
 DE Human cytokine receptor, Zcytor18 splice variant nucleotide sequence.
 XX
 KW Cytokine receptor; Zcytor18; cell proliferation; antiproliferic; human;
 KW pulmonary alveolar proteinosis; familial periodic fever; antitumor;
 KW erythroleukemia; chromosome 3p14.3; gene therapy; splice variant; ds.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 86..2305
 FT /*tag= a
 FT /product= "Zcytor18 splice variant"
 XX
 XX MO200208259-A2.
 XX
 PD 31-JAN-2002.
 XX
 PP 23-JUL-2001; 2001MO-US023253.
 XX
 PR 26-JUL-2000; 2000US-0220747P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Kuestner RE, Gao Z;
 XX
 DR WPI; 2002-217048/27.
 DR P-PSDB; ABB07628.
 XX
 PT New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor growth,
 PT and modulating immune system by binding to endogenous zcytor18 ligand.
 XX
 PS Claim 5; Page 102-106; 119pp; English.
 XX
 CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
 CC and localize Zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human Zcytor18 splice variant nucleotide sequence
 XX
 SQ Sequence 2341 BP; 550 A; 668 C; 625 G; 498 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 0 Length: 2341
 Score: 3918.00 Matches: 734
 Percent Similarity: 99.6% Conservative: 1
 Best Local Similarity: 99.5% Mismatches: 3
 Query Match: 99.2% Indels: 0
 DB: Gaps: 0
 US-10-616-788-2 (1-738) x ABA95035 (1-2341)
 QY 1 MetAlaProTTrpLeuGlnLeuYsSerValPhePheThrValAlaAlaCysLeuAangly 20
 DB 86 ATGGCCCGGCGGCTGAGCTCTGCTCGCTCTTAAAGGCTCAACGCTCCTCAAGGC 145
 QY 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTrpGlyValAlaPTrpCysGly 40

DB 146 TGGCAGGTGGCTGTGGCCGCTGGCGGGGTCCGCCGCCGCCGCCCAACCTGTGGC 205
 QY 41 TTPArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheIleTyr 60
 DB 206 TGGAGGGGAGGTGGGGCAGCGACAGAAAACAGTGGGCTGTAAACATCACTCAATAT 265
 QY 61 AspAsnCysThrThrThrLeuAsnProValGlyValHisValIleAlaAspAlaGlnAsn 80
 DB 266 GACAAATGTACCACTTAAATCCAGTGGGAGCAATGTGATGCTGAGCGCCAGAAAT 325
 QY 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrSerPro 100
 DB 326 ATCAACATCAGCCAGATGCTTGGCATGACCAAGTGGCATCACTTCTTGTGCCCA 385
 QY 101 GlyAlaLeuGlyIleGlnPheLeuIleGlyPheArgValIleLeuGlnLeuLeuSer 120
 DB 386 GGGGCCCTCGGCTCAATTCCTGAAAGATTTCCGGGTATATCTGAGGAGCGTGAAGTCG 445
 QY 121 GlnGlyArgGlnCysGlnGlnLeuIleLeuIleLeuIleAspProIleGlnLeuAsnSerPhe 140
 DB 446 GAGGAAAGACAGTGCACCAACATGATTTAAAGATCCAGAGAGCTCAACAGTACCTTC 505
 QY 141 LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGlyIleThrAspTyrPhe 160
 DB 506 AAAAGAACTGGAAATGGAATCTCAACCTTCTCGAATATGAAATTTGAACGGATTAATTC 565
 QY 161 ValLysValValProPheProSerIleLysAsnGlnSerAsnTyrHisProPhePhe 180
 DB 566 GTAAAGTTTCCCTTTCTTCTTCAATTAAGAAAGAAATATCAACCTTCTTCTT 625
 QY 181 ArgThrArgAlaCysAspLeuLeuLeuGlnProAspAsnLeuAlaCysLysProPheTrp 200
 DB 626 AGAACCCGAGCTGTACCTGTGTGTAACGCCGCAACATCTTACTGTGAACCTTCTTG 665
 QY 201 LysProArgAsnLeuAsnIleSerGlnIleGlySerAspMetGlnValSerPheAspHis 220
 DB 686 AAGCTTCGAGACTGAACTCAACATCAACGATGCTCGGACATGAGGTGCTTCGACAT 745
 QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrLysLeuLysIleGlnGly 240
 DB 746 GCACCCGACAACTTCGCTTCGCTTCTTCTTCTTCACTCAACAGCTCAAGCAGAAAGA 805
 QY 241 ProPheLysArgLysThrCysLysGlnGlnIleThrGlnIleThrThrSerCysLeuLeu 260
 DB 806 CCTTCAACCGAAAGCCGTGAAGCAGGAAACATCAACAGACGACCGCTGCCCTT 865
 QY 261 GlnAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspThrAsnThrArg 280
 DB 866 CAAATGTTTCTCCAGGGGATTTATATTAATGACTGTGATGACATCAACACAAAGA 925
 QY 281 LysValMetHisTyrAlaLeuLysProValHisSerProTyrAlaGlyProIleArgAla 300
 DB 926 AAAGTATCATTTATGCTTTAAAGCAGACATCCCGCGGGCGGCGCATCAAGGC 985
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 DB 986 GTGGCCATCAAGTGCACGTGATCATATGCTGATGCGCACCTCTTCACTGTGARG 1045
 QY 321 CysArgLysLysGlnGlnLeuAsnIleTyrSerHisLeuAspGlnIleSerGlnSer 340
 DB 1046 TGGCGAAGAGCAACAAAGAAATATATATTCATTTAGATGAAGAGCTGTAGTCT 1105
 QY 341 SerThrTyrThrAlaAlaLeuProArgGlnArgLysArgProArgProLysValPheLeu 360
 DB 1106 TCCACATACACAGCACTCCCAAGAGAGAGGCTCCGCGCGCGCAAGGCTTCTTC 1165
 QY 361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
 DB 1166 TGTCTATTCCAGTAAGATGCGCAATCATCAAGATGTGCTCAAGTGTTCCTTCACTTC 1225
 QY 381 LeuGlnAspPheCysGlyCysGlyValAlaAlaAspLeuTrpGlnAspPheSerLeuCys 400
 DB 1226 CTCAGGAACTTGT 1285

QY 401 ArgGluGlnArgGluTrpValIleGlnIleHisGlnSerGlnPheIleIleVal 420
 DB 1286 AGAGAAAGGAGAGAGAGATGGGTATCATCAAGATCCAGATCCAGATTCATTCATG 1345
 QY 421 ValCysSerIleGlyMetLeuTyrPheValAspIleValAsnTyrIleGlyGly 440
 DB 1346 GTTGTTCAGAGATGAGTACTTGTGGACAGAAAGATCAAGAACCAAGAGAGGT 1405
 QY 441 GlnArgGlySerGlyLeuGlyGlnPheLeuValAlaValSerAlaIleAlaGlnLeu 460
 DB 1406 GGGCGAGGCTGGGGAGAGAGAGCTCTCTGGTGGCGGTGACAGCTTCGAGAAAG 1465
 QY 461 LeuArgGlnAlaIleGlnSerSerSerAlaIleLeuSerPheIleAlaValTyrPhe 480
 DB 1466 CTCGGCCAGGCGCAGAGAGATGCTCCGGCGCTTCAGCAAGTTATTCGCGCTTACTTT 1525
 QY 481 AspTyrSerCysGlnGlnIleAspValProGlyIleLeuAspLeuSerThrIleTyrArgLeu 500
 DB 1526 GATTATTCCTGGCAGGAGAGAGCTCCCGGTATCTTAAGCTGAGTACCAAGTACAGACTC 1585
 QY 501 MetAspAsnLeuProGlnIleuCysSerHisLeuHisSerArgAspHisGlyLeuGlnGlu 520
 DB 1586 ATGAGCAATCTTCCTCAGCTCTGTTCCACTTGCACTCCGAGACCCAGGCTTCAGAGAG 1645
 QY 521 ProGlyValIleHisThrArgGlnGlnIleSerArgArgAsnTyrPheArgSerIleYsSerGlyArg 540
 DB 1646 CCGGGGAGAGACAGCGACAGGGGAGAGAGAGAACTACTTCGGAGCAAGTCAAGGCCCG 1705
 QY 541 SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGlnGlnIleProAspTyrPhe 560
 DB 1706 TCCCTATACCTGGCATTTTGCATCATGCAAGATTATTCAGAGAGAGCCGAGCTGTTTC 1765
 QY 561 GlnIleGlnPheValProPheHisProProProLeuArgTyrArgGlnProValIleGln 580
 DB 1766 GAAAGAGAGTTCCTTCCTTCATCTCCCTCCAGCTGGGCTACCGGGAGCCAGCTTCGAG 1825
 QY 581 LysPheAspSerGlyLeuValIleuAsnAspValMetCysIlePyrProGlnIleSerAsp 600
 DB 1826 AATTTGATTCGGGCTTGTTGTTTAAATGATGTCATGTGCAAAACAGGGCTTCGAGATGAC 1885
 QY 601 PheCysLeuLysValGlnAlaProValIleuGlnValAlaThrGlnProAlaAspSerGlnHis 620
 DB 1886 TTCCTGCTTAAAGGATAGAGGGCGGTCTTGGGGCAACCGGACCGAGCTCCAGCAC 1945
 QY 621 GlnSerGlnHisGlyGlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
 DB 1946 GAGAGTCAGATGGGGCTGGGACCAAGACGGGGAGGCCCGGCTTCCTTGAACGTAGC 2005
 QY 641 AlaAlaLeuGlnProLeuLeuHisIleThrValIleAlaGlnIleSerProSerAspMetProArg 660
 DB 2006 GCGGCTTCGACCCCTGCTGACACCGGTAAAGCCCGGACCCCTGGACATGGCCGG 2065
 QY 661 AspSerGlyIleTyrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGln 680
 DB 2066 GACTCAGGAGATATGATGCTGTCGTCTCCCTCAACAGCTGCTCTGCCACATGATGAA 2125
 QY 681 GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSer 700
 DB 2126 GGAATCTCGACGACGACAGAGAAACCTTCCTTCCTGACGAGCGGTCTCTCTTCA 2185
 QY 701 GlnLeuGlnIleGlnGlnIleProProAlaLeuProSerIleLeuSerSerGlySerCys 720
 DB 2186 GGCCTGGGTAGAGAGAACTCTGCGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 2245
 QY 721 LysAlaAspLeuGlnCysArgSerTyrThrAspGlnLeuHisAlaValAlaPro 738
 DB 2246 AAGGAGATCTTGTGTTGCGGACGATACATGATGAATCTCAACGGGTGCGCCCT 2299
 RESULT 4
 ADU69241
 ID ADU69241 standard; DNA; 4477 BP.

AC ADU69241;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human SEF gene SEQ ID NO:1.
 XX
 KM de; gene; fibroblast growth factor; SEF; similar expression of FGF genes;
 KM cytotatic; cardiovascular-gen.; antiarteriosclerotic; cardiant;
 KM vasotropic; hypotensive; nephrotropic; gene therapy; diagnosis;
 KM prognosis; proliferative disorders; cardiovascular disorders;
 KM renal disease; glomerular disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 90..2309
 FT /tag= a
 FT /product= "SEF"
 XX
 PN US2004235104-A1.
 XX
 PD 25-NOV-2004.
 XX
 XX 07-MAY-2004; 2004US-00842006.
 XX
 XX 08-MAY-2003; 2003US-0469522P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Yang R;
 XX
 DR WPI; 2004-821320/81.
 DR P-PSDB; ADU69242.
 XX
 PT New isolated SEF nucleic acid and polypeptide, useful for monitoring,
 PT treating, or diagnosing proliferative and/or differentiative disorders,
 PT e.g. ovarian cancer, breast cancer, or cardiovascular disorder including
 PT arteriosclerosis.
 XX
 PS Claim 1; SEQ ID NO 1; 46pp; English.
 XX
 CC The invention relates to a novel isolated SEF (similar expression of FGF
 CC gene) nucleic acid molecule (I). An SEF of the invention has cyostatic,
 CC cardiovascular-gen., antiarteriosclerotic, cardiant, vasotropic,
 CC hypotensive, and nephrotropic activity, and may have a use in gene
 CC therapy. The SEF nucleic acids and polypeptides can be used for
 CC diagnostic assays, prognostic assays, and monitoring clinical trials.
 CC They can also be used for treating a subject at risk of or susceptible to
 CC a disorder or having a disorder associated with aberrant or unwanted SEF
 CC expression or activity. The SEF molecules can also be used for
 CC monitoring, treating, or diagnosing proliferative and/or differentiative
 CC disorders, e.g. ovarian cancer, breast cancer, colon cancer, prostatic
 CC cancer, FGF related disorder, cardiovascular disorder including
 CC arteriosclerosis, coronary artery disease, ischemia, reperfusion injury,
 CC restenosis, arterial inflammation, hypertension, endothelial disorders,
 CC and a kidney disorder, e.g. glomerulonephritis, vascular nephropathy,
 CC renal failure, or glomerular disease. The SEF molecules can also be used
 CC as markers of disorders or disease states, as markers for precursors of
 CC disease states, as markers for predisposition of disease states, as
 CC markers of drug activity, or as markers of the pharmacogenomic profile of
 CC a subject. The present sequence represents the SEF nucleic acid molecule
 CC of the invention.
 XX
 SQ Sequence 4477 BP, 1133 A, 1086 C, 1141 G, 1117 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 4477
 Score: 3908.00 Matches: 732
 Percent Similarity: 99.5% Conservative: 2
 Best Local Similarity: 99.2% Mismatches: 4
 Query Match: 99.0% Indels: 0
 DB: 13 Gaps: 0

US-10-616-788-2 (1-738) x ADU69241 (1-4477)

QY 1 MetAlaProThrLeuGlnLeuCySerValPhePheThrValAsnAlaCysLeuAsnGly 20
 Db ATGGCCCGGAGTGGAGCTCTGCTCGTCTTAAAGGTCAACGCTCCCAACGAGC 149
 QY 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTrpGlyValAspThrCysGly 40
 Db TCGGAGCTGCTGAGCGCGCTGGCGAGGTCCGCGCGCGCGCGCGCGCGCGCGCGCG 209
 QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyTrpAsnIleThrPheLeuTyr 60
 Db TGGAGGGGAGTGGGGCCAGCCAGAGAAACAGTGGGCTGTAAACAACATCACTTCAATAT 269
 QY 61 AspAsnCyThrThrThrTyrLeuAsnProValGlyValAsnIleValAlaAspAlaGlnAsn 80
 Db GACAAATTTGACCACTTAATTCAGTGGGAGAGATGTGATGTGTCGACGCCCAAGAT 329
 QY 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrPhePro 100
 Db ATACCAATACGCAAGATAGTGTGTCATGACCAAGTGCAGTCAACATTTCTTGGTCCCA 389
 QY 101 GlyAlaLeuGlyIleGluPheLeuGlyGlyPheArgValIleLeuGlnGluLeuLeuSer 120
 Db GGGGCGCTGGGCAATCGAATTCGTAAGATTTCCGGTATATCTGGAGAGCTGAAGTGC 449
 QY 121 GluGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
 Db GAGGGAAGACAGTGCACAACTGATTTCTAAAGATCCGAAGACGCTCAACAGTACGCTTC 509
 QY 141 LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGlnThrArgTyrPhe 160
 Db AAAAGAACTGGAATGGAATCTCAACCTTCTGAATATGAAATTTGAAAGGATTAATTTTC 569
 QY 161 ValLysValValProPheProSerIleLysAsnGlyLysAsnTyrHisProPhePhe 180
 Db GTAAAGTTTCCCTTTCTTCTTCAATTAAGAAAGCAATTAACCACTTTCTTCTTTC 629
 QY 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTyr 200
 Db AGAAGCCGAGCTGTGACCTGTGTATACAGCCGAGCAATCTAGCTGTAAACCTTCTGCG 689
 QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
 Db AACCTCTGGAACCTGAACATCAACAGCAAGCTCGGACATGACAGGTGCTTTCGACAC 749
 QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisIleTyrLysLeuLysHisGly 240
 Db GACCGGCACTTCGCTTCGCTTCCTTCTTCTTCACTTCAAGACTCAAGACAGAAAGA 809
 QY 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrThrGlnIleThrThrSerCysLeu 260
 Db CTTTCAAGGAAAGACCTGTGACAGAGCAAACTACAGAGTACAGACTGCTGCTTTC 869
 QY 261 GlnAsnValSerProGlyAspTyrIleIleGlnLeuValAspAspThrAsnThrArg 280
 Db CAAGAAGTTTCTCAGAGGATTAATATTAATGAGCTGTGTGATGACCTTAACAACAAGA 929
 QY 281 LysValMetHisTyrAlaLeuLysProValHisSerProTrpAlaGlyProIleArgAla 300
 Db AAGATATGATTAATGCTTAAAGCAAGTCACTCCCGTGGGCGGGGCCCAATCAAGACC 989
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 Db GTGGCATCATCAGTGCACCTGTAGTCAATTCGCAATTCGCAAGCTTCACTGATG 1049
 QY 321 CysArgLysLysGlnGlnGlnGlnIleTyrSerHisLeuAspGlnGlnLysSerGlySer 340
 Db TGGCGAGAGAGAAACAAATAATATTAATCACTTAATGATGAGAGAGAGCTGTGAGTCT 1109
 QY 341 SerThrTyrThrAlaAlaLeuProArgGluArgLeuArgProArgProLysValPheLeu 360
 Db TCCACATACCTGAGACATCCCAAGAGAGGCTCCGCGCGCGCGCGCGCGCGCGCGCTTC 1169

QY 361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
 Db TGTATTTCCAGTAAAGATGGCCAGAAATCAATGAATGTCTCAAGTGTTCGCTTACTTC 1229
 QY 381 LeuGlnAspPheCysGlyCysGluValAlaLeuAspLeuTrpGluAspPheSerLeuCys 400
 Db CTCACAGACTTCTGTGTGTAGAGTGTGAGTGTGAGCTGTGAGAGAGACTTCACTCTGT 1289
 QY 401 ArgGlnGlyGlnArgGlnTrpValIleGlnLysIleHisGlnSerGlnPheIleIleVal 1420
 Db AGAAGAGGCGAGAGAAATGGGTCAATCCAGAGATCCAGAGTCCAGATTCATCATGTG 1349
 QY 421 ValCysSerLysGlyMetLysTyrPheValAspLysLysAsnTyrLysHisLysGlyGly 440
 Db GTTGTGTCCAAAGATTAAGATCTTTGTGGAAGAAAGAACTTAACAACAAGAGAGGT 1409
 QY 441 GlyArgGlySerGlyLysGlyGlnLeuPheLeuValAlaValSerAlaIleAlaGlnLys 460
 Db GCGCGAGCTCGGGGAAAGAGAGCTTCTGTGTGTGCGGTGTCAAGCATTCGCGAAAG 1469
 QY 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
 Db CTCGCGCAGGCCAAGCAGAGTGTGTCGCGCGCTCAGCAAGTTATCCGCGCTACTTTC 1529
 QY 481 AspTyrSerCysGlnGlyAspValProGlyIleLeuAspLeuSerThrLysTyrArgLeu 500
 Db GATTAATCTGTGCAAGAGAAACGTCCCGGTATCTTGAAGCTGTGACCAAGTCAAGATC 1589
 QY 501 MetAspAsnLeuProGlnLeuCysSerHisLeuHisSerArgAspHisGlyLeuGlnLys 520
 Db ATGGAACAATTTCTTCAAGCTGTGTTCACCTGCACTCCGAGACCAAGCTTCCAGAG 1649
 QY 521 ProGlyGlnHisThrArgGlnLysArgArgAsnTyrPheArgSerLysSerGlyArg 540
 Db CCGGGCAGACACCGGACAGGGCAGACAGAGAACTATCTCCGAGCAAGTCAAGCCGG 1709
 QY 541 SerLeuTyrValAlaIleCysAsnMetHisGlnPheIleAspGlnGluProAspTyrPhe 560
 Db TCCCTATACGTCCCACTTTGCAACATGCAACAGTTTATTAACAAGAGCCGCACTGGTTC 1769
 QY 561 GluLysGlnPheValProPheHisProProLeuArgTyrArgGluProValLeuGln 580
 Db GAAAGCAAGTGTCTTCCCTTCACTCTCCCACTGCGCTACCGGAGCCAGCTTGGAG 1829
 QY 581 LysPheAspSerGlyLeuValLeuAsnAspValMetCysLysAspProGlyLysAsp 600
 Db AATTTGATTCGGGCTTGGTTTAATGATGTCAATGCAACAGGGCTGAGAGTGAAC 1889
 QY 601 PheCysLeuLysValGlnAlaProValLeuGlyAlaThrGlyProAlaAspSerGlnHis 620
 Db TTCTGCTTAAGGTAAAGGAGCGGCTGTCTTGGGGCAACCGGACCACTCCAGAC 1949
 QY 621 GluSerGlnHisGlyGlyLysAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
 Db GAAAGTCAAGTGGGGCTGTGACCAAGACGAGGAGCCCGGCTTCCCTTGAAGGTAGC 2009
 QY 641 AlaAlaLeuGlnProLeuLeuHisThrValIleValGlySerProSerAspMetProArg 660
 Db GCGGCGCTCCCAACCTGCTGTGACACGTGAAGACCGGAGCCCTCGGACATGCCGCG 2069
 QY 661 AspSerGlyIleTyrAspSerSerValProSerSerGlnLeuSerLeuProLeuMetGln 680
 Db GACTCAGGATCATATACCTGTGTGCGCTTCCAGACTGTCTGTGCACTGATGAGAA 2129
 QY 681 GlyLeuSerThrAspGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSer 700
 Db GAACTCTCAAGCAGACCAAGAAAGTCTTCCCTGAAGAGAGCTGTCTCTCTTCA 2189
 QY 701 GlyLeuGlyGlnGlnLysProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
 Db GGCCTGGTGAAGAGAACTCTGCTGCTTCTTCAAGCTCTCTTCTGAGTATGC 2249

QY 721 LysAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
DB 2250 AAGGAGATCTGTGGCCGACGTAACATGATGAATCCACCGGGTCCGCCCT 2303
RESULT 5
ADW23599
ID ADW23599 standard; DNA; 4477 BP.
XX
AC ADW23599,
XX
DT 10-MAR-2005 (first entry)
XX
DE Human IL-17RLM DNA.
XX
KM Neuroprotective; Immunosuppressive; Cytostatic; IL-17RLM;
XX rheumatoid arthritis; asthma; carcinoma; ds; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS /tag= a
FT /product= "IL-17RLM"
XX
PN CNI463982-A.
XX
PD 31-DEC-2003.
XX
PF 28-JUN-2002; 2002CN-00123447.
XX
PR 28-JUN-2002; 2002CN-00123447.
XX
PA (UYOI) UNIV QINGHUA.
XX
PI Xiong S, Chang Z, Fu X;
XX
DR MPI; 2004-248693/24.
XX P-PSDB; ADW23600.
XX
PT New polynucleotide encoding IL-17RLM polypeptide, useful in preparing a
PT composition for treating e.g., neurological or autoimmune disease, such
PT as rheumatoid arthritis or asthma, or kidney- or testis-related
PT carcinoma.
XX
PS Disclosure; SEQ ID NO 1; 14pp; Chinese.
XX
CC The present invention relates to a new isolated IL-17RLM polynucleotide.
CC The polynucleotide encoding the IL-17RLM polypeptide is useful in
CC preparing a composition for treating an individual in need of an
CC increased or decreased level of IL-17RLM polypeptide, e.g. neurological
CC or autoimmune disease, such as rheumatoid arthritis or asthma, or kidney-
CC or testis-related carcinoma. The present sequence represents human IL-
CC 17RLM DNA.
XX
SQ Sequence 4477 BP; 1133 A; 1086 C; 1141 G; 1117 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 4477
Score: 3908.00 Matches: 732
Percent Similarity: 99.5% Conservative: 2
Best Local Similarity: 99.2% Mismatches: 4
Query Match: 13 Indels: 0
DB: 13 Gaps: 0
US-10-616-788-2 (1-738) x ADW23599 (1-4477)
QY 1 MetAlaProTyrLeuGlnLeuCysSerValPhePheThrValAlaAlaCysLeuAangly 20
DB 90 ATGGCCCCGCGGCTGACGCTCTGCTCCGCTCTTTACGATCAACGCTCTCAACGGC 149
QY 21 SerGlnLeuAlaValAlaAlaGlyGlySerGlyArgAlaTrpGlyValAlaAspThrCysGly 40
DB 150 TCGCACTGGCTGTGGCCGCTGGCGGGGTCCGGCCGCGGGGAGCCGCACTGTGGC 209

QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLeuTyr 60
DB 210 TGGAGGGGAGGTGGGGCCACCCAGCAAGAACAGTGGCTGTACACACTTCCTCAATAT 269
QY 61 AspAsnCysThrThrTyrLeuAsnProValGlyValHisValIleAlaAspAlaGlnAsn 80
DB 270 GACAAATTGTACCACTTACTGAATCCAGTGGGAGCATGTGATCTGACCGCCCAAAAT 329
QY 81 IleThrIleSerGlnTyrAlaCysHisAspGlnValAlaValThrIleLeuTyrPsrPro 100
DB 330 ATCAACCATCAGCAGATATCTTGCACATGACCAAGTGGCGTCACTTCTTGGTCCCA 389
QY 101 GlyAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGlnGluLeuLeuSer 120
DB 390 GGGGCGCTCGGATCGAAATCTCTGAAGAGATTTCCGGTAAATCTGAGAGAGCTGAAGTGG 449
QY 121 GlnGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe 140
DB 450 GAGGGAAGACAGTGGCCAACTGATTTAAAGATCCGAAAGCACTCAACAGTACCTTC 509
QY 141 LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGluThrAspTyrPhe 160
DB 510 AAAAGAACTGGAAATGGAATCTCAACCTTCTCGAAATATGAAATTGGAACGGAATTATTC 569
QY 161 ValLysValValProPheProSerIleLysAsnGlnSerAsnTyrHisProPhePhePhe 180
DB 570 GTTAAGGTGTCCCTTTCTTCTTCAATTAAAGCAAGAACTTACCACTTCTTCTTT 629
QY 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPheTyr 200
DB 630 AGAACCCGAGCCTGTGACCTGTGTGACAGCGGACAACTAGCTGTGAACCTTCTG 689
QY 201 LysProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis 220
DB 690 AAGCCTCGGAACCTGAACATCAAGCCAGTGGCTCGAATGAGGTGTCCTTCGACCA 749
QY 221 AlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrTyrLeuLysHisGlnGly 240
DB 750 GCAACGCAACAATTGGCTTCCCTTCTTCTTCACTTCACTCAAGCTCAAGCAAGAGA 809
QY 241 ProPheLysArgLysThrCysLysGlnGlnGlnThrGlnThrThrSerCysLeuLeu 260
DB 810 CCTTCAAGCAAGAACTGTGACGAGCAAGCAAACTACAGATGACAGTGGCCCTT 869
QY 261 GlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrArg 280
DB 870 CAAAATGTTTCTCAGAGGAGATTATATATGAGCTGGTGGATGACATTAACAACAAGA 929
QY 281 LysValMetHisTyrAlaLeuLysProValHisSerProTyrAlaGlyProIleArgAla 300
DB 930 AAGATGATCATTTATGCTTTAAAGCCAGTGCCTCCCGTGGGCGGGCCATCAAGGCC 989
QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
DB 990 GTGGCATCAGAGTGCATCTGGATGATGATGCGGATTCGCGAGCTTCACTGTGATG 1049
QY 321 CysArgLysLysGlnGlnGlnLeuIleTyrSerHisLeuAspGlnGlnSerSerGlnSer 340
DB 1050 TGCCTGCAAGAACCAACAAATAATATATTTCACTTGAAGAAAGAGCTCTGAGTGT 1109
QY 341 SerThrTyrThrAlaAlaLeuProArgGlnArgLeuArgProArgProArgValPheLeu 360
DB 1110 TCCACATACCTGGACATCTCCCAAGAGAGAGCTTCGCGCGCCCAAGTCTTCTTC 1169
QY 361 CysTyrSerSerLysAspGlyGlnAsnHisMetAsnValValGlnCysPheAlaTyrPhe 380
DB 1170 TGTATTTCAAGTAAGATGAGCCAGATCACTAAGATGTGTCAAGTGTTCGCTACTTC 1229
QY 381 LeuGlnAspPheCysGlyCysGlyValAlaAlaLeuAspLeuTyrGlnAspPheSerLeu 400
DB 1230 CTCACAGACTCTGTGGCTGTGAGGTGCTTGCACCTGTGGGAAGACTTCAAGCCCTGT 1289

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QY 401 ArgGluGlyValArgGluTrpValIleGlnIleValIleHisGluSerGlnPheIleIleVal 420
DB 1290 AGGAGAGGCGAGAGAAATGGTCAATCCAGAAATCCAGATCCCAAGTTCAATCATTTG 1349
QY 421 ValCysSerIleValIleValIleValIleValIleValIleValIleValIleVal 440
DB 1350 GTTGTGTTCCAAAGATGAAATGATCTTTGTCAGCAAGAAATCAACAACCAAGAGGT 1409
QY 441 GlyAlaGlySerGlyIleValIleValIleValIleValIleValIleValIleVal 460
DB 1410 GGCCTGGGCTCGGAGAAAGAGAGCTCTTCTGCTGGCTGTCAGCAATTCGCGTCACTT 1469
QY 461 LeuArgGlnAlaIleValIleValIleValIleValIleValIleValIleValIleVal 480
DB 1470 CTCCGCGAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1529
QY 481 AspTyrSerCysGluGlyValIleValIleValIleValIleValIleValIleVal 500
DB 1530 GATTATTCCTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1589
QY 501 MetAspAsnLeuProGlnLeuValIleValIleValIleValIleValIleValIleVal 520
DB 1590 ATGCAAAATCTTCTCAGCTCTGTTCCACCTGCACTCCGAGAGAGAGAGAGAGAGAG 1649
QY 521 ProGluGlnIleValIleValIleValIleValIleValIleValIleValIleVal 540
DB 1650 CCGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1709
QY 541 SerLeuTyrValAlaIleValIleValIleValIleValIleValIleValIleVal 560
DB 1710 TCCCTATAGCTGCTCCCTTTCAGACATGCACTTTATTCAGAGAGAGAGAGAGAGAG 1769
QY 561 GluValGlnPheValIleValIleValIleValIleValIleValIleValIleVal 580
DB 1770 GAAAGCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1829
QY 581 LysPheAspSerGlyLeuValIleValIleValIleValIleValIleValIleVal 600
DB 1830 AAATTTGATTCGGGCTGTTTAAATGATGATGCAAAACAGAGGCTGAGAGAGAGAG 1889
QY 601 PheCysLeuValIleValIleValIleValIleValIleValIleValIleValIleVal 620
DB 1890 TTCTGCTTAAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1949
QY 621 GluSerGlnIleValIleValIleValIleValIleValIleValIleValIleVal 640
DB 1950 GAGAGTCAGCATGGGAGGCTGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2009
QY 641 AlaAlaIleValIleValIleValIleValIleValIleValIleValIleValIleVal 660
DB 2010 GCGGCTCTCAACCTCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2069
QY 661 AspSerGlyIleValIleValIleValIleValIleValIleValIleValIleVal 680
DB 2070 GACTCAGGAGCTTAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2129
QY 681 GlyLeuSerThrAspGlnThrGlnThrSerSerSerLeuThrGluSerValSerSerSer 700
DB 2130 GGACTCTCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2189
QY 701 GlyLeuGlyValIleValIleValIleValIleValIleValIleValIleValIleVal 720
DB 2190 GGCCTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2249
QY 721 LysAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
DB 2250 AAAGCAATCTTGTGTGCGAGCTCACTGATGAACCTCCAGCGGTCGCCCT 2303

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RESULT 6
ABA95031
ID ABA95031 standard; DNA; 2383 BP.
XX
AC ABA95031;

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XX 20-MAY-2002 (first entry)
DT
XX Human cytokine receptor, Zcytor18 nucleotide sequence.
DE
XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;
XX erythroleukemia; chromosome 3p14.3; gene therapy; de.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 86..2347
FT /tag= "a
FT /product= "Zcytor18"
FT
XX
PN W0200208259-A2.
PD
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-US023253.
XX
XX 26-JUL-2000; 2000US-0220747P.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Presnell SR, Kuestner RE, Gao Z,
XX
XX WPI; 2002-217048/27.
XX
XX P-PDSB; ABB07626.
XX
XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
XX
XX Claim 5; Page 85-90; 119pp; English.
XX
XX
XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumor growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial
XX periodic fever and erythroleukemia, and erythroleukemia associated with
XX CC polymorphisms of cytokine receptors. The present sequence represents a
XX human Zcytor18 nucleotide sequence
XX
SQ Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 U; 0 Other;

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Alignment Scores:

Pred. No.: 0 Length: 2383
 Score: 3901.00 Matches: 734
 Percent Similarity: 97.7% Conservative: 1
 Best Local Similarity: 97.6% Mismatches: 3
 Query Match: 98.8% Indels: 14
 DB: 6 Gaps: 1

US-10-616-788-2 (1-738) x ABA95031 (1-2383)

```

QY 1 MetAlaProTrpLeuGlnLeuValIleValIleValIleValIleValIleValIleVal 20
DB 86 ATGGCCCGAGGCTGAGCTCTGCTCTCTTTCAGTCAAGCCCTGCTCAACGCG 145
QY 21 SerGlnLeuAlaValAlaIleValIleValIleValIleValIleValIleValIleVal 40
DB 146 TCGCAGCTGCTGTGGCGGCTGCGCGGCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCG 205
QY 41 TrpArg-----GlyValGlyPro 46

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|||||
Db      206  TCGAGAGATGAAGCGGCTGCCGACCCCGCTTGTGTTGCTAATGAGGAGTGGGGCCA 265
Qy      47  AAsarArgAsnserrglYleuYrAenlleThrPheYerYrApsenCySrrThrTrYr 66
Db      266  GCCAGCGAAGAAAGTGGCTGTCAACATCACCTTCAAAATATGACAATTTATCCACCTTAC 325
Qy      67  LeuAsnProValglYlysh:sval11ealAspAlaglnAsnilleThr11eserGlnYr 86
Db      326  TTGAATCCAGTGGGGAGAGCATGTGATGTCGAGCCCAAGAAATATCACCACTCACCGCAT 385
Qy      87  AlaCyshAspGlnValAlaVal1Thr11eLeu1TrSerProglYalAleuglY11eglu 106
Db      386  GCTTGCATGACCAAGGCGAGTCCATTCCTTGGTCCCCAGGGGCGCTCGGCATCGAA 445
Qy      107  PheLeu1yglYpheaArgVal111eleuGlugluLeuYserGlnYalYargGlnYnYsgln 126
Db      446  TTCCTGAAGAGATTTCCGTAATATCTGGAGAGACTGAAGTGGAGGGAGACAGTGGCAA 505
Qy      127  GlnLeu111eleuYsAspProLYsGlnLeuAsnSerSerPheYsArgThrglYmetGlu 146
Db      506  CAATCATTTTAAAGATCCGAAGCAGCTCAACATGCTTCAAAAGACTGGAAATCGAA 565
Qy      147  SerGlnProPheLeuAsnMetLYsPheGluThrAspYrPheValYVal1ProPhe 166
Db      566  TCTCAACCTTTCCTGAATATGAATTTGAACGGAATTTCCGTAAGGTTGCCCTTTT 625
Qy      167  ProSer111eYsAsnGlnUserAemYrH1eProPhePhePheArgThrArgAlaCyAsp 186
Db      626  CTTTCATTTAAAGACAAAGCAATTCACACCTTTCTTTTGAACCCAGGCTGTGAC 685
Qy      187  LeuLeuLeuGlnProAspAsnLeuAlaCyelysProPheTrpLYsProArgAsnLeuAsn 206
Db      686  CTCTTTTACAGCCGCGACATCTAAGCTTGTAAACCTTTCGAAAGCTCGGAACCTGAAC 745
Qy      207  11SerGlnH11sg1YserAspMetGlnVal1SerPheAspH11sAlaProH11sAsnPheGly 226
Db      746  ATCAGCAGCATGAGCTCGGACATGAGAGTGTCTTTCGACCATGACACGCGCAACTTCGCG 805
Qy      227  PheArgPhePheYrYleuH1sYrYlybLeuYsh11sg1ug1YProPheLYsArgLYsThr 246
Db      806  TTCCGGTTTCTTCTATCTTCACTACAGCTCAACAGCACAAAGACCTTTCAGCCAAAGACC 865
Qy      247  CyelysGln1ug1nThrThrg1uThrThrSerCyelysLeuGlnAsnVal11serProGly 266
Db      866  TGTAAAGAGAGCAAACTACAGAGACGACGCTCTCTTCAAAATGTTTCTCCAGGG 925
Qy      267  AspYr11e11eg1uLeuValAspAspThrAsnThrThrArgLYsVal1MetH1sYrYAla 286
Db      926  GATTATATATTTGAGCTGGTGATGACACTAACACAAAGAAAGTGCATTTATGCC 985
Qy      287  LeuLYsProValH11sSerProTrpAlag1YPro11eArgAlaMetAla11eThrValPro 306
Db      986  TTAAACCCAGTGCATCCCGTGCGCGCGGCCCATCGAGCCGTCGATCAACAGTGGCCA 1045
Qy      307  LeuValVal111eserAlaPheAlaThrLeuPheThrVal1MetCyAsArgLYsLYsGln 326
Db      1046  CTGGTATGCTATTCGGCATTCGCGAGCTCTTCACTGTATGTGCGCAAGAAAGCAACAA 1105
Qy      327  GlnAsn11eYrSerH1sLeuAspGln1uSerSerGlnYserSerThrYrThrAla11a 346
Db      1106  GAAATATATATATTCACATTTAAGATGAAGAGAGCTGTAGTCTTCCACATACCTGACGA 1165
Qy      347  LeuProArgGluArgLeuArgProArgProLYsVal1PheLeuCYsYrYrSerSerLYsAsp 366
Db      1166  CTCGCCAAGAGAGGCTCCGCGCGCGCGCGCGAGAGTCTTCTCTGTGCTAATTCAGATAAGAT 1225
Qy      367  G1YGLAsnH1sMetAsnVal11GlnCybPheAla1YrPheLeuGlnAspPheCyAsGly 386
Db      1226  GGCCAGATTCATGAATGTGTCAGGTGTTGCTTACTTCTCCAGGACTTGTGGC 1285
Qy      387  CybGluValAlaLeuAspLeuTrpGluAspPheSerLeuCyAsArgGln1ug1nArgGlu 406
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Db      1286  TGTAGGTGCTCTTGCAGCTGTGGAGAGACTTCAGCTCTGTATAGAGAGGACAGAGAA 1345
Qy      407  TrpVal111eGlnLYs11eH1sg1UserGlnPhe11eVal1Val1CyserSerLYsYmet 426
Db      1346  TGGGTATCCAGAAAGATTCACAGAGTCCAGTTTCATATGTGTGTTTGTTCAAAGGTAAAG 1405
Qy      427  LYsYrPheVal1AspLYsAsnYrLYsH1sLYsGlyGlyGlyYArgGlyserGlyLYs 446
Db      1406  AGTACTTTGTGGACAAAGAAACTACAAACAAAGAGAGGTGGCGGAGCTCGGGGAAA 1465
Qy      447  G1YGLuLeuPheLeuValAlaVal1serAla11eAlagluLeuArgGlnAlaLYsGln 466
Db      1466  GAGAGCTTCTCTGTGTGGCGGTGTCCAGCATTTCCGAAAGCTTCGCAAGGCGCAAGCAG 1525
Qy      467  SerSerSerAla1aleuSerLYsPhe11eAlaVal1YrPheAspYrYrSerCybGlnY 486
Db      1526  AGTTGTCGCGGCGCTTCAGCAAGTTATTCGCGCTTACTTTGATTTATTCCTGCGAGGGA 1585
Qy      487  AspVal1ProGly111eLeuAspLeuSerThrLYsYrArgLeuMetAspAsnLeuProGln 506
Db      1586  GAGTCCCGGATATCTTACAGCTGAGTACCAAGTACAGCTATGGACATCTTCTCTCAG 1645
Qy      507  LeuCySerH1sLeuH1sSerArgAspH1sGlyLeuGlnGluProGlyGlnH1sThrArg 526
Db      1646  CTCTGTTCACATTCGACTCCCGAGACACAGGCTTCAGAGACCCGGGCGAGCACAGCGGA 1705
Qy      527  GlnLYsSerArgArgAsnYrPheArgSerLYsSerGlyArgSerLeuYrValAla11e 546
Db      1706  CAGGGCAGCAAGAAAGTACTTCCGAGCAAGTCAAGGCGGCTCTTATACCTCGGCATT 1765
Qy      547  CyAsnMetH1sGlnPhe11eAspGln1uProAspTrpPheGluLYsGlnPheVal1Pro 566
Db      1766  TCGAATCATCACAGTTTATTGACGAGAGCCGAGCTGTTTGAAAGAGATTCGTTCCC 1825
Qy      567  PheH1sProProLeuArgYrArgGluProVal1LeuGluLYsPheAspSerGlyLeu 586
Db      1826  TTCCATCTCTCTTCCACTGTGCTACCGGAGCCAGTCTTGAGAAATTTATTCGCGGCTTG 1885
Qy      587  Val1LeuAsnAspVal1MetCyelysProGlyProGlnUserAspPheCyelysVal1Glu 606
Db      1886  GTTTAAATGATGTCATGTGCAACAGGAGCTGAGAGTGACTTCTTGCTTAAAGTTAGAG 1945
Qy      607  AlaProVal1leuGlyAlaThrg1YProAlaAspSerGlnH1sg1UserGlnH1sg1Ygly 626
Db      1946  GCGGCTGTTCTTGCGGCAACCGGACCGAGCTCCACACAGAGTCAAGCATGGGGGC 2005
Qy      627  LeuAspGlnAspGlyGluAlaArgProAlaLeuAspGlySerAla11eLeuGlnProLeu 646
Db      2006  CTGACCAAGAGCGGGAGGCGCGGCTGTGACGTTGACGTTAGCGCGCCCTGCAACCCCTG 2065
Qy      647  LeuH1sThrValLYsAlag1YserProSerAspMetProArgAspSerGly11eYrAsp 666
Db      2066  CTGCACAGGTGAAGACCGGAGCGCTCTCGACATGCCGGAGACTCAAGACATCTATAGAC 2125
Qy      667  SerSerVal1ProSerSerGlnYserLeuProLeuMetGln1YleuSerThrAspGln 686
Db      2126  TGGTGTGTCCTTCATCCGAGGCTGTCTCGCCATGATGAAGACTTCGACGAGCAAG 2185
Qy      687  Thrg1uThrSerSerLeuThrg1uSerVal1SerSerSerSerGlyleuGlyGluGlu 706
Db      2186  ACAAGAAAGCTTTCCTTGCAGAGAGCGAGTGTCTCTTTCAGGCGCTGGGTGAGAGAA 2245
Qy      707  ProProAlaLeuProSerLYsLeuLeuSerSerGly11eCybLYsAlaAspLeuGlyCYs 726
Db      2246  CTTCTGCGCTTCTTCCAAAGCTCTCTTCTTGGGGTCAAGCAAGACATCTTGTTGC 2305
Qy      727  ArgSerYrThrAspGluLeuH1sAlaValAlaPro 738
Db      2306  CGAGCTTACATGATGAATCTCAACGCGGTGCGCCCT 2341
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RESULT 7
ABA95033
ID ABA95033 standard; DNA; 2383 BP.


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QY 387 C Y E G I L V A L A L e u a b p l e u t r p g l u a s p h e s e r l e u c y a r g l u g l i n a r g l u 406
DB 1286 T G T G A G G T G C T C T G A C C T T G G G A A G A C T T C A G C C T C T G T A G A A G G G C A G A G A A 1345
QY 407 T T P V A I I l e g l u y s l i e h i g l u s e r g l n p h e i l e i l e v a l C y s e r l y g l y m e t 426
DB 1346 T G G G T C A T C C A G A A G A C C A G A G T C C A G T T C A T C A T T G G T T G T C C A A G A G T A T G 1405
QY 427 L y e T y P h e V a l A b p l y s l y a n t y r l y e h i a l y a g l y g l y a r g l y s e r g l y l y s 446
DB 1406 A A G A C T T T T G G C A A A G A A C T A C A A C A A A G A G T G C C A G G C T C G G G A A A 1465
QY 447 G l y g l u l e u p h e u v a l a v a l s e r a l i l e a l a g l u l y l e u a r g l n a l y l e g l n 466
DB 1466 G A G A G C T T C T C G T G G G C G T C A G C C A T T G C C A A A A G C T C C C C A G G C C A G C A G 1525
QY 467 S e r S e r S e r A l a l e u s e r l y p h e i l a l a v a l y r p h e a p r y s e r C y s g l u g l y 486
DB 1526 A G T T C G T C C G G G C T C A G C A A G T T A T G C C G T C A C T T G A T T A T T C T C G A G A G G A 1585
QY 487 A a p V a l P r o g l y l l e l e u a b p l e u s e r t h r l y e t r a r g l e u e t a p a n t l e u p r o g l n 506
DB 1586 G A G G T C C C G G T A C C T A G A C C T A G A C A A G A C A C T C A T G A C A A T C T T C C T C A G 1645
QY 507 L e u C y s e r h i s t r e u h i s e r a r g a s p h i g l y l e u g l n g l u p r o g l y g l n h i s t h a r g 526
DB 1646 C T C T G T T C C A C C T G C A C T C C C A G A C C A G G C C T C C A G A A G C G G G G C A G C A C C G A 1705
QY 527 G l n g l y s e a r g a r g a n t y r p h e a r g s e r l y s e r g l y a r g s e r l e u t y r v a l a l i l e 546
DB 1706 C A G G G A G C A G A A G A A C T A C T T C C G A G A C A G C A G C C G G T C C C A T A C G T C G C A A T T 1765
QY 547 C y a a m e r h i g l n p h e i l e a b p l u g l u p r o a s p r t p h e g l u l y s g l n p h e v a l p r o 566
DB 1766 T G G A C A T G A C A G A T T A T T A C A G A G A C C C A C A C T G T T C A A A A G A C A T T C G T C C C 1825
QY 567 P h e i s p r o p r o b l e u a r g t y r a r g l u p r o v a l l e u g l u l y p h e a s p e r g l y l e u 586
DB 1826 T T C A A C T C T C C A C T G C C C T A C C G G A C C A G T C T T G A A A A T T G A T T C G G C T T G 1885
QY 587 V a l l e u a b a p v a l m e c y s l y s p r o g l y p r o g l u s e r a p h e c y l e u l y s v a l g l u 606
DB 1886 G T T T T A A T G A T G A T G T C A A A C C A G G C C T G A G A G T A C T T G C C T A A A G T A G A G 1945
QY 607 A l a p r o v a l l e u g l y a l t h r g l y p r o a l a a s p e r g l n h i g l u s e r g l n h i g l y l y 626
DB 1946 G C G G C T G T T C T T G G G A C C G G A C C A G C C A C T C C A G A C A G A G T C A G A T G G G G G C 2005
QY 627 L e u a s p g l n a s p g l y g l u a l a r g p r o a l a l e u a b p l y s e r a l a l a l e u g l n p r o l e u 646
DB 2006 C T G G A C C A A A C G G G A G C C C G C C T T G A C G T A G C C C C C C C T G C A A C C C C T G 2065
QY 647 L e u h i e t h r v a l l y s a l a g l y s e r p r o s e r a s p m e r p r o a r g a s p e r g l y l e t y r a s p 666
DB 2066 C T G C A C A C G G T G A A A G C C G C A C C C C T C G A C A T G C C G G G A C T C A G C A C T A C T A T G A C 2125
QY 667 S e r S e r V a l P r o s e r S e r g l u s e r l e u p r o l e u m e t l u l y l e u s e r t h r a p g l n 686
DB 2126 T C G T C T G T G C C C A T C C G A G C G T C T C T C C A C T A T G A A G A G A C T T G A C G A C C A G 2185
QY 687 T h r g l t h r s e r S e r l e u t h r g l u s e r V a l s e r S e r S e r g l y l e u g l y g l u g l u g l u 706
DB 2186 A C G A A A C G T T C C C T G A C G A A G C G T C T C T C C T T C A G G C C T G G T G A G A G A A 2245
QY 707 P r o p r o a l a l e u p r o s e r l y s l e u s e r S e r g l y s e r C y s l y s a l a a p l e u g l y C y s 726
DB 2246 C C T C G C C C T C T C T C C A G C C T C T C T T T G G G T C A G C A A A G A G A C A T T T G G T T G C 2305
QY 727 A r g s e r t y r t h r a p g l u l e u h i a l a v a l a p r o 738
DB 2306 C G C A G C T A C T A T G A A C T C C A C G G C G C C C C T 2341

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RESULT 8

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ABK62082
ID ABK62082 standard; cDNA; 4392 BP.
XX
AC ABK62082;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human cDNA encoding novel secreted protein LP253.
XX
KW Human; ss; gene; secreted protein; cancer; autoimmune disease; arthritis;
KW osteoporosis; Alzheimer's disease; Parkinson's disease; meningitis;
KW encephalitis; neoplasia; trauma; ischemia; infection; mania; stroke;
KW cardiovascular disease; atherosclerosis; sepsis; anaemia;
KW rheumatoid arthritis; hypothyroidism; allergic response; liver failure;
KW multiple sclerosis; haemorrhage; paranoia; obsessive compulsive disorder;
KW autism; panic disorder; learning disability; feeding disorder;
KW sleep pattern disorder; balance; perception; Th1-dependent insulinitis;
KW adult respiratory distress syndrome; ARDS.
XX
OS Homo sapiens.
XX
PN WO200214358-A2.
XX
PD 21-FEB-2002.
XX
PF 30-JUL-2001, 2001MO-US021124.
XX
PR 11-ANG-2000; 2000US-0224642P.
XX
PR 19-OCT-2000; 2000US-0241779P.
XX
PA (ELIL) LILLY & CO ELL.
XX
PI Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;
XX WPI; 2002-304057/34.
XX DR P-PSDB; AAU91330.
XX
PT Novel polypeptides and polynucleotides of secreted proteins useful for
PT treating various diseases such as multiple sclerosis, cancer, autoimmune
PT diseases, osteoporosis, Alzheimer's disease and Parkinson's disease.
XX
XX Claim 1; Page 166-171; 235pp; English.
XX
XX The invention relates to a novel human secreted polypeptide having
XX sequence 90% identical to the polypeptide sequences of LP105, LP61,
XX LP224, LP240, LP239(a), LP243(a), LP243(b), LP253, LP218), LP251(a),
XX LP252, LP239(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP255(b), or
XX LP223(b). Also included are the nucleic acids encoding the LP proteins
XX (including complement, fragments encoding mature forms of the polypeptide
XX or variant), a vector comprising the nucleic acid, a host cell comprising
XX the vector, the preparation of the protein, an anti-LP antibody,
XX ant/agonists of LP and anti-LP-encoding mRNA ribozymes. The secreted
XX protein or its agonist is useful in the manufacture of a medicament for
XX treating a mammal suffering from a disease (and in diagnosis), condition
XX or disorder associated with aberrant levels of the secreted protein e.g.
XX cancer, autoimmune diseases, arthritis, osteoporosis, Alzheimer's
XX disease, Parkinson's disease, meningitis, encephalitis, neoplasia,
XX trauma, ischemia and infection, mania, stroke, cardiovascular disease,
XX atherosclerosis, rheumatoid arthritis, hypothyroidism, anaemia, sepsis,
XX allergic response, multiple sclerosis, liver failure, haemorrhages,
XX paranoia, obsessive compulsive disorder, autism, panic disorder, learning
XX disability, ALS (amyotrophic lateral sclerosis) psychoses, disorders
XX in feeding, sleep patterns, balance, and perception. Th1-dependent
XX insulinitis, adult respiratory distress syndrome (ARDS). The secreted
XX protein is further useful for identifying compounds that bind to the
XX secreted protein. The present sequence encodes a novel secreted protein
XX of the invention
XX
SQ Sequence 4392 BP; 1125 A; 1050 C; 1101 G; 1116 T; 0 U; 0 Other;

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Alignment Scores: 0 Length: 4392
Pred. No.: 3857.00 Matches: 732

Percent Similarity: 98.8%
 Best Local Similarity: 98.7%
 Query Match: 97.7%
 DB: 6
 Conservative: 1
 Mismatches: 5
 Indels: 4
 Gaps: 0

US-10-616-788-2 (1-738) x ABK62082 (1-4392)

QY 1 MetAlProTleuGlnleuCySerValPhePheThrValAlaAlaGly 20
 DB 1 ATGGCCCGGCTGGAGCTCTGCTCCGCTCTTACGGTCAACGCTCCACAGGC 60
 QY 21 SerGlnleuAlaValAlaAlaGlySerGlyAArgAlaTrpGlyValaAptThrCyGly 40
 DB 61 TCCACACTGGCTGGCGCCGCTGGCGGGTCCGCGCGCGCGCGCCGACCTGGGC 120
 QY 41 TrpArgGlyValGlyProAlaSerArgApsSerGlyLeuTyraSerIleThrPheLeuTyr 60
 DB 121 TGGAGGGGAGTGGGGCCAGCCAGCAAGACAGTGGGCTGACCAATCATCTTCAATAT 180
 QY 61 AspArgCysThrThrThrThrLeuApsProValGlyValIleAlaAlaAlaGlnAps 80
 DB 181 GACAATTTGACCACTTAACTTGAATCCAGTGGGAGAGATGATGCTGAGCCCAAGAT 240
 QY 81 IleThrIleSerGlnTyraIaCySerApsGlnValAlaValThrIleLeuTrpSerPro 100
 DB 241 ATACACATCAGCCAGATGCTTGCATGACCAAGTGGCACTCACTTCTTGGTCCCA 300
 QY 101 GlyAlaLeuGlyIleGlnPheLeuLeuGlyPheArgValIleLeuGlnleuLeuSer 120
 DB 301 GGGGCGCTCGGCACTCAATCTGAAAGATTTCCGGGTATATCTGAGAGAGCTGAAGTGC 360
 QY 121 GlnGlyArgGlnCySerGlnleuIleLeuLeuApsProGlyLeuLeuApsSerPhe 140
 DB 361 GAGGAGAGACAGTGCACCAATCTGATTAAGATCCGAAAGCAAGCTCAACACTAGCTTC 420
 QY 141 LysArgThrGlyMetGlnSerGlnProPheLeuApsMetLysPheGlnThrAptTyPhe 160
 DB 421 AAAAGACCTGGATGGAATCTCAACCTTCTGAAATGAAATTTGAAACGATATTTTC 480
 QY 161 ValLysValValProPheProSerIleLysApsGlnSerApsThrIlePhePhePhe 180
 DB 481 GTAAAGTGTGCTCTTCTTCTTCAATTAAGAAAGCAATTAACACCTTCTTCTTCTT 540
 QY 181 ArgThrArgAlaCyApsPheLeuLeuGlnProApsPheLeuAlaCyValPProPheTrp 200
 DB 541 AGAAGCCGAGCTGTGACCTGTGTGTTACAGCCGGAACATCTAGCTGTAAACCTTCTG 600
 QY 201 LysProArgApsLeuApsIleSerGlnIleGlySerApsMetGlnValSerPheApsIle 220
 DB 601 AGGCTTCGGAACCTGAACATCAGCAGCATGGCTCGGACATGGAGTGTCTTCGACAT 660
 QY 221 AlaProIleApsPheGlyPheArgPhePheTyrlleuIleTyrlleuLeuValIleGlnGly 240
 DB 661 GACCCGCAACAATTCGGCTTCTTCTTCTTCACTTCACTCAAGCTCAAGCAAGAGGA 720
 QY 241 ProPheLysArgLysThrCyValSerGlnGlnGlnThrThrGlnThrSerCyValleu 260
 DB 721 CCTTTACAGGAAAGACCTGTAAAGAGGAACTTACAGAGAGCACTGCTCTCTT 780
 QY 261 GlnApsValSerProGlyApsTyrlleGlnleuValApsApsThrApsThrApsArg 280
 DB 781 CAAGATGTTCTCCAGGGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
 QY 281 LysValMetIleTyrlleuLeuLysProValIleSerProTrpAlaGlyProIleArgAla 300
 DB 841 AAAGTATGATTAATGCTTAAAGCAAGTCACTCCCGTGGGCGCGGCGCCATCAAGGCC 900
 QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
 DB 901 GTGGGCATCACTGAGCACTGTAGTATCATATCGGCAATTCGCAAGCTCTTCACTGTAG 960
 QY 321 CyAArgLysValSerGlnGlnIleTyrlleuSerIleLeuApsGlnGlnSerSerGlySer 340

DB 961 TGGCGAAGAGCAACAAGAAATATATATATATATATATATATATATATATATATATAT 1020
 QY 341 SerThrThrThrAlaAlaAlaLeuProArgLysGlnLeuArgProArgProArgValPheLeu 360
 DB 1021 TCCACATTAACCTGACACACTCCCAAGAGAGAGCTCCGCGCGCGGCGGCGGCTTCTC 1080
 QY 361 CySerSerSerLysApsGlyGlnApsIleMetApsValValGlnCyPheAlaTyPhe 380
 DB 1081 TGCATTTCCAGTAAATGAGCCAGAAATCAATGATGCTGCTCAAGTCTTCCGCTACTTC 1140
 QY 381 LeuGlnApsPheCyGlyCySerValAlaAlaLeuApsLeuTrpGlnApsSerLeuCy 400
 DB 1141 CTCACAGACTTCTGTGCTGTAGAGTGTGCTGTGACCTGTGGAGACATTCACCTCTGT 1200
 QY 401 ArgGlnGlyGlnArgLysTrpValIleGlnLysIleIleGlnSerGlnPheIleIleVal 420
 DB 1201 AGAAGAGGCGAGAAATGGGTCACTAGAAATCAGAGATCCAGATTCATCATTTG 1260
 QY 421 ValCySerSerLysGlyMetLysTyrlleuValApsLysApsThrIleLysGlyGly 440
 DB 1261 GTTGTTCAGAGATGATGATGATCTTGTGACAGAAAGATTAACAAACAGAGAGGT 1320
 QY 441 GlyArgGlySerGlyLysGlyLeuPheLeuValAlaValSerAlaIleAlaGlnLys 460
 DB 1321 GGGCGAGGCTCGGGAAGAGAGCTCTTCTGTGGCGGTGTCAAGCATTCGCGAAG 1380
 QY 461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyPhe 480
 DB 1381 CTCGCGCAGGCGCAAGAGAGTCTGTCGCGCGCTCAGAAAGTTATCCGCTACTT 1440
 QY 481 ApsTyrlleuSerCySerGlnLysApsValProGlyIleLeuApsLeuSerThrLysTyArgLeu 500
 DB 1441 GATTATTCCTGAGGAGAGAGCTCCCGGTATCTGACCTGATGACCAATGACAGATC 1500
 QY 501 MetApsApsLeuProGlnleuCySerSerIleLeuIleSerArgApsIleGlyLeuGln 520
 DB 1501 ATGACAAATCTTCCCTCAGCTGTTCCACTCTGCACTCCGAGACAGAGGCTCCAGG 1560
 QY 520 LysProGlyGlnIleThrArgGlnGlySerArgApsThrPheArgSerLysSerGly 539
 DB 1561 AGCGGGGATGACACAGGAGAGGAGGAGGAGAACTACTTCCGAGGCAAGTCAAG 1620
 QY 539 LysSerLeuTyrlleuAlaIleCyApsMetIleGlnPheIleApsGlnGlnProApsTrp 559
 DB 1621 CCGTCTCTTAACGTCGCAATTTGACAGTCACTTATGACAGAGAGCCAGCTG 1680
 QY 559 PheGlnLysGlnPheValProPheIleProProProLeuArgTyArgGlnProValIle 579
 DB 1681 GTTCGAAAGCACTTCTTCTTCTTCTTCACTCTTCACTGCGGTACGGGAGCACTT 1740
 QY 579 GlnLysPheApsSerGlyLeuValIleuApsApsValMetCyValPProGlyProGln 599
 DB 1741 GAGAAATTTGATTCGGGCTTGTGTTTAAATGATGATGATGATGATGATGATGATG 1800
 QY 599 ThrPhePheLeuLysValGlnApsProValIleGlnGlyAlaThrGlyProAlaApsSerGly 619
 DB 1801 TGACTTCTCTTAAGATGAGAGGCTGTCTTGTGGGAGAAACGAGCACTGCTTCCA 1860
 QY 619 MetLysSerGlnIleGlyGlyLeuApsGlnApsGlyGlnAlaArgProAlaLeuApsGly 639
 DB 1861 GACAGAGATCAGCATGGGGGCTTGAACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
 QY 639 LysAlaAlaLeuGlnProLeuLeuIleThrValLysValIleGlySerProSerApsMetPr 659
 DB 1921 TAGCGCGGCTGCAACCTCTGCTGCAACGAGGAAAGCGGAGGAGGAGGAGGAGGAGG 1980
 QY 659 ArgApsSerGlyIleTyrlleuApsSerValProSerSerGlnLeuSerLeuProLeuMet 679
 DB 1981 GCGGAGCTAGGAGATTAATGATCTGCTGTGCTTATCCAGCTGTCTCTGCACTGAT 2040
 QY 679 GlnGlyLeuSerThrApsGlnThrGlnThrSerSerLeuThrGlnSerValSerSerSe 699
 DB 2041 GAAAGACTTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2100

QY 699 rsergylleuglglupproalaaleuproserlyleuenseergerglyse 719
 DB 2101 rtagagcttgagagagaaacctctgacctcttccaaagctctctcttgagctc 2160
 QY 719 rcylyalaaapleuglycyaragerlyrthaspglyleuhsialaValaapro 738
 DB 2161 atccaaagcagacttggttgccgacactacatgaagaaCTCAGCGGTCCGCCCT 2218
 RESULT 9
 AAS18134
 ID AAS18134 standard; cDNA; 2786 BP.
 AC AAS18134;
 XX 26-MAR-2002 (first entry)
 DT Human DNAX cytokine receptor subunit 8 (DCRS8) cDNA.
 XX Human DNAX cytokine receptor subunit 8; DCRS8: phosphate labelling; ss;
 KM Human; DNAX cytokine receptor subunit 8; DCRS8: phosphate labelling; ss;
 KM gene therapy; protein therapy; immunological disorder.
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS /tag= a /product= "Human DCRS8"
 FT
 FT MO200190358-A2.
 XX 29-NOV-2001.
 PD 23-MAY-2001; 2001MO-US016767.
 XX 24-MAY-2000; 2000US-0206862P.
 PR (SCHE) SCHERING CORP.
 PA Gorman DM;
 PI WPI; 2002-106198/14.
 XX P-PSDB; AAU11355.
 DR
 DR
 XX
 XX
 PT Isolated antigenic human or mouse DNAX receptor subunit-like polypeptide
 PT useful for detecting antibodies generated in response to presence of
 PT increased protein levels or immunological disorders.
 CC Claim 16; Page 21-25; 148bp; English.
 XX
 XX The invention relates to primate and rodent DNAX cytokine receptor
 CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The
 CC receptors, or their portions may be useful as phosphate labelling enzymes
 CC to label general or specific substrates. The subunits may also be
 CC functional immunogens to elicit recognising antibodies, or antigens
 CC capable of binding antibodies. A combination e.g., including a DCRS can
 CC be used as an immunogen for the production of antisera or antibodies
 CC capable of distinguishing between other cytokine receptor family members.
 CC A purified DCRS can also be used as a reagent to detect antibodies
 CC generated in response to the presence of elevated levels of expression,
 CC or immunological disorders which lead to antibody production to the
 CC endogenous receptor. This sequence represents cDNA encoding the human
 CC DCRS8 polypeptide
 XX
 SQ Sequence 2786 BP; 673 A; 760 C; 709 G; 637 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.: 0 Length: 2786
 Score: 3835.50 Matches: 722
 Percent Similarity: 98.2% Conservative: 3
 Best Local Similarity: 97.8% Mismatches: 12
 Query Match: 97.2% Indels: 1
 DB: 6 Gaps: 1

US-10-616-788-2 (1-738) x AAS18134 (1-2786)
 QY 1 MetAlaPProTfPLeuGlnLeuCySerValPhePheThValAlaAlaCybleuAengly 20
 DB 70 ATGGCCCGCTGGGTGAGCTGTCTCCGTCTTCTTACCGGTCAACCCCTGCCCAACGGC 129
 QY 21 serGlnLeuAlaValAlaIaGlySerGlyATGAlaTTPGlyValaAphThCySerGly 40
 DB 130 TCGCAGCTGCTGTGACCGCTGCGGAGTCCGGCCGCGCCGCGCCCAACCTTAC 189
 QY 41 TTPATGlyValGlyProAlaSerArgaenSerGlyLeuTyraenileThPheTy 60
 DB 190 TGGANGGAGGTGGGGCCAGCAGCAAGAAACATGGGCTGTACAACTCACTTCAATAT 249
 QY 61 AspaenCyThThTy 80
 DB 250 GACAAATGTATCCACTTATGATCCATGGGGAGACATGTATGTCTTACCGCCGAAT 309
 QY 81 ILeThrIleSerGlnTyraIaCySHsaapGlnValAlaValThrIleLeuTfPserPro 100
 DB 310 ATCACCATCAGCCAGTATCTGTGCAATGACCAAGTGGCACTCACTTGTGGTCCCA 369
 QY 101 GAlaIaLeuGlyIleGlnPheLeuLySGlyPheArgValIleLeuGlnGlnLeuLySer 120
 DB 370 GGGGCCCTGGCATGGAATTCGAAAGATTTCCGGTAAATCTGGAGAGGTGAAGTGG 429
 QY 121 GlnGlyArgGlnCySglnGlnLeuIleLeuLyAspProLyGlnLeuAenSerSerPhe 140
 DB 430 GAGGAGAGACAGAGCCCAACACTGATTTAAAGATCCCAACAGTCAAGTACCTTC 489
 QY 141 LyAsArgThGlyMecGlnSerGlnProPheLeuAenMetLyPheGlnThraPryPhe 160
 DB 490 AAAGAACTGAAATGGAATCTCACTTCTGATATGAAATTTGAAACGGAATTTATTC 549
 QY 161 ValLyValValProPheProSerIleLyAsaGlnSerAspTyriAsPhePhePhe 180
 DB 550 GTAAAG---TGTGCTTTCTCTTCACTTAAAGAAAGCAATTAACACCTTTCTTT 606
 QY 181 ArgThArgAlaCyAspLeuLeuGlnProAspLeuAlaCyLyAspProPhePhe 200
 DB 607 AGAAACCGAGCCGTGTACCTGTGTGTAACGGGCAACTGTGCTTGAACCTTCTG 666
 QY 201 LyPProArgAsnLeuAsnIleSerGlnIleGlySerAspMetGlnValSerPheAsp 220
 DB 667 AAGCCTGGAACTGTGAACATGACCAAGCATGGCTGGAATGAGGTGCTTCAACAC 726
 QY 221 AlaProHisAsnPheGlyPheArgPhePheTyTyLeuHisTyTyLeuLeuLySglnGly 240
 DB 727 GACCCGCAACCTTGGCTTCCGTTCTTCTTCACTTCACTTCAAGCTCAAGCAAGGA 786
 QY 241 ProPheLyArgLySerThCyLySglnGlnThThGlnThThSerCybleuLeu 260
 DB 787 CTTTCAACCGAAAGCTGTAAAGCAGAGCAAACTACAGATGACAGCTGCCCTCTT 846
 QY 261 GlnAsnValSerProGlyAspTyriIleGlnLeuValAspAspThraenThraArg 280
 DB 847 CAATAAGTTTCTCAGGGGAAATTAATTAATTAAGCTGTGATGACCTTACACACAA 906
 QY 281 LyValMetHisTyTyAlaLeuLyProValHisSerProTfPAlaGlyProIleArgAla 300
 DB 907 AAAGTATCATTAATTCCTTAAAGCCAGTCACTCCCGTGGGCGGCGCATCAAGCC 966
 QY 301 MetAlaIleThTyAlaProLeuValValIleSerAlaPheAlaThrLeuPheThValMet 320
 DB 967 GTGGCCATCAGATGCGCATGTGATGATCATATGCGCATTGGCAGCGCTTCACTGAGAG 1026
 QY 321 CyArgLyLyGlnGlnGlnLeuAsnIleTySerHisLeuAspGlnLeuSerSerGly 340
 DB 1027 TGGCGCAAGAGCAAGAAATATATATTCACATTATGATGAAGAGGCTGTGAGTCT 1086
 QY 341 SerThTyThraAlaLeuProArgGlnArgLeuArgProArgProLyValPheLeu 360

Db 1087 TCCACATACAGCTGACGACCTCCCAAGAGAGGCTCCGGCCGCGGCGCAAGTCTTTCTC 1146
 Qy 361 CgATrSerSerlysaaprglyglinaenhiemecanvalaiglnCyspheilaATyrPhe 380
 Db 1147 TGCATATCCAGTAAGATGCGACGAAATCACATGAAATGCTCCAGTCTTCCGCTTACTTC 1206
 Qy 381 LeuGlnaapPheCysgllyCysgllyValaIaleuapleuTrpGluapPheSerLeuCys 400
 Db 1207 CTCACGACCTTCTGTGCTGTAGTGGCTCTGACCTTGAGAGAGAGCTTCAAGCTCTGT 1266
 Qy 401 ArgGlnGlyGlnaarglurValaIleGlnlylehiaglyserGlnpheileilaVal 420
 Db 1267 AGAGAGGCGAGAGAAATGGGTCAATCCAGAAATCCACAGATCCCAAGTTCATCATTTGTC 1326
 Qy 421 ValCysSerlysegllywellytyrPheValaaplylyabnTytylyvhiaglyGly 440
 Db 1327 GTTGTGTCCAAGATGAAATGAACTTGTGTGACAAAGAAATCAAAACCAAGAGAGT 1386
 Qy 441 GLYArgGlySerGlylyGlnlyleuPheleuValaIaleuSerailaileaglylye 460
 Db 1387 GGCCTAGGCTCGGGGAAAGAGAGCTTCTGTGGCGGTGTCAGCCATTTGCCAAAG 1446
 Qy 461 LeuArgGlnaIalysegllyserSerailaIaleuSerlyspheilealaIalyrPhe 480
 Db 1447 CTCGCGCAGGCCAAGCAGATTCGTCCGCGCGCTCAGCAAGTTTATCCGCGTACTTT 1506
 Qy 481 AapTyTrSerCysgllysaapvalProGlyTyleuapleuSerThylytyrArgLeu 500
 Db 1507 GATTATTTCCCGCAGGAGAGAGTCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTC 1566
 Qy 501 MetAapapleuProGlnlyCysSerhiIleuhiIsearArgapRhiaglyleuGlnly 520
 Db 1567 ATGAGACATTTCTCCAGCTCTGTCTCCACCTGACTCCGAGACCAAGCCCTCCAGAG 1626
 Qy 521 ProGlyGlnhiIsthrArgGlnlyserArgArgabnTytyrPheArgSerlysegllyArg 540
 Db 1627 CCGCGGAGAGACACGCGACAGGCGAGAGAAAGAACTTCCGAGCAAGTCAAGCGCG 1686
 Qy 541 SerleuTyralaIaleCysaamMehiGlnpheileapgllyleuProapTrpPhe 560
 Db 1687 TCCCTATACGTCGACATTTGCAACATGACCAAGTTTATGACAGAGAGCCGACTGGTTC 1746
 Qy 561 GlnlyleGlnpheValProPhehiIProProProleuArgTytyrArgGluProvalleuGln 580
 Db 1747 GAAAGAGAGTTCCTTCCTTCATCTCCCTCCACTGGCTACCGGAGGCGAGCTTGGAG 1806
 Qy 581 LysPheAapSerGlyleuValleuAapAapValMetCyslyspProGlyProGlyserAap 600
 Db 1807 AAATTGATTCGGGCTTGGTTTAAATGATGTCAITGCAAAACAGGCGCTGAGAGTGAAC 1866
 Qy 601 PheCysleuTyralaIaleCysaamMehiGlnpheileapgllyleuProapTrpPhe 620
 Db 1867 TTCTGCTAAAGTAAGAGCGCGCTTCTTGGGCAACCGGACGAGCGACTCCAGCAC 1926
 Qy 621 GlnSerGlnhiaglyleuAapGlnaapGlyGlnaIaargProalaIaleuapGlySer 640
 Db 1927 GAAAGTCAAGATGGGGCTTGGACCAAGAGCGGAGGCGCTGCTTGGCGGTAGC 1986
 Qy 641 AlaAlaIleuGlnProleuLeuhiIsthrValaIaleGlyserProserAapMetProArg 660
 Db 1987 GCGGCGCTGCAACCTCTGCTGACACGCTGAAAGCCGCGAGCCCTTGGACATGCCCGG 2046
 Qy 661 AapSerGlyTyleTyraPseSerValProSerSerGlnleuSerleuProleuMetGln 680
 Db 2047 GACTCAGGAGTATGATCTGCTGTGCTCCCTCATCCGAGCTGTCTGCCACATGATGAA 2106
 Qy 681 GlyleuSerThrapGlnThrapGlnThrapSerSerleuThrapGlnSerValSerSerSer 700
 Db 2107 GGAATCTCGACGAGACCAAGAAACCTTCTCCCTGACGAGACGCGTCTCTCTTCA 2166
 Qy 701 GlyleuGlyGlnlyGlnlyProProalaIaleuProSerlyspheleuSerSerGlySerCys 720
 Db 2167 GGCTGCTGAGAGAGAACTCTGCGCTTCTTCCAGCTCTCTCTTCTGGGCTATGC 2226

Qy 721 LysAlaIleuGlnlyCysArgSerTytyrThrapGlnleuhiIaleValaIalePro 738
 Db 2227 AAAGCATCTTGTGTCGCGAGCTACCTGATGAATCTCCAGCGGCTGCGCCCT 2280
 RESULT 10
 AEB55653
 ID AEB55653 standard; cDNA; 2786 BP.
 AC AEB55653;
 XX
 XX 22-SEP-2005 (first entry)
 DT
 XX
 DE Human DCR8 polypeptide encoding cDNA.
 XX
 XX Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
 KM DCR8; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
 KM Interstitial lung disorder; asthma; allergy; atherosclerosis;
 KM Gastrointestinal-gen.; antiinflammatory; antiasthmatic; antiallergic;
 KM antipneumatic; antiarteriosclerotic; respiratory-Gen.; immunosuppressive;
 KM antidiabetic; DCR9 agonist; DCR9 antagonist; IL-17C antagonist;
 KM IL-17C agonist; human; DCR8; gene; ss; antisense therapy; RNAi therapy.
 OS
 XX Homo sapiens.
 FH
 FH Key Location/Qualifiers
 FT CDS
 FT /tag= b
 FT /product= "DCR8"
 FT /transl_except= (pos: 169..171, aa: Xaa)
 FT /transl_except= (pos: 193..195, aa: Xaa)
 FT /transl_except= (pos: 442..444, aa: Xaa)
 FT /transl_except= (pos: 475..478, aa: Xaa)
 FT /transl_except= (pos: 517..519, aa: Xaa)
 FT /note= "Xaa = unknown"
 FT sig_peptide 70..117
 FT /tag= a
 FT mat_peptide 118..2283
 FT /tag= c
 PN MO2005065711-A2.
 XX
 PD 21-JUL-2005.
 XX
 XX 22-DEC-2004; 2004MO-US042935.
 PF
 XX 29-DEC-2003; 2003US-00749144.
 PR
 XX (SCHER) SCHERING CORP.
 PA
 XX Gorman DM;
 PI
 XX WPI; 2005-506792/51.
 DR P-PSDB; AEB55654.
 XX
 PT Modulating activity of cell, involves contacting cell with an agonist or
 PT antagonist of DNAX cytokine receptor subunit.
 PS
 XX Example 5; SEQ ID NO 9; 130bp; English.
 CC The invention relates to modulating (M1) activity of cell, by contacting
 CC cell with an agonist or antagonist of DNAX cytokine receptor subunit
 CC (DCR9) or of interleukin (IL)-17C where the cell modulates psoriasis,
 CC inflammatory bowel disorder (IBD), interstitial lung disorder, asthma or
 CC allergy, or atherosclerosis. Also provided are methods for treating (M2)
 CC the disorders which involves administration of the modulator and
 CC diagnosing (M3) a disorder as mentioned above that involves contacting a
 CC sample from a test subject with a binding composition that specifically
 CC binds to a polypeptide or nucleic acid of DCR9 or IL-17C. (M1) is useful
 CC for modulating an activity of a cell. (M2) is useful for treating a
 CC subject suffering from a disorder such as psoriasis, IBD, interstitial
 CC lung disorder, asthma or allergy, or atherosclerosis, where the
 CC interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic

CC granuloma, or hypersensitivity pneumonitis. The IBID is Crohn's disease or
CC ulcerative colitis. The present sequence represents a human DKRS8
CC polypeptide encoding cDNA.

XX Sequence 2786 BP; 673 A; 760 C; 709 G; 637 T; 0 U; 7 Other;

Alignment Scores:

Pred. No.:	Length:	Matches:
Score:	3835.50	722
Percent Similarity:	98.2%	Conservative: 3
Beet Local Similarity:	97.8%	Mismatches: 12
Query Match:	97.2%	Indels: 1
DB:	14	Gaps: 1

US-10-616-788-2 (1-738) x AEB55653 (1-2786)

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QY 1 MetAlaProTrrLeuGlnLeuCySerValPhePheThrValAlaMetAlaCySLeuMetGly 20
Db 70 ATGGCCCCGTGGCTGAGCTCTGCTCCGTCCTTTACGGTCAACGCGCTCCACAGGC 129
QY 21 SerGlnLeuAlaValAlaAlaGlySerGlyValArgAlaTrpGlyValAspThrCySLeu 40
Db 130 TCGCAGCTGGCTGTGGCGGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 189
QY 41 TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLeuTyr 60
Db 190 TGGAGGAGATGGGGCCAGCCAGCAAGAAACAGTGGCTGTACAACTACCTTCAATAT 249
QY 61 AspAsnCySerThrThrTyrLeuAsnProValGlyValMetAlaValAlaAlaAlaAla 80
Db 250 GACAAATGTACCACTTCAATCCAGTGGGGAAGCATGTGATGCTGACGCCCAAGAT 309
QY 81 IleThrIleSerGlnTrrAlaCySAsnAlaValAlaValAlaValAlaValAlaValAla 100
Db 310 ATCAACATCAGCAAGATAGCTGTGCATGACCAAGTGGCAGCTACCATTTCTTGGTCCCA 369
QY 101 GlyAlaLeuGlyIleGlnPheLeuLeuGlyPheArgValIleLeuGlnGlnLeuLeuSer 120
Db 370 GGGGCCCTCGGCATCGAATTCCTGAAAGATTCGGGTATATCTGAGAGAGCTGAAGTGG 429
QY 121 GlnGlyValArgGlnCySLeuGlnLeuIleLeuValAspProLeuGlnLeuAsnSerPhe 140
Db 430 GAGGGAAGACAGAGCCCAACATGATCTTAAGGATCCGAAGCAAGTCAAGTACCTTC 489
QY 141 ValArgThrGlnIleMetGlySerGlnProPheLeuAsnMetLeuPheGlnIleAspTyrPhe 160
Db 490 AAAAGAACTGGAAATGGAAATCTCAACCTTTCGATATATGAATTTGAAGAGGATATATTC 549
QY 161 ValIleValValProPheProSerIleLeuAsnGlnSerAsnTyrIleAspPhePhe 180
Db 550 GTAAAG---TTGTCCTTTCTTCAATTAAAGCAAAATTACCAACCTTTCTTCTTT 606
QY 181 ArgThrArgAlaCySAspLeuLeuGlnProAspAsnLeuAlaCySLeuPhePheTyr 200
Db 607 AGAAGCCGAGCTGTGACCTGTGTATACAGCCGACAAATCTAGCTGTATAACCTTCTG 666
QY 201 LeuProAspAsnLeuAsnIleSerGlnIleGlySerAspMetGlnValIleSerPheAsn 220
Db 667 AACCCCTCGAAGCTGAACATGACGAGCATGGCTCGGACATGACGAGGTCTTCTGACAC 726
QY 221 AlaProIleAsnPheGlyPheArgPhePheTyrIleMetAlaTyrIleLeuLeuValIleGlnGly 240
Db 727 GCAACCCGACAACTTCGGCTTCGTTCTTCTTCACTTCACTCAAGCTCAAGCAGAGAGGA 786
QY 241 ProPheLeuValArgIleTyrCySLeuGlnGlnIleThrThrGlnIleThrThrSerCySLeuLeu 260
Db 787 CCTTTCAGGGAAGACCTGTAAAGCAGAGCAAACTACAGAGATGACCACTGCTCTTCT 846
QY 261 GlnAsnValSerProGlyLeuAspTyrIleIleGlnLeuValAspAspThrAsnThrThrArg 280
Db 847 CAAAAGTTTCTCAGGAGATTAATATATGAGCTGTGTGATGACATTAACACAAACAGA 906
QY 281 LeuValIleMetIleTyrAlaLeuLeuProValIleSerProTrrAlaGlyProIleArgAla 300

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Db 907 AAAGTATCATTAATCTTTAAAGCAGTGCATCCCGCTGGCCGAGCCCATCAAGGCC 966
QY 301 MetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMet 320
Db 967 GTGGCCATCAAGTGCAGTGTGATGATATGAGATTCGACAGGCTTTCATGTGAATG 1026
QY 321 CySArgLeuLeuGlnGlnIleLeuAsnIleTyrSerIleLeuAspGlnIleSerSerGlnSer 340
Db 1027 TGGCGAAGAGCAACAAAGAAATATATATTCATTAATGATGAAAGAGCTTGAGTCT 1086
QY 341 SerThrTyrThrAlaAlaLeuProArgGlnValGlnLeuValArgProArgProLeuValPheLeu 360
Db 1087 TCCACATACATGACGACATCCCAAGAGAGAGGCTCCGCGCGCGCGCAAGGCTTCTC 1146
QY 361 CySThrSerSerLeuAspGlnIleAsnIleMetAsnValValGlnCySAspAlaTyrPhe 380
Db 1147 TGCTATTTCCAGTAAATGAGCCAGAAATCAATGAATGTGTGTCAAGTTCGCTTCTTC 1206
QY 381 LeuGlnAspPheCySLeuValAlaLeuAspLeuTrpGlnAspPheSerLeuCyS 400
Db 1207 CTCACGACTTCTGTGGCTGTGAGTGTGCTTGACCTTGAGAGACTTCAGCTCTGT 1266
QY 401 ArgGlnGlyLeuArgGlnTrpValIleGlnIleIleGlnIleIleGlnIleIleVal 420
Db 1267 AGAGAAAGGCAAGAGAAATGGGTCAACAAGATCCAGAGTCCAGTTCATCATTTGTG 1326
QY 421 ValCySerLeuGlnIleMetIleTyrPheValAspLeuValAsnTyrIleIleValGly 440
Db 1327 GTTGTTCAAAGATATGAAGTATCTTGTGACAAAGAACTCAAAACAAAGAGGT 1386
QY 441 GlyArgGlySerGlyLeuGlnLeuPheLeuValAlaValSerAlaIleAlaGlnIle 460
Db 1387 GGGCGAGGCTCGGGGAAAGAGAGCTTCTGTGTGGCTGTGACCTTCGCAAAAG 1446
QY 461 LeuArgGlnAlaLeuGlnSerSerSerAlaAlaLeuSerLeuPheIleAlaValTyrPhe 480
Db 1447 CTCGCGCAGCCCAAGCAGAGATTCGTCCGCGGCGCTCAGCAAGTATTCGCCGTACTTT 1506
QY 481 AspTyrSerCySLeuGlnIleAspValProGlyIleLeuAspLeuSerThrTyrTyrArgLeu 500
Db 1507 GATTATTTCTGGAGGGAACGTCCTCCGGTATCTTGAAGCTTGAACAAAGTACAACTC 1566
QY 501 MetAspAsnLeuProGlnLeuCySerIleIleMetIleSerArgAspIleGlyLeuGlnIle 520
Db 1567 ATGCAAACTTCTCTGAGCTGTGTCCACCTGCACCTCCGAGACCAAGGCTTCCAGAG 1626
QY 521 ProGlyGlnIleThrArgGlnIleSerArgAsnTyrPheArgSerLeuSerGlyArg 540
Db 1627 CCGGGGCAACACACGCGCAGGAGGAGAGAGAACTACTCCGAGCAAGTCAAGGCCG 1686
QY 541 SerLeuTyrValAlaIleCySAsnMetIleGlnPheIleAspGlnIleProAspTrrPhe 560
Db 1687 TCCCTATAGCTGCGCAATTTGCAACATGACACAGTATTAATGAAGAGGCGCACTGGTTC 1746
QY 561 GlnIleGlnPheValProPheIleProProLeuArgTyrArgGlnIleProValIleGlnIle 580
Db 1747 GAAAGCAATTCCTTCTTCATCTCTCCATGCGGTACCGGAGGCAAGCTTGGAG 1806
QY 581 LeuPheAspSerGlyLeuValIleuAsnAspValMetCySLeuProGlyProGlnSerAsp 600
Db 1807 AATTTGATTCGGGCTGTGGTTTAATATGATGATGCAATGCAAAACAGGCGCTGAGAGTAC 1866
QY 601 PheCySLeuValValGlnAlaProValIleuGlyAlaThrGlyProAlaAspSerGlnIle 620
Db 1867 TTCTGTCTAAAGGTAGAGCGGCTGTCTTGGGGCAACCGGACCAAGCTCCAGCAC 1926
QY 621 GlnSerGlnIleGlyIleLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySer 640
Db 1927 GAGAGTCAACATGGGGCTGTGACCAAGAGCGGGAGGCGCGGCTTGAAGGTAGC 1986
QY 641 AlaAlaLeuGlnProLeuLeuIleThrValIleValGlySerProSerAspMetProArg 660

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Db      870 CAAAAGTTCTCCAGGGGATATATATGAGCTGGATGACATTAACACAAAGA 929
Qy      281 LysValMetHisIstYrAlaLeuLysProValHisSerProTPrAlaGlyProIleAla 300
Db      930 AAGGTATGATATGCTTAAAGCCAGTCACTCCCGTGGCGCCCATCAGGCC 989
Qy      301 MetAlIleThrValProLeuValIleIleSerAlaPheAlaThrLeuPheThrValMet 320
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Qy      321 CysArgLysLysGlnGlnGlnAmlIeTyrSerHisLeuApgLugIuseSerGlySer 340
Db      1050 TGC CGAAGAAGCAACAAGAAATATATATTCACATTAGTAGAAGAGACTCGAGTCT 1109
Qy      341 SerThrTyrThrAlaAlaLeuProArgGluArgLeuArgProArgPheValPheLeu 360
Db      1110 TCCACATACACTCAGACATCCCAAGAGAGGCTCCGGCCGCGCAAGGCTTTCTC 1169
Qy      361 CysTyrSerSerLysApgGlyGlnApmHisMetApmValIleGlnCysPheAlaTyrPhe 380
Db      1170 TGCCTATTCAGTAAAGATGCGCAATCACTGAATGCTGCTCCAGTCTTCGCTACTTC 1229
Qy      381 LeuGlnApgPheCysGlyCysGluValAlaLeuApgLeuTPrGluApgPheSerLeuCys 400
Db      1230 CTCACAGACTTCTGTGGCTGTGAGGTGGCTCTGGACCTGTGGAGACTTCAGCTCTGT 1289
Qy      401 ArgGluGlyGlnArgGluTPrValIleGlnLysIleHisGluSerGlnPheIleVal 420
Db      1290 AGAGAAAGGAGAGAGATGGTCTATCCAGAAAGATCCACAGATCCCATCATTTGTG 1349
Qy      421 ValCysSerLysGlyMetLysTyrPheValApgLysLysApmTyrLysHisLysGlyGly 440
Db      1350 GTTGTGTTCCAAAGTATGAGTACTTTGTGCAAGAAAGACTHCAAAACAAGAGAGGT 1409
Qy      441 GlyArgGlySerGlyLysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluLys 460
Db      1410 GCGCGAGGCTCGGGGAAAGAGAGCTCTCTGGTGGCGGTGTGACGCAATTCGCAAAAG 1469
Qy      461 LeuArgGlnAlaLysGlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPhe 480
Db      1470 CTCGCGCAGGCCAAAGAGAGTGTGTCGCGCGCTCGCAAGGTTTAACTCGCGCTACTTT 1529
Qy      481 AspTyrSerCysGluGlyApgValProGlyIleLeuApgLeuSerThrLysTyrArgLeu 500
Db      1530 GATTATTCCTGCGAGGAGAGCTCCCGGTATCTTAAGCTGAGTACCAAGTACAGACTC 1589
Qy      501 MetApgApmLeuProGlnLeuCysSerHisLeuHisSerArgApmHisGlyLeuGlnGlu 520
Db      1590 ATGGAACATCTTCCTCAGCTCTGTCCCACTGCACTCCGAGACCAAGGCTCCAGAG 1649
Qy      521 ProGlyGlnHisThrArgGlnGlySerArgArgApmTyrPheArgSerLysSerGlyArg 540
Db      1650 CCGGGGAGACACGCGCACAGGGGAGAGAACTTCCGAGCAAGTCAAGGCGCG 1709
Qy      541 SerLeuTyrValAlaIleCysApmMetHisGlnPheIleApgLugIuseProApmTPrPhe 560
Db      1710 TCCCTATACCTCGCATTTGCAACATGCAACAGTTTATTAAGAGAGCCGCACTGGTTC 1769
Qy      561 GluLysGlnPheValProPheHisProProLeuApgTyrArgGluProValLeuGlu 580
Db      1770 GAAGAAGAGTTGCTGCTCCATCTCCCTCACTGGGCTACCGGAGCCAGCTTGGAG 1829
Qy      581 LysPheApgSerGlyLeuValLeuApmApmValMetCysLysProGlyProGlySerApm 600
Db      1830 AATTTGATTCGGGCTTGTGTTTAAATGATGTCTATGTGCAAAACAGGCGCTGAGAGTGC 1889
Qy      601 PheCysLeuLysValGluAlaProValLeuGlyValaThrGlyProAlaApgSerGlnHis 620
Db      1890 TTTCGCTTAAAGTAAAGGCGGCTGTTCTTGGGGCAACCGGACCGGACTCCAGCAC 1949
Qy      621 GluSerGlnHisGlyGlyLeuApgGlnApgGlyGluAlaArgProAlaLeuApgLysSer 640

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Db      1950 GAGAGTCACAGTGGGGGCTGGACCAAGACGGGAGGCCCGGCTGCTTCAGCGTAGC 2009
Qy      641 AlaAlaLeuGlnProLeuLeuHisThrValLysAlaGlySerProSerApmMetProArg 660
Db      2010 GCGCCCTCAACCCCTGTGGACACGCTGAAGCCGAGGCCCTCGGACATGCGCGG 2069
Qy      661 AspSerGlyIleTyrApgSerSerValProSerSerGluLeuSerLeuProLeuMetGlu 680
Db      2070 GACTCAGGATCATATACCTGCTGTGCCCTATACCGACTGTCTTGCACATGAGAA 2129
Qy      681 GlyLeuSerThrApgGlnThrGluThrSerSerLeuThrGluSerValSerSerSer 700
Db      2130 GGACTCCAGCGACAGACAGAAAGCTTCTTCACCGAAGCGTGTCTCTCTTCA 2189
Qy      701 GlyLeuGlyGluGluProProAlaLeuProSerLysLeuLeuSerSerGlySerCys 720
Db      2190 GGCCTGGTGAAGAGAACCTCTGCTCTTCCATCAAGCTCTCTTCTGGGTATGC 2249
Qy      721 LysAlaApgLeuGlyCysArgSerTyrThrApgGluLeuHisAlaValAlaPro 738
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RESULT 12
ADM7619 standard; DNA; 4508 BP.
XX
XX ADM7619;
AC
XX 24-MAR-2005 (first entry)
DT
XX
XX Human Interleukin-17 (IL-17) receptor DNA.
DE
XX
XX Interleukin-17 receptor; IL-17 receptor; ds; gene.
KM
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 553..2340
FT CDS /tag= a
FT /product= "Human Interleukin-17 (IL-17) receptor protein"
FT
XX
XX CN1465592-A.
PN
XX
XX 07-JAN-2004.
PD
XX
XX 01-JUL-2002; 2002CN-00123540.
PF
XX
XX 01-JUL-2002; 2002CN-00123540.
PR
XX
XX (UYOI ) UNIV QINGHUA.
PA
XX
XX Xiong S, Chang Z, Fu X;
PI
XX WPI; 2004-248799/24.
XX P-PSDB; ADM76620.
DR
XX
XX Human Interleukin-17 receptor sample protein, coding gene and its uses.
PT
XX
XX Claim 3; SEQ ID NO 1; 14pp; Chinese.
PS
XX
XX The invention relates to a novel human interleukin-17 (IL-17) receptor
CC protein, the coding gene and application. The current sequence is that of
CC the human interleukin-17 receptor DNA of the invention.
XX
XX
SQ Sequence 4508 BP; 1175 A; 1061 C; 1141 G; 1131 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 4508
Score: 3706.00 Matches: 694
Percent Similarity: 99.7% Conservative: 2
Best Local Similarity: 99.4% Mismatches: 2
Query Match: 93.9% Indels: 0
DB: Gaps: 13

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US-10-616-788-2 (1-738) x ADM76619 (1-4508)

QY 41 TTPARGLYVALGIPROALASERARGASERGLYLEUTYRAENIIETHRPHELYTYR 60
DB 241 TGGCAGGAGTGGGGCCAGCCAGCAAGAACAGTGGGCTGTACACATCACCTTCATAATAT 300
QY 61 AAGASNCYETHRTHRYTLEAENPROVALGILEUYEHIISVALIIIEALAAAPALAGLAAEN 80
DB 301 GACAAATGTACCACTTAACTTGAATCCAGTGGGAAAGATGATGTCTGACGCCCAAAAT 360
QY 81 ILETHRILESERGLNYRALACYSNIIASPPGLNVALALAVALTNRILLEUTRPSERPRO 100
DB 361 ATGACACATGACCCAGATGCTGTCCATGACCAAGTGGCAGTCCATCTTGGTCCCA 420
QY 101 GILVALALEUGLYILEGIPHEULEUYEGILEYARGLYVALLIELEUGLJULEUYESER 120
DB 421 GGGGGCCCTCGGCAATCGAATTCCTGAAAGATTTCGGGTAAATACGTGAGAGCTGAAGTCG 480
QY 121 GLUGLYARGLINCYSGLINGIENLEUILEUYASAPROLYSGILEUAENSERSERPHE 140
DB 481 GAGGAAAGACAGTGCACCAACATGATCTAAAGGATCCGAAGCAGTCAACAGTAGCTTC 540
QY 141 LYSARGTHRGLYMECTGUSERGLNPROPHLEUAENMETLYSPHEGLUTNRASPTYRPH 160
DB 541 AAAAGAACTGGAATGGAATCTCAACCTTCTGAAATGAAATTTGAAACGGAATTAATTC 600
QY 161 VALLYVALVALPROPHEROSERTILEYASNGIUSERANTYRHIISPROPHEPHE 180
DB 601 GTAAAGGTTCCTCTTTCCTTCAATTAAGAACAAATTAACCACTTCTTCTTCTT 660
QY 181 ARGTHRARGALACYSAPRLEULEUGLNPORASPHALEUAIACYSLYBPORPHETTP 200
DB 661 AGAAGCCGAGCCCTGTGACCTGTGTACACCCGCAATCTAGCTTTAAACCCCTTCTG 720
QY 201 LYSAPROGRASMLEUAENIIISERGLNIIISGLISERAPMETGLNVALISERPHENPHIS 220
DB 721 AAGCTTCGAACTGAACTGAACTGACCAATGCTCGCAATGCAAGGTCTCTTCAGCAC 780
QY 221 ALAPROHIIASAPHEGLYPHEARGPHEPHETYRLEUHIISYRILYVLEUYVSHISGLUGLY 240
DB 781 GACCCGCAACACTTCGGCTTCGGTTCTTCTCATCTTCACTACAAAGCTCAAGCAAGAGA 840
QY 241 PROPHELYARGLYTHRCYLYSGINGLUGLINTHRGLUTNRHSERYVLEULEU 260
DB 841 CCTTTCAAGGGAAGACCTGTAGCAGAGCAAACTACAGAGTAGCAGCTGCTCTCT 900
QY 261 GLIASAPVASERPROGLYASPTYRILEILEGILEUVALIASAPERTHRANPTHRARG 280
DB 901 CAHAATGTTCTCCAGGGGAATTAATAATGAGCTGAGTAGCACTTAACACAAACAGA 960
QY 281 LYSVALMETHISTYRALALEULYPROVALHIIISERPROTPRALAGIYPROILEARGALA 300
DB 961 AAAGTAGATGATATGCTTAAAGCCAGTGCATCCCCGTGGCGGGCCCATACAGGCC 1020
QY 301 METALALIETHRVALPROLEUVALIILESERALAPHEALATHREUPHERTHVALMET 320
DB 1021 GTGGCCATCAAGTGCACCTGTAGTATCGGCATTCGCGAGCTTCATCATGATG 1080
QY 321 CYAARGLYLYSGINGLINGIENLEUILEYSERHIIISLEUAPRGLUGIUSERSERGLUSER 340
DB 1081 TGGCGCAAGAGCAACAAATAATATTAATTCATATTGATGAAGAGAGCTCTGAGTCT 1140
QY 341 SETTHRITRHALALALEUPROARGLUAARGLEUARGPROARGPROLYSVALPHELEU 360
DB 1141 TCCACATACACTGACAGACTCCCAAGAGAGAGGTCCGGCCGCGAGAGGTCTTCTC 1200
QY 361 CYEYTSERISERYASRGLYGINAENHIIISMETASNAVALAGINCYSRHEALATYRPH 380
DB 1201 TGGCTATTCAGTAAAGATGCGCAAGATCATGATGCTCTCCAGTGTTCGCTACTTC 1260
QY 381 LEUGLIASAPHECYSGLYCYSGIUVALLIILEUASPRLEUTRGLIAPRPHESERLEUCYS 400

DB 1261 CTCAGGACTTCTGTGGCTGTGAGTGGCTGTGGAACCTGTGGGAAGACTTCAGCTCTGT 1320
QY 401 ARGGLUGLYGINARGGLUTRPVALIIIEGLINLYEHIISGLUSERGLNPHELLEIVALL 420
DB 1321 AAGAAAGGAGAGAGAAATGGGTTCATCCAGAAATCCACAGATCCCAAGTTCATCATTTGTG 1380
QY 421 VALCYSERISERYASRGLYRPHLEVALASRGLYLYASANTYRILYVSHISLYSGLY 440
DB 1381 GTTTGTTCCAAAGATATGAATGATCTTTGTGCAAGAAAGAACTACAAACCAAGAGAGT 1440
QY 441 GILYARGGLYSEGLYLYSGIULEUPHELEUVALIIVALSERALIIIEALAGLULYS 460
DB 1441 GGGCGAGGCTCGGGGAAAGAGAGCTCTTCCTGTGGCGGTGTGAGCATTTGCCGAAAG 1500
QY 461 LEUARGGLNALALYSGINUSERSERVALIILEUSERLYSPHEIIIEALATYRPH 480
DB 1501 CTCGCGCAGGCCAAGCAGAGATTCGTCCGCGCCCTCAGCAAGATTTATCGCCGTACTTT 1560
QY 481 ASPTYRSECYSGIUGIYASPVALLPROGLYIIILEUASPRLEUSETHRILYRARGLEU 500
DB 1561 GATTAATTCCTCGAAGGAGAGCGTCCCGGATCTTGAACCTTGATACCAATACAGACTC 1620
QY 501 METASPHASMLEUPROGLINLEUCYSERHIIISLEUHIISERARGASPHISGLYLEUGLNU 520
DB 1621 ATGACAAATCTTCTCAGCTCTGTCCATCTGCACTCCGAGACCAAGCCCTCCAGAG 1680
QY 521 PROGLYGLNHIISTHRARGGLINGLYSERARGATASANTYRPHASRISERYASRGLYARG 540
DB 1681 CCGGGCAGACACACGCGACAGGCGACAGAAAGAACTACTCCGAGCAAGTCAAGGCCGG 1740
QY 541 SERLEUTYRVALIIECYASMETHISGLINPHILEASPRGLUGIUPROASPTTPHE 560
DB 1741 TCCCTATACGTCCCAATTTGCAACATGACCAAGATTAATTAACAGAGAGCCGAGTGTTC 1800
QY 561 GLULYGLINPHEVALPROPHENIISPROPROPROLEUARGTYRARGIUPROVALLEUGLU 580
DB 1801 GAABAAGAGTTCCTTCCCTTCATCTCTCCCATGCGCTACCGGAGCCAGTCTTGAG 1860
QY 581 LYSAPHEASPSERGLYLEUVALILEUAENAPVALMETCYALYAPROGLYPROGLUSERASP 600
DB 1861 AAATTTGATTCGGGCTTGTTTAAATGATGTATGTCATGTGCACAAACAGGGCTGAGAGTAC 1920
QY 601 PHECYLEULEUYVALIGLUALPROVALLEUGLYALATHRCIYPROLIIASPSERGLNHIIS 620
DB 1921 TTCTGCTTAAAGGTGAGAGGGCGTGTCTTGGGCAACCGGACAGCCCATCCAGCAC 1980
QY 621 GLUSERGLNHIISGLYGLYLEUASPRGLIAPRGLIAPRPROLIIASAPRGLYSER 640
DB 1981 GAAAGTACGATGGGGGCTGTGACCAAGACGGGAGAGGCCGCTGCTTGACGTTAGC 2040
QY 641 ALALALEUGLINPROLEULEUHIISTHRVALIIVALSGLYSEAPROSERAPMETPROARG 660
DB 2041 GCGCCCTGCAACCCCTGTCGACACAGTGAAGCCGGGAGCCCTTCGACATGCCGCG 2100
QY 661 AASPSEGLYILEYTRAPSERSERVALPROSERSERGLILEUSERLEUPROLEUMETGLU 680
DB 2101 GACTCAGGCACTTATACCTGTCTGTGCCCTCATCCGAGCTGTCTCTGCCATGATGAA 2160
QY 681 GLYLEUSERTHRAPGINTHRGLUTNRHSERSERLEUTHRCIUSERVALISERSERSER 700
DB 2161 GAACTTCGACGAGCAACAGACAAAGAGCTTCTCTTACGAGAGGCTGTCTCTCTTCA 2220
QY 701 GILYLEUGLYGLUGIUPROPROLIIALEUPROSERLYSLEUUSERSERGLYSECY 720
DB 2221 GGCCTGGGAGAGAGAACTCTGCTCTCTCTTCAAGTCTCTCTTCTGTGGGTATGC 2280
QY 721 LYSALIASAPRLEUGLYCYBASRSEYTRTHRAPRGLILEUHIISALIVALLIAPRO 738
DB 2281 AAAGCAGATCTTGTGGCGCACTACATGATGAATCCACGCGGTGCGCCCT 2334
RESULT 13
ABX71363
ID ABX71363 standard; cDNA; 2406 BP.

QY 500 LeuMetAspAsnLeuProGlnLeuCySeSerHisLeuHisSerArgAspHisGlyLeuGln 519
 DB 1411 CTATGACACATCTTCTTCCAGCTCTGTTCCACCTGACCTCCGAGACACGGGCTCCAG 1470
 QY 520 GluProGlyGlnHisThrArgGlnGlySerArgArgAsnArgPheArgSerGlySerGly 539
 DB 1471 GAGCCGGGAGGACACACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1530
 QY 540 ArgSerLeuArgValAlaIleCyAsnMetHisGlnPheHisGlnGluProArgTyr 559
 DB 1531 CGGTCTCTATACGTCGCGCATTTGCAATGACACGAGTTTATGACGAGGAGGAGGAGGAGG 1590
 QY 560 PheGluLeuArgHisPheValProPheHisProProProLeuArgTyrArgGluProValLeu 579
 DB 1591 TTGAAAGAGAGGATTCGTTCCCTTCATCTCTCCATCTGCGACACCGGAGCCAGCTTGG 1650
 QY 580 GluLeuPheAspSerGlyLeuValLeuAspAspValMetCysGlySerProGlyProGluSer 599
 DB 1651 GAGAAATTTATTCGGGCTTGTTTAAATGATTCATCTGCAACCGAGGAGGAGGAGGAGGAGT 1710
 QY 600 AspPheCysLeuArgValGluAlaProValLeuGlyValAlaThrGlyProAlaAspSerGln 619
 DB 1711 GACTTCTGCTAAAGAGAGAGGCGCTGTTCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1770
 QY 620 HisGluSerGlnHisGlyLeuAspGlnAspGlyGluAlaArgProAlaLeuAspGly 639
 DB 1771 CACGAGAGTACAGATGGGGGCTGGAGCAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1830
 QY 640 SerAlaAlaLeuGlnProLeuLeuHisThrValAlaGlySerProSerAspMetPro 659
 DB 1831 AGGCGCCGCTGCAACCCCTGCTGACACGCTGAAACCGGAGGAGGAGGAGGAGGAGGAGT 1890
 QY 660 ArgAspSerGlyIleTyrAspSerSerValProSerSerGluLeuSerLeuProLeuMet 679
 DB 1891 CGGAGCTCAGGACATCTATGACTGCTGCTGCTCCCTCATCCGAGGAGGAGGAGGAGGAGT 1950
 QY 680 GluGlyLeuSerThrArgGlnThrGlnThrSerSerLeuThrGluSerValSerSerSer 699
 DB 1951 GAAGGACATCTGACGAGCAGACAGAAACGCTCTCTGACGAGGAGGAGGAGGAGGAGGAGT 2010
 QY 700 SerGlyLeuGlyGluGluProProAlaLeuProSerHisLeuSerSerGlySer 719
 DB 2011 TCGAGCTGAGTGAAGAGAACTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2070
 QY 720 CysAlaAlaAspLeuGlyCysArgSerTyrThrAspGluLeuHisAlaValAlaPro 738
 DB 2071 TGCAGAGCAATCTGCTTCCGAGCTACATGATGATCCACGCGGTGCGCCCT 2127
 RESULT 14
 AAS09517
 ID AAS09517 standard; cDNA, 2319 BP.
 AC AAS09517,
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DB Human cDNA encoding Interleukin 17 receptor, IL-17RH4.
 XX
 KM Human; Interleukin-17 receptor; IL-17RH4; agonist; antagonist; ss;
 KM PRO20026; DNA 154095-2998; systemic lupus erythematosus;
 KM rheumatoid arthritis; osteoarthritis; diabetes mellitus;
 KM allergic disease; asthma; demyelinating disease;
 KM degenerative cartilaginous disorder; transplantation associated disease.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..2255
 FT /tag= a
 FT /product= "IL-17RH4"
 XX
 PN MO200146420-A2.

XX PD 28-JUN-2001.
 XX PF 20-DEC-2000; 2000MO-US034956.
 XX PR 23-DEC-1999; 99US-0172096P.
 XX PR 30-DEC-1999; 99MO-US031274.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 02-MAR-2000; 2000MO-US05841.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000MO-US07532.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 22-JUN-2000; 2000US-0213807P.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 24-OCT-2000; 2000US-0242837P.
 PR 10-NOV-2000; 2000MO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000MO-US032678.
 XX
 PA (GETH) GENENTECH INC.
 PI Chen J, Filvaroff E, Fong S, Goddard A, Godowski P, Grimaldi CJ,
 PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lockeren M, Vandlen RL,
 PI Watanabe CK, Williams PM, Wood WI, Yansura DG;
 DR WPI; 2001-451708/48.
 DR P-PSDB; AAU04958.
 XX
 PT Novel pro polypeptides homologous to interleukin-17, useful for the
 PT diagnosis and treatment of immune related disease e.g. rheumatoid
 PT arthritis and diabetes.
 PS Claim 1; Fig 17; 188bp; English.
 XX
 CC The sequence (DNA 154095-2998) encodes a PRO polypeptide (PRO20026) which
 CC is the human Interleukin 17 receptor, IL-17RH4. A composition containing
 CC ant/agonists to the PRO polypeptides or individual components are useful
 CC for treating a mammal with an immune related disease, e.g. systemic lupus
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
 CC arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease, a
 CC demyelinating disease, an autoimmune or immune-mediated skin disease,
 CC contact dermatitis, an allergic disease e.g. food hypersensitivity,
 CC asthma, a transplantation associated disease, or a chronic inflammatory
 CC demyelinating polynuropathy. Treating a degenerative cartilaginous
 CC disorder comprises administering a PRO1031 or PRO112 polypeptide
 CC agonist, or antagonist to the mammal. Numerous examples of the diseases
 CC and disorders are given in the specification
 XX
 SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other.
 Alignment Scores:
 Pred. No.: 0 Length: 2319
 Score: 3690.00 Matches: 702
 Percent Similarity: 96.0% Conservative: 2
 Best Local Similarity: 95.8% Mismatches: 11
 Query Match: 93.5% Indels: 18
 DB: 4 Gaps: 3
 US-10-616-788-2 (1-738) x AAS09517 (1-2319)
 QY 24 AlaValAlaAlaGlyGlySerGlyArg-----AlaTrpGlyValAsp-----Thr 38
 DB 52 GCGGTGAGAGGGGAGAGATGCCAGCGCTTCTGCTCAGGATCTCTCGGCTGTTGTC 111
 QY 39 CysGlyTrpArgGlyValGlyProAlaSerArgAspSerGlyLeuTyrAsnIleThrPhe 58
 DB 112 AGTGAAGACAGGAGATGGGGCCAGCCAGCAAGAAACATGAGCTGTACAAACATCACCTTC 171

QY 59 LysTyrAspAsnCyethrThrTyrLeuAsnProValGlyLysHISValIleAlaAspAla 78
 Db 172 AAlATATGACATGTGTACCACTACTGTAATCCAGTGGGAGAGATGATGTCTGACGCC 231
 QY 79 GlnAsnIleThrIleSerGlnTyrAlaCyethrAspGlnValAlaValThrIleLeuTyr 98
 Db 232 CAGAAATATCCATCAGCCAGCTAGTATGCTGTGCATAGCAACAGTGGCAGCTCATCTTTGG 291
 QY 99 SerProGlyValAlaLeuGlyIleGlnPheLeuLysGlyPheArgValIleLeuGlnGlnLeu 118
 Db 292 TCCCCAGGGGGCCCTCGCATCGAATTCCTGAAGAGATTCGGGTAATACTGGAGAGCTG 351
 QY 119 LysSerGlnGlyYArgGlnCyethrGlnLeuIleLeuLysAspProLysGlnLeuAsnSer 138
 Db 352 AGTCCGAGGAGAGACAGCTGCCAACATGATCTTAAAGATTCGAGAGCGCTCAACAGT 411
 QY 139 SerPheLysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGlnThrAsp 158
 Db 412 AGCTTCAAAAGAACTGGAATGGAAATCTCAACCTTCTGAAATAGAAATTTGAAACGGAT 471
 QY 159 TyrPheValLysValValProPheProSerIleLysAsnGlnSerAsnTyrHISProPhe 178
 Db 472 TATTTGTAAGAGGTGTCTCTTTCTTCATTAAAAAGAAAGCAATTACCACTCTTTC 531
 QY 179 PhePheArgThrArgAlaCyethrLeuLeuGlnProAspAsnLeuAlaCyethrPro 198
 Db 532 TTCTTAAAGAACCGAGCGCTGTGACCTGTGTACAGCCGAGCAATCTAGCTTTAAACCC 591
 QY 199 PheTrpLysProArgAsnLeuAsnIleSerGln----- 209
 Db 592 TTCTGGAAGCTCGGAACCTGGAACATCAGCCAGCATGCTCGGACATGCAAGTGTCTTC 651
 QY 210 -----HISGlySerAspMetGlnValSerPheAspHISAlaProHISAsnPhe 225
 Db 652 GACACGCAACCGATGAGCTCGACATGCAAGTGTCTTCGACCAAGCAACCGCAACCTTC 711
 QY 226 GlyPheArgPhePheTyrLeuHISLysTyrLysLeuLysHISGlnGlyProPheLysArgLys 245
 Db 712 GGTTCGCTTCTTCTTATCTTCACTCAAGCTCAAGCAAGAGACCTTTCAGAGCAAG 771
 QY 246 ThrCysLysGlnGlnGlnThrThrGlnThrThrSerCysLeuLeuGlnAsnValSerPro 265
 Db 772 ACCTGTAGAGAGAGCAACTACAGAGATGACAGAGCTCTCTCAAAATGTTTCCCA 831
 QY 266 GlyAspTyrIleIleGlnLeuValAspAspThrAsnThrThrArgLysValMetHISLys 285
 Db 832 GGGGATTTATATATGAGCTGTGTGAGTACATTAACAACAAAGAAAGTATGACATTA 891
 QY 286 AlaLeuLysProValHISerProTrpAlaGlyProIleArgAlaMetAlaIleThrVal 305
 Db 892 GCCTTAAGCGCATCTCCCGTGGCCGGCCCATACAGACCGTGGCCATCACAGTG 951
 QY 306 ProLeuValValIleSerAlaPheAlaThrLeuPheThrValMetCysArgLysLysGln 325
 Db 952 CCACTGTAGTACATATCGGCATTCGCGACGCTCTTCACTGTGATGTGCCCAAGAGCAA 1011
 QY 326 GlnGlnAsnIleLysSerHISLeuAspGlnGlnSerSerGlnSerSerThrTyrThrAla 345
 Db 1012 CAAGAAATATATATTCACATTTAGATGAAGAGAGCTGTAGTCTTCCATATCACCTGCA 1071
 QY 346 AlaLeuProArgLysArgLeuAspProArgProLysValPheLeuCyethrSerSerLys 365
 Db 1072 GCATCTCCAGAGAGAGAGCTCCGGCCGGCCGAGAGTCTTTCTGTGCTATTCAGTAA 1131
 QY 366 AspGlyGlnAsnHISMetAsnValValGlnCysPheAlaTyrPheLeuGlnAspPheCys 385
 Db 1132 GATGGCCAGATACATGAATGTGTGTCAAGTGTTCGCTACTTCCCGAGCACTTGTGT 1191
 QY 386 GlyCysGlnValAlaLeuAspLeuTrpGlnAspPheSerLeuCyethrGlnGlnArg 405
 Db 1192 GGTGTGAGGTGTCTGTGACCTGTGTGGAAGACTTCAGCTCTGTGTGAGAGAGGAGAGA 1251
 QY 406 GlnTrpValIleGlnLysIleHISGlnSerGlnPheIleIleValValCysSerLysGly 425

Db 1252 GAATGGTCATCCAGAAATCCACGAGTCCAGTTCATATGTGGTGTTCAAAGCT 1311
 QY 426 MetLysTyrPheValAspLysLysAsnTyrLysHISLysGlyGlyLysArgLysArgLys 445
 Db 1312 ATGAAGTACTTGTGTGACAAAGAACTACAAACAAAGAGAGTGGCCGAGCTGGGG 1371
 QY 446 LysGlyGlnPhePheLeuValAlaValSerAlaIleAlaGlyLysLeuArgGlnAlaLys 465
 Db 1372 AAGAGAGACTCTTCTGTGGCGGTGTGACGCAATTCGCGAAAGCTCCGCAAGCGCAAG 1431
 QY 466 GlnSerSerSerAlaAlaLeuSerLysPheIleAlaValTyrPheAspTyrSerCysGln 485
 Db 1432 CAGAGTTCGTCCGGCGCTCAGCAAGTTTATCGCGCTACTTGTATTTCTCTCGAG 1491
 QY 486 GlyAspValProGlyLysLeuAspLeuSerThrLysTyrArgLeuMetAspAsnLeuPro 505
 Db 1492 GAGAGCTCCCGGTATCTTAAGCTGAGTACCAAGTACAGACTCAATGACAAATCTCT 1551
 QY 506 GlnLeuCysSerHISLeuHISSerArgAspHISGlyLeuGlnGlnProGlyGlnHISThr 525
 Db 1552 CAGCTGTATTCACCTGCACTCCGAGACAGCGCTCCAGAGCCGGGCAAGCAAG 1611
 QY 526 ArgGlnGlySerArgArgAsnTyrPheArgSerLysSerGlyArgSerLeuTyrValAla 545
 Db 1612 CAGACAGGCGAGAGAGAACTACTTCCGAGCAAGTCAAGCCGGTCCCTATACGTGGCC 1671
 QY 546 ILeCysAsnMetHISGlnPheIleAspGlnGlnProAspTrpPheGlnLysGlnPheVal 565
 Db 1672 ATTTGCAATGACACAGATTATATGACGAGAGCCGAGCTGTTCAAAAGCAATTCGTT 1731
 QY 566 ProPheHISProProLeuAspArgTyrArgGlnProValIleGlnLysPheAspSerGly 585
 Db 1732 CCTTTCATCTCTCTCACTCGCGCTACCGGAGCCAGCTTTGAGAAATTTGATTCGGGC 1791
 QY 586 LeuValIleuAsnAspValMetCysLysProGlyProGlnSerAspPheCysLeuLysVal 605
 Db 1792 TTGGTTTAAATGATGTATGTGCAAAACAGGGCTGAGAGTGAATCTTGTCTTAAAGTGA 1851
 QY 606 GlnAlaProValLeuGlnValLarThrGlyProAlaAspSerGlnHISGlnSerGlnHISGly 625
 Db 1852 GAGGCGGCTGTCTTGTGGGCAACCGGACCAAGCTCCACACAGAGTCAAGCATGGG 1911
 QY 626 GlyLeuAspGlnAspGlyGlnAlaArgProAlaLeuAspGlySerAlaIleLeuGlnPro 645
 Db 1912 GGCCTGACCAAGACGAGAGGCGCGCTGTGCTTGAAGTACGCCGCCCTGCAACCC 1971
 QY 646 LeuLeuHISThrValLysAlaGlySerProSerAspMetProArgAspSerGlyIleTyr 665
 Db 1972 CTGCTGCAACGGTGAAAGCCGGCAAGCCCTCGAATGCTCGGGGACTCAAGCATCTAT 2031
 QY 666 AspSerSerValProSerSerGlnLeuSerLeuProLeuMetGlnGlyLeuSerThrAsp 685
 Db 2032 GACTCGTGTGTGCTTCATCCAGCTGTCTGTGCCATATGAGAGACTCTTCAGAGGAGC 2091
 QY 686 GlnThrGlnThrSerSerLeuThrGlnSerValSerSerSerSerGlyLeuGlnGlnGln 705
 Db 2092 CAGACAAAGCTCTTCTCTGACGAGAGAGCGTGTCTCTCTTCAGGCTGGGTGAGAG 2151
 QY 706 GlnProProAlaLeuProSerLysLeuLeuSerSerGlySerCysLysAlaAspLeuGly 725
 Db 2152 GAACCTCGTCCCTTCTTCAAGCTCTCTTGTGGGTATGAGCAAGCATCTTGGGT 2211
 QY 726 CysArgSerTyrThrAspGlnLeuHISAlaValAlaPro 738
 Db 2212 TGCCTGAGCTTACATGATGAATCCACGCGGTGACCCCT 2250

RESULT 15

ACA89858

ID ACA89858 standard, cDNA, 2319 BP.

AC ACA89858;

XX

DT 10-JUL-2003 (first entry)
 XX Human cDNA encoding PRO20026.
 XX Human; ss; gene; Interleukin 17; IL-17; IL17 receptor; angiogenesis;
 KM T-lymphocyte proliferation; inflammatory cell infiltration;
 KM immune related disorder; systemic lupus erythematosus; osteoarthritis;
 KM rheumatoid arthritis; spondyloarthritis; systemic sclerosis;
 KM Sjogren's syndrome; sarcoidosis; autoimmune hemolytic anaemia;
 KM thyroditis; diabetes mellitus; immune-mediated renal disease;
 KM demyelinating disease; Guillain-Barre syndrome; hepatobiliary disease;
 KM hepatitis; inflammatory bowel disease; Whipple's disease; psoriasis;
 KM immune-mediated skin disease; erythema multiforme; contact dermatitis;
 KM allergic disease; asthma; atopic dermatitis; food hypersensitivity;
 KM ulcerative colitis; idiopathic pulmonary fibrosis; eosinophilic pneumonia;
 KM idiopathic pulmonary fibrosis; transplantation associated disease;
 KM graft-versus-host disease.
 OS Homo sapiens.
 XX US2003003546-A1.
 XX 02-JAN-2003.
 XX 22-MAR-2001; 2001US-00816744.
 XX 15-MAY-1998; 98US-0085579P.
 XX 23-DEC-1998; 98US-0113621P.
 XX 08-MAR-1999; 99WO-US005028.
 XX 21-APR-1999; 99US-0130232P.
 XX 26-APR-1999; 99US-0131022P.
 XX 14-MAY-1999; 99US-00311832.
 XX 14-MAY-1999; 99US-0134287P.
 XX 14-MAY-1999; 99WO-US010733.
 XX 09-JUN-1999; 99US-0138387P.
 XX 23-DEC-1999; 99US-0172096P.
 XX 30-DEC-1999; 99WO-US031274.
 XX 11-JAN-2000; 2000US-0175481P.
 XX 18-FEB-2000; 2000WO-US004341.
 XX 01-MAR-2000; 2000WO-US005601.
 XX 02-MAR-2000; 2000WO-US005841.
 XX 21-MAR-2000; 2000US-0191007P.
 XX 21-MAR-2000; 2000WO-US007532.
 XX 02-JUN-2000; 2000WO-US015264.
 XX 22-JUN-2000; 2000US-0213807P.
 XX 24-AUG-2000; 2000WO-US023328.
 XX 24-OCT-2000; 2000US-0242837P.
 XX 26-OCT-2000; 2000US-0244072P.
 XX 10-NOV-2000; 2000WO-US030873.
 XX 28-NOV-2000; 2000US-0253646P.
 XX 01-DEC-2000; 2000WO-US032678.
 XX 20-DEC-2000; 2000WO-US034956.
 XX 28-FEB-2001; 2001WO-US006520.
 XX (GETH) GENENTECH INC.
 XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski P, Grimaldi C,
 PI Gurney A, Li H, Hillan K, Tumas D, Vanlokeren M, Vandlen R,
 PI Matanabe C, Williams PM, Wood WI, Yansura D;
 XX WPI; 2003-428843/40.
 XX P-PDB; AB089705.
 XX New PRO polypeptides and polynucleotides homologous to interleukin-17,
 PT useful for treating e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, or systemic
 PT sclerosis.
 XX Claim 2; Fig 17, 129pp; English.
 XX The invention relates to a nucleic acid having similarity to interleukin-
 CC 17 (IL-17) or IL-17 receptor comprises at least 80% nucleic acid sequence
 CC identity to a nucleotide sequence which: (a) encodes a polypeptide having

CC a sequence of appearing as AB089697-AB089700 and AB089702-AB089705 (PI-
 CC pe), lacking or having its associated signal peptide; (b) encodes an
 CC extracellular domain or PI-P8 lacking its associated signal peptide; (c)
 CC consists of a sequence of appearing as ACA89850-ACA89853 and ACA89855-
 CC ACA89856887; or (d) consists of the full-length coding sequence of
 CC selected from SI-S8, and of the cDNA deposited under ARCC accession
 CC number 209866, 203552, PTA-1185, PTA-2108, PTA-202, PTA-1555, PTA-1082 or
 CC PTA-2591. Also included are expression vectors, host cells, encoded
 CC proteins, chimeric proteins, antibodies, ant/agonists, compounds
 CC inhibiting the expression of SI-S8 or activity (or mimicking the activity
 CC of) of PI-P8, stimulating/inhibiting the proliferation of T-lymphocytes
 CC using the polypeptides or ant/agonists, enhancing the infiltration of
 CC inflammatory cells into a tissue of a mammal by administering a PRO1031
 CC polypeptide, its an agonist or antagonist, and inhibiting angiogenesis
 CC induced by a PRO1031 polypeptide or its agonist in a mammal by
 CC administering a PRO1031 polypeptide, its an agonist or an anti-PRO1031
 CC antibody. The proteins, antibodies, ant/agonists and compounds are useful
 CC for treating an immune related disorder such as systemic lupus
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
 CC arthritis, a spondyloarthritis, systemic sclerosis, an idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,
 CC thyroditis, diabetes mellitus, immune-mediated renal disease, a
 CC demyelinating disease of the central or peripheral nervous system,
 CC idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, a
 CC chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence encodes an IL17 or IL17
 CC receptor homologue of the invention
 XX SQ Sequence 2319 BP; 585 A; 633 C; 602 G; 499 T; 0 U; 0 Other;
 XX Alignment Scores:
 XX Pred. No.: 0 Length: 2319
 XX Score: 3690.00 Matches: 702
 XX Percent Similarity: 96.0% Conservative: 2
 XX Best Local Similarity: 95.8% Mismatches: 11
 XX Query Match: 93.5% Indels: 18
 XX DB: Gaps: 3
 XX US-10-616-788-2 (1-738) x ACA89858 (1-2319)
 QY 24 AlVaAlaAlaAlaGlySerGlyArg-----AlaTPrGlyValAsp-----Thr 38
 Db 52 GCGGTGGAGAGGAGGAGGATGCCAGCGGCTTGCGCTCAGGTGTCTCGGTGTTGTC 111
 QY 39 CyGGLYTPArgGLyValGLyProAlaSerArgAsnSerGlyLeuTyraAlaIleThrPhe 58
 Db 112 AGTGAAGAGAGAGAGAGTGGGCGAGCCAGCAAAACAGTGGGTGTGAACAATCACCTTTC 171
 QY 59 LyeTYrAspAsnCyThrThyTyrLeuAsnProValGLyLysIleValIleAlaAspAla 78
 Db 172 AAATATACAAATTGTATCACTTACTTGAATCCAGTGGGAGACATGTGATGCTGACGCC 231
 QY 79 GlAsnIleThrIleSerGlnTyrAlaCyGnIAspGlnValAlaValThrIleLeuTyr 98
 Db 232 CAGAAATACCAATCAAGCAGCGATGCTTGCATGACCAACATGGCAGATCACTTCTTGG 291
 QY 99 SerProGlyValAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGluGluLeu 118
 Db 292 TCCCAAGGGGCGCTCGCATCGAATTCGTAAGAGATTTCGGGTAATATCTGGAGAGCTG 351
 QY 119 LysSerGluGlyArgGlnCyGnIleGlnIleLeuIleLysAspProLysGlnLeuAsnSer 138
 Db 352 AAGTGGAGGAGAGACAGTCCCAACATGATTTCTAAAGATTCGAAAGCTCAACAGT 411

QY 139 SerPheValArgThrGlyMetGluSerGlnProPheLeuAmMetLysPheGluThrAsp 158
 DB AGCTTCAAAAGAACTGGAAATGAAATCTCAACCTTCTGAAATGAAATGAAACGAT 471
 QY 159 TyrPheValIleValAlaProPheProSerIleLysAmGluSerAntyTrhIAspPhe 178
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Search completed: March 1, 2006, 08:31:20
 Job time : 1064 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 1, 2006, 06:19:54 ; Search time 7487 Seconds
(without alignments)
4611.843 Million cell updates/sec

Title: US-10-616-788-2
Perfect score: 3948
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Scoring table:
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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues
Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/abs/ABSSWEB.spool/US10616788/rnac 28022006 160430 14453/app query.fasta_1
-DB=EST -QPMF=fastap -SUFFIX=ret -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=pro -NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs07
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-NARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:
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11: gb_esc11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3698	93.7	2406	4	HSMB05220
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3	2858.5	72.4	1677	10	AY408490 Homo sapi
4	2355	59.7	1674	10	AY408491 Pan trogl
5	1522	38.6	908	7	CJ025168 Mus muscu
6	1481	37.5	856	8	CJ025168 Mus muscu
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					DN283597 1184215 M

8	1183	30.0	724	3	BP154750
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10	1084	27.5	632	5	BU221978
11	1058	26.8	907	5	BU909956
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13	1024.5	25.9	583	3	BP275741
14	1023.5	25.9	717	5	BU479802
15	1022	25.9	748	7	CV126214
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23	937	23.7	665	2	BB641245
24	906	22.9	547	2	BE750478
25	890	22.5	494	8	DR003317
26	879.5	22.3	664	8	DN432360
27	873	22.1	548	5	BQ830554
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ALIGNMENTS

RESULT 1	HSMB05220	2406 bp	mRNA	linear	HTC 20-JAN-2005
LOCUS	HSMB05220				
DEFINITION	Homo sapiens mRNA; cDNA DKFp434L0320 (from clone DKFp434L0320).				
ACCESSION	AL833913				
VERSION	AL833913.1	GI:21739453			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 2406)				
AUTHORS	Ockenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaupp,A., Mewes,H.W., Weill,B., Amid,C., Oesanger,A., Fobo,G., Han,M. and Wiemann,S.				
CONSRMT	The German CDNA Consortium				
TITLE	Direct Submision				
JOURNAL	Submitted (20-JAN-2005) MIPB, Ingolstaedter Landstr.1, D-85764				
COMMENT	Neuberberg, GERMANY				
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the CDNA sequencing Consortium of the German Genome Project.				
	This clone (DKFp434L0320) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/ci.cgi?cloneID=DKFp434L0320				
	Further information about the clone and the sequencing project is available at http://mipb.gcf.de/projects/cdna/.				
FEATURES	Location/Qualifiers				


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ORIGIN

Alignment Scores:

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Pred. No.: 0 Length: 2406
Score: 3698.00 Matches: 694
Percent Similarity: 99.6% Conservative: 2
Best Local Similarity: 99.3% Mismatches: 3
Query Match: 93.7% Indels: 0
DB: 4 Gaps: 0

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US-10-616-788-2 (1-738) x HSM605220 (1-2406)

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DB 91 TATGACAAATTGACCACTTACTTGAAATCCAGTGGGAGAGCATGTGATGTCGACGCCAG 150
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DB 271 TCGGAGGAGAGACAGTGGCAGCAACATGATTTCTAAAGGATCCGAAAGCACTCAACATGAGC 330
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DB 331 TTCAAAAGAACTGGAAATGGAATCTCAACCTTTCTGAAATATGAATTTGAAAGGATTAAT 390
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QY 220 HISALAPROHISASNPHEGLYPHEARGPHEPEYRLEUHSITYRILEULYSHISGLU 239
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Qy      600  AspPheCysLeuIyValGlnIyValProValLeuGlyValAlaThrGlyProAlaAspSerGln 619
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            Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
            Adams,M.D. and Cargill,M.
            Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL    Science 302 (5652), 1960-1963 (2003)
PUBMED     14671302
REFERENCE  2 (bases 1 to 1677)
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            Direct Submission
            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
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COMMENT    This sequence was made by sequencing genomic exons and ordering
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Beet Local Similarity: 93.3%      Mismatches:  2
Query Match:    74.0%      Indels:     37
DB:             10      Gaps:         2

US-10-616-788-2 (1-738) x AY408489 (1-1677)
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Db      1  ATGGAAATTCACACCTTCTCGAATATGAAATTTGAAGGATATTTCGTAAGCTGTC 60
Qy      165  ProPheProSerIleIyAsnGluSerAsnTyrHisProPhePheAspThrArgAla 184
Db      61  CTTTTCCTTCCATTAAAAACGAAAGCAATTACACCTTCTTCTTGAACCCGAGTC 120
Qy      185  CysAspLeuLeuGlnProAspAsnLeuAlaCysIyPhePheThrIyPheProArgAsn 204
Db      121  -----TGGAAAGCTCGGAAC 135
Qy      205  LeuAsnIleSerGlnHisGlySerAspMetGlnIySerPheAspHisAlaProHisAsn 224
Db      136  CTGAACATACAGCAGATGCGCTCGACATGCAAGTGCTCTTGACCATCAGCCGACAAAC 195
Qy      225  PheGlyPheAspPhePheTyrLeuHisTyrIyIyLeuIyHisGlnIyProPheIyArg 244
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Qy      245  IyThrCysIyGlnGlnGlnIyThrGlnIyThrSerCysLeuLeuGlnAsnValSer 264
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Qy      265  ProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrThrArgIyValMetHis 284
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Qy      285  TyrAlaLeuIyProValHisSerProTyrAlaGlyProIleArgAlaMetAlaIleThr 304
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Qy      305  ValProLeuValValIleSerAlaPheAlaThrLeuPheThrValMetCysArgIyIyArg 324
Db      370  GTGCCACTGCTGATCATATCGGCACTTCGAGAGCTCTTACATGTATGTGCGGCAAGAG 429
Qy      325  GlnGlnGluAsnIleTyrSerHisLeuAspGlnGluSerSerGlySerSerThrTyrThr 344
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Qy      345  AlaAlaLeuProArgIyGlnIyArgLeuArgProArgProIyValIyPheLeuCysTyrSerSer 364
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Db      550  AAAGATGGCAAAATCACAATGATGCGTCAAGTGTTCGCTTACTCTCCAGAGACTTC 609
Qy      385  CysGlyCysGluValAlaLeuAspLeuTyrGlnAspPheSerLeuCysArgIyGlnIyGln 404
Db      610  TTGGCTGTAGAGTGCTGTGACCTGTGGAAAGCTTCAAGCTCTTGTGAGAAAGGCGAG 669
Qy      405  ArgGluThrValIleGlnIyIleHisGluSerGlnPheIleIyValIyCysSerIyArg 424
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 DEFINITION genomic survey sequence.
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 VERSION AY408490.1 GI:39764461
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 SOURCE Pan troglodytes (chimpanzee)

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 Homidae; Pan.
 REFERENCE 1 (bases 1 to 1677)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITL Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 1677)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferrieri,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITL Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
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 QY 165 ProPheProSerLleLysAngLysSerAenTyrHisProPhePhePheArgThArgAla 184
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 QY 725 GlyCysArgSerTyrThrAspGluLeuIleAlaValAlaPro 738
 DB 1630 GGTTCGCGAGTCAATGATTAATCTCCAGCGGTGCGCTT 1671
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 DEFINITION Mus musculus HCM3241 gene, VIRUTAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY408491
 VERSION AY408491.1 GI:39764462
 KEYWORDS GSS.
 SOURCE
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 Mus musculus
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Mus.
 REFERENCE
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civeallo, D.R., Lu, F., Murphy, B.,
 Ferrieres, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
 Adams, M.D. and Cargill, M.
 1 (bases 1 to 1674)
 TITLE
 Inferred nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE
 2 (bases 1 to 1674)
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejaritwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civeallo, D.R., Lu, F., Murphy, B.,
 Ferrieres, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
 Adams, M.D. and Cargill, M.
 TITLE
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 US-10-616-788-2 (1-738) x AY408491 (1-1674)
 QY 145 MetGluSerGlnProPheLeuAniMetLysPheGluThrAspTyrPheValValVal 164
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Sus.

REFERENCE
1 (bases 1 to 908)
Uenishi,H., Esuchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamaeima,N. and Awata,T.
PEDS (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
14681463
COMMENT
Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STRF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library

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Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319 low quality bases were trimmed based on the quality values.

FEATURES

source

Location/Qualifiers

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/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult trachea"

ORIGIN

Alignment Scores:

Pred. No.: 8,14e-146 Length: 908
Score: 1522.00 Matches: 280
Percent Similarity: 95.6% Conservative: 5
Best Local Similarity: 94.0% Mismatches: 13
Query Match: 38.6% Indels: 0
DB: 7 Gaps: 0

US-10-616-788-2 (1-738) x CJ025168 (1-908)

QY 1 MetAlaProTTrpLeuGlnLeuCySerValPhePheThrValAlaAlaCysLeuAnGly 20
DB 11 ATGGCCCGGCGTGGCGCT 70
QY 21 SerGlnLeuAlaValAlaAlaGlySerGlyValGAlaTrpGlyValAlaPheThrGly 40
DB 71 TCCCAATTGGCCCTGGCCGAGGTGGCTCCAGCAAGCTGGGGCCGCGACCTTGGGC 130
QY 41 TPpArgLyValGlyProAlaSerArgAsnSerGlyLeuTyranilLeuThrPheLy 60
DB 131 TGGAGGGAGGTGGCGCGCCGCGCAGAGAAACAGTGGCTGCACAACTCCTCAGATAT 190
QY 61 AspAsnGlyThrThrTyLeuAsnProValGlyLyHisValIleAlaAlaAlaGln 80
DB 191 GACAACTGCACCACTTACTTGGTGGTGGAGAGATGATGCGCCGCGCAGAAAT 250
QY 81 IleThrIleSerGlnTyranilCysHisAspGlnValAlaValThrIleLeuTrpSerPro 100
DB 251 ATACACATCAGTACGATGAGCTGCACAGCAAGTGCACATCTCTCTGCTCCCA 310
QY 101 GlyAlaLeuGlyIleGluPheLeuLyGlyPheArgValIleLeuGluGluLeuLySer 120
DB 311 GGGGCGCTGGGATCGAATTCCTTAAAGATTTCCGGTATATCTGAGAGAGCTGAAGTCA 370
QY 121 GlnGlyArgGlnCysGlnGlnLeuIleLeuLyAspProLyGlnLeuAsnSerSerPhe 140
DB 371 GAAGGAAGACAGTGCACAACTGATTTCTGAGAGACCCGAGCCTCAACAGTACTTC 430
QY 141 LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLyPheGluThrAspTy 160
DB 431 AAAAGAGCTGGAATGGAATCTCAGCTTCTCTAAATGAAATGAAACAGATTAATT 490
QY 161 ValLyValValProPheProSerIleLyAsnGlnSerAsnTyranilAspPhePhe 180
DB 491 GTCAAGATTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 550
QY 181 ArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLyProPheTrp 200
DB 551 AGAAGCCGCACTGTGACCTGCTATTAAGCCGAGCAACCTGGCTGTAAACCTTCTGG 610
QY 201 LysProArgAsnLeuAsnIleSerGlnIleSerAspMetGlnValSerPheAspHis 220
DB 611 AAGCTCTGGAACTCAACATCAACCAACAGCTCAGACATGAGGTCTTCTGACAC 670
QY 221 AlaProHisAsnPheGlyPheArgPhePheTyranilGlyTyranilGlyValIleAlaAlaGln 240
DB 671 GCGCCACATACCTTGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 730

QY 241 ProPheLyArgLyThrCysLyGlnGlnIleGlnThrGluThrSerCysLeuLeu 260

DB 731 CTTTAAAGAGAAAGCTTGCAGAGCAAAATACAGAGCAACAGCTCTCTCT 790

QY 261 GlnAsnValSerProGlyAspTyranilIleGluLeuValAspAspThrAsnThrArg 280

DB 791 CAATATGATCTCTCTGGGATTTATATATATGAGCTGTGAGTCAACATATCAACAGA 850

QY 281 LysValMetHisTyranilLeuLyProValHisSerProTTrpAlaGlyProIle 298

DB 851 AAGATGATCATTAATGCTTANNACAGTCAATTCCTCCATGGGCTGGGCCATTA 904

RESULT 6

DN282586/ 856 bp mRNA linear EST 02-MAR-2005
LOCUS 1182679 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
DEFINITION DN282586
ACCESSION DN282586.1 GI:60451196
VERSION EST.
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Bos taurus

REFERENCE

1 (bases 1 to 856)
Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of Bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov

AUTHORS

Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLB015 row: B column: 19
Seq primer: TAGAAGCAGCTGCGAGG.
Location/Qualifiers

FEATURES

source 1..856
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 7BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN

Alignment Scores:

Pred. No.: 1.27e-141 Length: 856
Score: 1481.00 Matches: 272
Percent Similarity: 97.9% Conservative: 6
Best Local Similarity: 95.8% Mismatches: 5
Query Match: 37.5% Indels: 0
DB: 8 Gaps: 0

US-10-616-788-2 (1-738) x DN282586 (1-856)

QY 40 GlyTPpArgLyValGlyProAlaSerArgAsnSerGlyLeuTyranilLeuThrPheLy 59
DB 854 GCGTGGAGGGAGGTGGGCTGGCCAGCAAAACAGGGCTGTACATCACTTCAAA 795
QY 60 TyAspAsnCySerThrThrTyLeuAsnProValGlyLyHisValIleAlaAlaGln 79
DB 794 TATGACAACTGCACCACTTACTTGAATCCAGTGGGAGACACATGATGCGTCAAGCCG 735
QY 80 AenIleThrIleSerGlnTyranilCysHisAspGlnValAlaValThrIleLeuTrpSer 99


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Db 734 AACATCACCATGCTAGTATGCTGCGACGACCAAGTGCCTGACCATTTCTTGGTCC 675
Qy 100 ProGlyValAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGluGluLeuLeu 119
Db 674 CCGGGGGCCCTCGGACATCGAATTCCTTAAAGATTCGAGTCAATACGAGGAGCTGGAAG 615
Qy 120 SerGluGlyArgGlnCysGlnGlnLeuIleLeuLeuAspProGlySerGlnLeuLeuSerSer 139
Db 614 TCAGAGGAGCAGCAGTGCACAACTGATTTCTTAAAGAACCCGAGACGCTCAACAGTAGC 555
Qy 140 PheLeuArgThrGlyMetGluSerGlnProPheLeuAsnMetLeuPheGluThrAspTyr 159
Db 554 TTCAAAAGAGCTGGAGGATGGAATCTCAACCTTTCTGGAATATGAATTTGAAACGATTAAC 495
Qy 160 PheValIleValValProPheProSerIleLeuAsnGluSerArgTyrHisProPhePhe 179
Db 494 TTTGTAAAGATCGCTCTTCTTCTTCAATTAATAAAGCAATTAATCACTTCTTCTTC 435
Qy 180 PheArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLeuProPhe 199
Db 434 TTCAGAACCCGACAGCTGATGACTGCTATTGACAGCCGACAACTGGCTTTAAACCTTTC 375
Qy 200 TrpLeuProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAsp 219
Db 374 TGGAGGCTCGGAACCTCAACATCAGCAGCAGGTTCCGACATGACAGGTGCTTTTGAC 315
Qy 220 HisAlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrTyrLeuLeuValHisGlu 239
Db 314 CATGCGCCCGACACCTTGTGCTTCCTGCTTCTTCTTCAATTAATAAAGCAATTAATGACATGAA 255
Qy 240 GlyProPheLeuArgLeuThrCysLeuGlnGlnLeuThrGluThrThrThrSerCysLeu 259
Db 254 GGACCCCTTCAAGGAGAAAGACCTGTAAACAGAGCAAAATACAGAGATTAACAGCTGCTT 195
Qy 260 LeuGlnAsnValSerProGlyAspTyrIleIleGluLeuValAspAspThrAsnThrThr 279
Db 194 CTTCAAAATGTGCTCTCTGGGAGTATATATTAATGAGTGTGCATGACAGTAATACAGACA 135
Qy 280 ArgLeuValMetHisTyrAlaLeuLeuProValHisSerProTrpAlaGlyProIleArg 239
Db 134 AGAAAAGTATGATTAATGCTTAAACAGATGATTCCTCCGAGGCTGGGCCCCATCAGA 75
Qy 300 AlaMetAlaIleThrValProLeuValValIleSerAlaPheAlaThrLeuPheThrVal 319
Db 74 GCTGTGGCCATCTGTGCGCATGATGCTGCTATTCGCAATTCGAGCGCTTTCACAGGTG 15
Qy 320 MetCysArgLeu 323
Db 14 ATGTGCGCGCAA 3

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RESULT 7      851 bp      mRNA      linear      EST 02-MAR-2005
LOCUS        DN283973
DEFINITION   118415 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION    DN283973
VERSION      DN283973.1 GI:60452583
KEYWORDS
SOURCE       Bos taurus (cow)
ORGANISM     Bos taurus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 851)
Smith,T.P.L., Roberts,A.D., Scherhamp,S.E., Chitko-McKown,C.G.,
Way,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

```

Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: RLB015 row: B column: 19
 Seq primer: GTAATACGACTCATTTAGG.
 Location/Qualifiers

FEATURES

source

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1..851
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_id="MARC 7BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

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ORIGIN

Alignment Scores:

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Pred. No.:      1,72e-140      Length:      851
Score:          1470.00      Matches:      270
Percent Similarity: 97.5%      Conservative: 6
Best Local Similarity: 95.4%      Mismatches: 7
Query Match:      37.2%      Indels:      0
DB:              8      Gaps:      0

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US-10-616-788-2 (1-738) x DN283973 (1-851)

```

Qy 40 GlyTrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTyrAsnIleThrPheLeu 59
Db 3 GCGTGAAGGGAGGTGGGCTGGCCAGCAGAAACAGGGGCTGTACACATCACTTCAACA 62
Qy 60 TyrAspAsnCysThrThrTyrLeuAsnProValGlyValHisValIleAlaAspAlaGln 79
Db 63 TATGACAACTGGACCACTTAATCAATGAGTGGGAGACATGATGCTGACGCCAG 122
Qy 80 AsnIleThrIleSerGlnTyrAlaCysHisAspGlnValIleValThrIleLeuTrpSer 99
Db 123 AACATCACCATGATGATGATGCTGCGACGACAAAGTGGCTGTCACATTTCTTGGTCC 182
Qy 100 ProGlyValAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGluGluLeuLeu 119
Db 183 CCGGGGGCCCTCGGACATGATTTCTTAAAGATTTCCGGTCAATCTGAGGAGCTGGAAG 242
Qy 120 SerGluGlyArgGlnCysGlnGlnLeuIleLeuLeuAspProGlySerGlnLeuLeuSerSer 139
Db 243 TCAGAGGAGCAGCAGTGCACAACTGATTTAAAGAACCCGAGACGCTCAACAGTAGC 302
Qy 140 PheLeuArgThrGlyMetGluSerGlnProPheLeuAsnMetLeuPheGluThrAspTyr 159
Db 303 TTCAAAAGAGCTGGAGGATGGAATCTCAACCTTTCTGGAATATGAATTTGAAACAGATTAC 362
Qy 160 PheValIleValValProPheProSerIleLeuAsnGluSerArgTyrHisProPhePhe 179
Db 363 TTTGTAAAGATGCTCTTCTTCTTCAATTAATAAAGCAATTAATCACTTCTTCTTC 422
Qy 180 PheArgThrArgAlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLeuProPhe 199
Db 423 TTCAGAACCCGACAGTGCATGCTGATTTGACCGGACGACAACTGGCTTGTAAACCTTTC 482
Qy 200 TrpLeuProArgAsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPheAsp 219
Db 483 TGGAGCCCTCGGAACCTCAACATCACTGACAGCGTTCCGACATGACAGGTGCTTTTGAC 542
Qy 220 HisAlaProHisAsnPheGlyPheArgPhePheTyrLeuHisTyrTyrLeuLeuValHisGlu 239
Db 543 CATGCGCCCGACACCTTGGCTTCCTTCTTCTTCAATTAATAAAGCAATTAATGACATGAA 602
Qy 240 GlyProPheLeuArgLeuThrCysLeuGlnGlnLeuThrGluThrThrThrSerCysLeu 259
Db 603 GGACCTTCAAGGAGAAAGACCTGTAAACAGAGCAAAATTAACAGATTAACAGCTGCTCCTT 662

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Qy	260	LeuGlnAanValISerProG1YAAspYr1et1eg1ue1ueValAAspAspThrAAsnThr	279
Db	663	CTTCAAAATGCTCTCTCCGGGGATTATTAATTGACGTGCGATGACAGTAATACGACA	722
Qy	280	Arg1yValMetH1sT1yAlAluLeuAbProValH1sSerProT1pAlG1yPro1leArg	299
Db	723	AGAAAGATGATCATATATGATCCCTTAAACACAGTCAATTCGCCGTGGGCGCCATCAGA	782
Qy	300	AlaMetAla1etHrValProLeuVal1all1eserAlaPheAlaThrLeuPheThrVal	319
Db	783	GCTGTGGCATCAGTGGCCATTTGGTCTGTCAATTCGCGATTCGACGCTCTTCAACGGTG	842
Qy	320	MetCysArg	322
Db	843	ATGTGCCGC	851
RESULT 8			
LOCUS	BP154750	724 bp	mRNA linear EST 30-DEC-2003
DEFINITION	BP154750 full-length enriched swine CDNA library, adult ovary Sus		
ACCESSION	BP154750		
VERSION	BP154750.1	GI:40404223	
KEYWORDS	EST.		
SOURCE	Sus scrofa		
ORGANISM	Sus scrofa (pig)		
REFERENCE			
AUTHORS	1 (bases 1 to 724) Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasina,N. and Awata,T.		
TITLE	PERE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries		
JOURNAL	Nucleic Acids Res. 32 (1), D484-D488 (2004)		
PUBMED	14681463		
COMMENT	Contact: Hirohide Uenishi Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627 Fax: +81-29-838-8627 Email: huenishi@affrc.go.jp EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute Single pass sequencing of clones derived from oligo-capped cDNA library Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319 Low quality bases were trimmed based on the quality values.		
FEATURES			
Source			
	1..724		
	/organism="Sus scrofa"		
	/mol_type="mRNA"		
	/db_xref="taxon:9823"		
	/clone="OVRM10115H10"		
	/tissue_type="ovary"		
	/dev_stage="adult"		
	/clone_idb="full-length enriched swine CDNA library, adult		
	ovary"		
ORIGIN			
Alignment Scores:			
Pred. No.:	5.73e-111	Length:	724
Score:	1183.00	Matches:	217
Percent Similarity:	96.3%	Conservative:	5
Best Local Similarity:	94.8%	Mismatches:	7
Query Match:	30.0%	Indels:	0
DB:	3	Gaps:	0

Oy	1	MetLAPoTfPLeuGlnLeuCySerValPhePheTrValLanAlaCyLeuAnGly	20
Db	38	ATGGCCCCGGTGTGGACCTGTGTTCTCTTCCACCGTCACAGCTGECTCAACGGC	97
Oy	21	SerGlnLeuAlaValAlaGlyGlySerGlyArgAlaTrpGlyValAspThrCysGly	40
Db	98	TGGCAATTGGCGCGTGGCGGAGGTGCTCCAGAGAGCTGGGGGGCGGACACCTGGCGG	157
Oy	41	TrpArgGlyValGlyProAlaSerArgAsnSerGlyLeuTrpAnIleThrPheLeuTr	60
Db	158	TGGAGGGGAGTGGGGCGGCGGACGAGAAACGTGGCTGCACCACTCACCTTCAGATAT	217
Oy	61	AspAsnCySerThrTrpTrpLeuAsnProValGlyLeuHisValIleAlaAspAlaGlnAn	80
Db	218	GACCACTGCACCACTTACTTGAGTCTGTGGGGAGGACATGTGATCGCGAGCCCAAGAT	277
Oy	81	IleThrIleSerGlnTrpAlaCyHisAspGlnValAlaValIleLeuTrpSerPro	100
Db	278	ATCACCACTCACTCACTGACCTGCGCAGACCAATGGCAGTCAACACTTCTGTGGTCCCA	337
Oy	101	GlyAlaLeuGlyIleGluPheLeuLeuGlyPheArgValIleLeuGlnGluLeuLysSer	120
Db	338	GGGGCCCTCGGCATCGAATTCCTTAAAGATTTGGGTAATATCGAGAGACTGAAGTCA	397
Oy	121	GluGlyArgGlnCysGlnGlnLeuIleLeuLysAspProLysGlnLeuAsnSerSerPhe	140
Db	398	GAAAGAAAGACAGTGTCCAACTGATTTCTGAAAGACCCGAAAGCAGCTCAACAGTAGCTTC	457
Oy	141	LysArgThrGlyMetGlnSerGlnProPheLeuAsnMetLysPheGluThrAspTrpPhe	160
Db	458	AAAAGACTGGAAAGGAATCTCAGCCTTTCTCTGAATATGAAATTTGAAACAGATTACTTT	517
Oy	161	ValLysValValProPheProSerIleLysAsnGlnSerAsnTrpHisProPhePhe	180
Db	518	GTCAGATGTGCCCTTTCTTCTTCATTAAACGAAAGCAATTATCAACCTTTCTTCTTT	577
Oy	181	ArgThrArgAlaCyAspLeuLeuLeuGlnProAspAsnLeuAlaCyLysProPheTrp	200
Db	578	AGAACCGGACACTGTGACTGTCTATTACAGCGGACAACCTGGCTGTAAACCTTCTGG	637
Oy	201	LysProArgAsnLeuAnIleSerGlnHisGlySerAspMetGlnValSerPheAspHis	220
Db	638	AAGCTCGGAACCTCAACATCAACCAACATGCTCAGACAGCAGCAGTGTCTTGGACAC	697
Oy	221	AlaProHisAsnPheGlyPheArgPhe	229
Db	698	GCGCCACATACCTTCGGGCTTCGGTTTC	724

	RESULT 9	
BM65550	LOCUS	
	DEFINITION	BM65550 full-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVRO067A07 5', mRNA sequence.
	ACCESSION	BM65550
	VERSION	BM65550..1 GI:71964881
	KEYWORDS	EST.
SOURCE		Sus scrofa (pig)
ORGANISM		Sus scrofa Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE		1. (bases 1 to 679) Uenishi,H., Eguchi,T., Suzuki,K., Sawaraki,T., Toki,D., Shinkai,H.....
AUTHORS	TITLE	PDEB (Pig EST Data Explorer) : construction of a database for ESTs derived from porcine full-length cDNA libraries
JOURNAL		Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED		14681463
COMMENT	Contact:	Hirohide Uenishi Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan

Tel: +81-29-838-8627
Fax: +81-29-838-8627
Email: huenishi@affrc.go.jp

EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library

Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

FEATURES

source

1..679
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVR010067A07"
/issue_type="ovary"
/dev_stage="adult"
/clone_lib="full-length enriched swine cDNA library, adult
ovary"

ORIGIN

Alignment Scores:

Pred. No.:	6,32e-102	Length:	679
Score:	1095.00	Matches:	202
Percent Similarity:	96.8%	Conservative:	7
Best Local Similarity:	93.5%	Mismatches:	7
Query Match:	27.7%	Indels:	0
DB:	5	Gaps:	0

US-10-616-788-2 (1-738) x BW65550 (1-679)

```

QY 1 MetAlaProTrrPleuGlnLeuCySeSerValPhePheThrValAlaAlaCylLeuAluGly 20
DB 32 ATGAGCCCGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 91
QY 21 SeGlnLeuAlaValAlaAlaGlyGlySerGlyYArgAlaTrpGlyValAlaPThrCySeGly 40
DB 92 TCGCAATGGCCGCTGCGCGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 151
QY 41 TrpAlaGlyValGlyProAlaSerArgAsnSerGlyLeuTyraAsnIleThrPheLeuTyr 60
DB 152 TGGAGGGGAGATGGGGCGCGCGAGCAACAGTGGCGCTGCAACAATCATCTTCAGATAT 211
QY 61 AspAsnCySeThrThrTyLeuAsnProValGlyLeuHisValIleAlaAspAlaGlnAsn 80
DB 212 GACAACCTGCACCACTTACTGAGTCTGCTGCGGAGAGCATGATGCGCGCAGCAAT 271
QY 81 IleThrIleSerGlnTyraCySeHisAspGlnValAlaValThrIleLeuTTPSerPro 100
DB 272 ATCCACCTCAGTCAAGTACGCTGCGCACAGCAAGTGGCAGTCCATCTCTGCTCCCA 331
QY 101 GtAlaLeuGlyIleGluPheLeuGlyGlyPheArgValIleLeuGluGluLeuLeuSer 120
DB 332 GGGGCCCTCGGCAATCGAATTCCTTAAGAGATTCGGGTAAATATCTGAGAGGCTGAATCA 391
QY 121 GluGlyAArgGlnCySeGlnGlnLeuIleLeuLeuAspProLysGlnLeuAsnSerSerPhe 140
DB 392 GAAAGGAAGACAGTGCACCAACATGATTCGAAAGGACCCGGAAGCAGCTCAACAGTACCTTC 451
QY 141 LysArgThrGlnIleGluSerGlnProPheLeuAsnMetLysPheGluTrpArgPhePhe 160
DB 452 AAAAGAGCTGAATGGAATCTCAGCTTCTCTGAATATGAATTTGAAACAGATTACTTT 511
QY 161 ValIleValValProPheProSerIleLysAsnGluSerAsnTyHisProPhePhe 180
DB 512 GTCAAGATTGCTCTTCTTCTTCATTAAAGAAAGCAATATATCACCCTTCTTCTTT 571
QY 181 ArgThrArgAlaCySeAspLeuLeuGlnProAspAsnLeuAlaCySeLysProPheTyr 200
DB 572 AGAAGCCGCACTGTGACTGTATATACAGCCGGAACCCGGCTGTAAACCCCTTCTGG 631

```

QY 201 LysProArgAsnLeuAlaAlaIleSerGlnIleGlySerAspMetGlnVal 216
DB 632 AGGCTGGAGACCTCATCAATCCCAACATGGTCAATGCAATGCAATG 679

RESULT 10
BU221978
LOCUS
DEFINITION
603105617F1 CSBQCHN04 Gallus gallus cDNA clone CHEST44a6 5', mRNA
sequence.
ACCESSION
BU221978
VERSION
BU221978.1 GI:25410688
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 692)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Boscch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES

source

1..692
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="CHEST44a6"
/issue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_lib="CSBQCHN04"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site 1: EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.:	8.91e-101	Length:	692
Score:	1084.00 <td>Matches:</td> <td>190</td>	Matches:	190
Percent Similarity:	95.2%	Conservative:	26
Best Local Similarity:	83.7%	Mismatches:	11
Query Match:	27.5%	Indels:	0
DB:	5	Gaps:	0

US-10-616-788-2 (1-738) x BU221978 (1-692)

```

QY 97 LeuTTPSerProGlyAlaLeuGlyIleGluPheLeuGlyGlyPheArgValIleLeuGlu 116
DB 10 GTTGGACGACCAATGCCATTGGGATTAATACCTGAAGAGATTCGCGTAAATCTTGA 69
QY 117 GluLeuLysSerGlyGlyArgGlnCySeGlnGlnLeuIleLeuLysAspProLysGlnLeu 136

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Db 70 GAGTAAATACAGGAGGACATGTCAGACAGTGGTTTAAAGATCCAAAGCACTC 129
 Qy 137 AasnSerPheleValThrGlyMetGluSerGlnProPheleuAemMetLysPheGlu 156
 Db 130 AGCCCAAGTTTAAAGACAGAAATGCAATCCATCCCTTTGCAAAATCGAAGTTTGA 189
 Qy 157 ThrAspPhePheValLysValValProPheProSerLelLysAengLysSerAsnThrHis 176
 Db 190 AGAGATTACTTGTGCAAGATTGTGCTTTTCCCTTCATTAATAATGAAGATTATTCAC 249
 Qy 177 ProPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 196
 Db 250 CCATTCCTTTCCGAAATCCGCAATCGCATTAATGCTTACAGCCAGAAACCTCATCTGC 309
 Qy 197 LysPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 216
 Db 310 AAACCTTACGTAAGCCAGCAATCTGAATGTTACCGACGAGGGTTTAAATATGCAAGTG 369
 Qy 217 SerPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 236
 Db 370 TCTTTGATCATGCTCCCAACATTTGATTAATTAATTAATTAATTAATTAATTAATTA 429
 Qy 237 LysHISgluGlyProPheLysArgLysThrCysLysGlnGluGlnThrGluThrThr 256
 Db 430 AAGCATTAAGGCGCATTCAGCAAAAGACCTGCAAAACAGATCAAAACAGATCAACA 489
 Qy 257 SerCysLeuLeuGlnAenValSerProGlyAspPhePhePhePhePhePhePhePhePhe 276
 Db 490 AGTTGTATCTTCGAAATGTAATCCAGGGGATTAATTAATTAATTAATTAATTAATTA 549
 Qy 277 AsnThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 296
 Db 550 AATACCAACCAAGAAACCAATGCACTATGCACTAAACCAAGATCACTTCGCTGGCTGGA 609
 Qy 297 ProLleArgLamEalIleThrValProLeuValValIleSerAlaPheAlaThrLeu 316
 Db 610 CCATTAAGACTATGCAATTCAGTCCCTTACTTGTCTCATTTGCGCATTCGCAACACTT 669
 Qy 317 PheThrValMetCysArgLys 323
 Db 670 TTCACAGTATGTCGCCA 690

RESULT 11
 BU909956 907 bp mRNA linear EST 17-OCT-2002
 LOCUS 10487146 NICHD XGC Emb1 Xenopus laevis cDNA clone
 DEFINITION IMAGE:6635685 5', mRNA sequence.
 ACCESSION BU909956
 VERSION BU909956.1 GI:24091870
 SOURCE EST.
 ORGANISM Xenopus laevis (African clawed frog)
 Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Xenopus.
 1 (bases 1 to 907)
 NCI-CCGATP http://www.ncbi.nlm.nih.gov/ncicgcp.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaap-remail.nih.gov
 Tissue Procurement: Martha Rabbert, Steven L. Klein, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: NCI-CCGATP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L1AM14210 row: d column: 21
 High quality sequence stop: 716.
 Location/Qualifiers

source 1..907
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:6635685"
 /issue_type="embryo (stage 10)"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NICHD XGC Emb1"
 /notes="Vector: pCMV-SF001; Site 1: NCI; Site 2: Salt; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.55 kb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:
 Pred. No.: 6,72e-98 Length: 907
 Score: 1058.00 Matches: 186
 Percent Similarity: 83.6% Conservative: 49
 Best Local Similarity: 66.2% Mismatches: 43
 Query Match: 26.8% Indels: 3
 DB: 5 Gaps: 1

US-10-616-788-2 (1-738) x BU909956 (1-907)

Qy 26 AlaAlaGlyGlySerGly-----ArgAlaLysPheValAspThrCysGlyTrpArgGly 43
 Db 63 GCGACGAGAGGTTCCGAGGACACAGAGGAGGAGTTAGCAAGTCGTGCGCTCCAGGGA 122
 Qy 44 ValGlyProLysSerArgAsnSerGlyLeuValAsnIleThrPhePhePhePhePhePhe 63
 Db 123 GCGTGTGCTGACGAGAACTGCGGCTGCGCAAGTCACTTCGATATGCAACTGC 182
 Qy 64 ThrThrThrLeuAsnProValGlyValIleAlaAspAlaGlnAsnIleThrIle 83
 Db 183 ACTGCTTACATGAACTCCGCGGGAGAACACAGATGGGATGTGAGAACATTAACCATC 242
 Qy 84 SerGlnTrpAlaCysHisAspGlnValAlaValThrIleLeuThrSerProGlyAlaLeu 103
 Db 243 AGCCAAATTCCTGCAACAGCAAGTGGCGTTTCTGTTCTTGGACGCGCAATGATATC 302
 Qy 104 GlyIleGluPheLeuLysGlyPheArgValIleLeuGluGluLeuLysSerGluArg 123
 Db 303 GGCATTGAATACCTGAAGGCTTCGCGGTGCTGTGAAGATGTAAGTGGAGGGAGG 362
 Qy 124 GlnCysGlnGluLeuLysAspProLysGlnLeuAsnSerPheLysArgThr 143
 Db 363 TTCGTGACGAGATGTGATGAAGATCCAGACACTGATGAATCAAAAGAGTT 422
 Qy 144 GlyMetGluSerGlnProPheLeuAemMetLysPheGluThrAspPheValLysVal 163
 Db 423 GTAATGGAACACAACTATTTGCAACTGAAATTTGAAACAGATTAATTTGCAAAATTT 482
 Qy 164 ValProPheProSerLelLysAengLysSerAsnThrHisProPhePhePhePhePhePhe 183
 Db 483 GTCCATTTCCTCCCGCAGAAATGAAGATTAATCAATCCGCTTCTTCAGAGCCGC 542
 Qy 184 AlaCysAspLeuLeuGlnProAspAsnLeuAlaCysLysProPhePhePhePhePhePhe 203
 Db 543 ACCTGCGAGTCGTTGTCAGCCGACAGCTGACCTGACCTGACCTGACCTGACCTGACCT 602
 Qy 204 AsnLeuAsnIleSerGlnHisGlySerAspMetGlnValSerPhePhePhePhePhePhe 223
 Db 603 AAGGTCAACGTCACCAACAGGAGCATCAATGACAGCTGCTTCGACCAACGCGCCGAG 662
 Qy 224 AsnPheGlyPheArgPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 243
 Db 663 AATTTGCGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 722
 Qy 244 ArgLysThrCysLysGlnGluGlnThrThrThrThrThrThrThrThrThrThrThrThr 263
 Db 723 CAGAAATATGCGCGAAGGTCGAAACAGACTTCAACCAAGCTGATCCAGAAAGTA 782
 Qy 264 SerProGlyAspPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 283

JOURNAL
PUBMED
COMMENT
CONTACT
Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
SOURCE
1. 583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KDN04362"
/tissue="kidney"
/clone_lib="Sugano cDNA library, kidney"

ORIGIN

Alignment Scores:
Pred. No.: 1.06e-94 Length: 583
Score: 1024.00 Matches: 191
Percent Similarity: 98.5% Conservative: 0
Best Local Similarity: 98.5% Mismatches: 3
Query Match: 25.9% Indels: 0
DB: 3 Gaps: 0

US-10-616-788-2 (1-738) x BP275741 (1-583)

QY 498 TyraArgLeuMetAspAlaLeuProGlnLeuCySerHisLeuHisSerArgAspHisGly 517
Db 2 TACAGACTTACGACCAATCTTCTCCAGCTCGTTCCACCTGACCTCCGAGACACGAGC 61

QY 518 LeuGlnGluProGlyGlnHisThrArgGlnGlySerArgArgAntyrPheHisGlySer 537
Db 62 CTCACAGAGCGCGGAGCAGACACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121

QY 538 SerGlyArgSerLeuTyraValAlaLeuCyAspMetHisGlnPheLeuAspGluGluPro 557
Db 122 TCAGGCGCGGCTCCATATGCTGCGCATTTGCAACATGCAAGTTATTATGAGAGAGCC 181

QY 558 AspTrpPheGlnuysGlnPheValProPheHisProProProLeuArgTyraGluPro 577
Db 182 GACTGGTTCCAAAGACGATTGTTCCCTTCATCTCTCCACGCGGCTACCGGAGCCA 241

QY 578 ValLeuGlnuysPheAspSerGlyLeuValLeuAspValMetCyluysProGlyPro 597
Db 242 GTCTTGAGAAATTTGATTCGGGCTTGTTTAATGATGTCATGTCAAACAGGCGCT 301

QY 598 GluSerAspPheCysLeuLysValGluAlaProValLeuGlnuysValThrGlyProAlaAsp 617
Db 302 GAGAGTACTTCTGCTTAAGGTAGAGCGGCTGTTCTTGCGGACCGAGCCAGCCGAC 361

QY 618 SerGlnHisGlnuysSerGlnHisGlyGlyLeuAspGlnAspGlyGlnuysAlaArgProAlaLeu 637
Db 362 TCCAGACAGAGAGTACGATCGGCGGCTGAGCCAAACGAGGAGCGCCGCTGCTT 421

QY 638 AspGlySerAlaAlaLeuGlnProLeuLeuHisThrValuysAlaGlySerProSerAsp 657
Db 422 GACGGTAGCCCGCCCTGCAACCCCTGCTCACACGCTGAAGCGGCGACCCCTCGGAC 481

QY 658 MetProArgAspSerGlyLeuTyraAspSerSerValProSerSerGlnuysLeuSerLeuPro 677
Db 482 ATCCCGGGAGACTCAGGACATCTAGACTCGCTGTGCTCTCATNCGAGCTGTCTTCCA 541

QY 678 LeuMetGlnuysLeuSerThrAspGlnThrGluThrSerSer 691
Db 542 CTATGAGAGGACTCTGAGGAGACACAGAGAACTTTTCC 583

RESULT 14
BU479802 717 bp mRNA linear EST 30-NOV-2002
LOCUS 603843254.F1 CSEQRBN22 Gallus gallus cDNA clone CHEST828k13 5', mRNA
DEFINITION
sequence.
ACCESSION BU479802

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

BU479802.1 GI:25973379
EST.
Gallus gallus (chicken)
Gallus gallus
Archaeopteryx; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
1 (bases 1 to 717)
Boardman, P.E., Sanz-Exquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, M.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
SOURCE
1. 717
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST828k13"
/sex="Male and female"
/tissue type="Chondrocytes isolated from growth plate cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBN22"
/note="Vector: pBluescript II KS(+), site 1: EcoRI; site 2: NotI. This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand and synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:
Pred. No.: 1.67e-94 Length: 717
Score: 1023.50 Matches: 193
Percent Similarity: 91.4% Conservative: 20
Best Local Similarity: 82.8% Mismatches: 18
Query Match: 25.9% Indels: 2
DB: 5 Gaps: 1

US-10-616-788-2 (1-738) x BU479802 (1-717)

QY 266 GlyAspTyrTleLeuLeuValAspAspThrAsnThrThrArguysValMetHisTyr 285
Db 3 GGGGATTATATCATCGAGCTGTCGATGACATTAATACAAAGAAACAAATGCACTAT 62

QY 286 AlaLeuLysProValHisSerProTPAlaGlyProIleArgAlaMetAlaIleThrVal 305
Db 63 GCATTAACAGTACTACTTCCGTGGCGCTGAGCACTAATAGACTATGTCATTACAGTC 122

QY 306 ProLeuValAlaIleSerAlaPheAlaThrLeuPheThrValMetCysArguysLysGln 325
Db 123 CTTTAGTTGTCACTTCGGCATTTGCAACCTTTTCAAGTATGATGCGCAAAAGCAG 182

QY 326 GlnGluAsnIleTyraHisLeuAspGlnuysSerSerGlnuysSerThrTyraAla 345

Db 183 CAAAGGATATATATATCCCATCTTACAAGAGAGACTCAGAATCTTCACGTTATGTCGA 242

QY 346 AAlaLeuProArgGluArgLeuArgProArgProIysValPheLeuCyenYrSerSerIys 365

Db 243 GATCTCCCTGTGGAAAGACTTCGCCCCGCCAAAGATATTCATCTGCTATTCAGTAAA 302

QY 366 AArgIylGlnMetIleMetAsnValValGlnCySPhealIaYrPheLeuGlnAspPheCyS 385

Db 303 GATTGCCAGAAACACATTAAATGATACAGAGCTTGGCTATTTCTCCAGGACTTCGT 362

QY 386 G1yCySgluValAlaLeuAspLeuTrpGluAspPheSerLeuCyArgGluGlyGlnArg 405

Db 363 GCGCTGTAGCTGCGCTCTGGATTGTGGGAAGATCTGAATAATTGTAAGAAAGTCAGAA 422

QY 406 G1uTrpValIleGlnIysIleHisGlnSerGlnPheIleIleValIaCySerIysGly 425

Db 423 GAATGCGTCATTAAAAAATATAATAGCTCAGTTATCATCATCTGTGTCTCCAAAGGA 482

QY 426 MetIysTrpPheValAspIleIysAsnYrIysHisIysGlyGlyGlyArgGlySerIy 445

Db 483 ATGAATAATCTTGTTGAAAAAAGATTGAAACCAAGAGAGTAAACCAAGACACAGGG 542

QY 446 LysGlyGluLeuPheLeuValAlaValSerAlaIleAlaGluIysLeuArgGlnAla-Ly 465

Db 543 AAAGAGAACTCTTCTCTGTGTGTGTACTGTTCAGAGAGAGCTTCGTCAAGCAAAA 602

QY 465 SGLnSerSerSerAlaAlaLeuSerLysPheIleAlaValYrPheAspYrSerCySgl 485

Db 603 GCAGATATCAAAAT--GACCTCTCGAAGATTCATTGCACTCACTTGAATTACTCCTGGA 659

QY 485 uG1AspValProGlyIleLeuAspLeuSerThrIys 497

Db 660 GGGAGACATTCCTGTATTCGTGATCTAAGTACCAAA 696

RESULT	15
LOCUS	CVI26214
DEFINITION	CVI26214 748 bp mRNA linear EST 02-SEP-2004
ACCESSION	AGNCOURT_31913B56 NIH_MGC_238 Rattus norvegicus cDNA clone IMAGE:145313 5', mRNA sequence.
VERSION	CVI26214
KEYWORDS	CVI26214.1 GI:51860897
SOURCE	EST.
ORGANISM	Rattus norvegicus (Norway rat)
REFERENCE	Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 748) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
AUTHORS	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NCI Bldg. 31 RM10A07 Bethesda, MD 20892
TITLE	Email: cgs@db-ref@mail.nih.gov
JOURNAL	Tissue Procurement: Howard Jacobo
COMMENT	cDNA Library Preparation: Express Genomics cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LLM15711 row: p column: 15 High quality sequence stop:669.

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FEATURES
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/db_xref="taxon:10116"
/clone="IMAGE:745313"
/tissue_type="testis, pooled"
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/lab_host="DH10B TONA"
 /clone_l1b="NIH_MGC_238"
 /note="Organ: testis; Vector: pExpress-1; Site 1: EcoRV;
 Site 2: NotI; RNA obtained from testis tissue of 8 wk old
 animal. Tissues were snap-frozen and kept at -80C before
 RNA extraction and purification (TRI-reagent method). cDNA
 was primed using oligo-dT primer:
 5'-pGACTGACTTGAATCCGAGCGGCCCCCT(T)25-3' and cloned into
 the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
 resulted in an average insert size of 1.9 kb. This primary
 library is normalized (non-normalized primary library is
 NIH_MGC 237) and was constructed by Express Genomics
 (Frederick, MD)"

[illegible]

US-10-616-788-2 (1-738) x CV126214 (1-748)

Oy	398	berleucyaaaguguguaaguguaaguttrpvallelgluyvlelengisuserglnphe	417
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Oy	418	llelevalvalcyserilyvglymetlyetyrphelvalnprlylvaaentytlyvnh	437
Db	63	atcatgttcgtgagctccaaagaccatgaagatctgttgatgataaagaaagcttcagacc	122
Oy	438	lygllygllyglng---glyserglyvlyglglylphenleuvalalvalserala	456
Db	123	aaagagagcagctgctggccgacagggccaaagaaagatcttccatggccggagacc	182
Oy	457	llelaaglylvleuarginalalyglinserserzlaalaleuserilyphele	476
Db	183	attgctcagaagatccgctcagacccaagacagatctctggcactgagacaaattcatc	242
Oy	477	alavaltyrphearptyrsercyvgluglyaaervalproglylleleuapleuserthr	496
Db	243	accctctacttggatgataattccttgaaaggggaatgctccctgacccctgacccagacacc	302
Oy	497	lyetyrargleumecarapenleuproglnleucyserhileuhsiseratgarpnh	516
Db	303	aaatracaaagctcatgacaaaccttccagactctgttccatcttaccatctcagagaaacag	362
Oy	517	glyleuglngluproglyglinhivthraarglnglyserarglrgaantyrpheatgser	536
Db	363	-----gagagagctggcgccacgacccacagacacagacagcagaaagaaactgttccgagcc	416
Oy	537	lyserglyrgerseleutyvalalallecyaamemehvglinpheleaprgluglu	556
Db	417	aaactggccgctccctcgtatggttgcattttgcacatgcacacagatttatgtagaagaa	476
Oy	557	prokaptprphegluyvglinphevalpropheniearobprobroleuaargtyrarglu	576
Db	477	cttgcactggttgcagaaagcagatttgatcccttcacacccgccctcgccctacagag	536
Oy	577	provalleugluyvphelapserglyleuvalleuanaarvalmetcylyvprogly	596
Db	537	ccaaactcttgagaaagttgactcagagtttggttttaantatgtcatnAACCAACCAAGG	596
Oy	597	progluserarphocyvleulyvalglualprovalleugllyalatrnglyproala	616
Db	597	ccagaaagtaactttctgcccctgaaagttgagacgttcataacttggggcactggcgacact	656
Oy	617	apserglnhis-----gluserglnhisglylyleuaprgln-----	629
Db	657	gactcttactcatatcctggaagatgacatgacagcccttgacacagacacatgagccagacc	716

Qy 630 -----AapGlyGluAlaArgProAlaLeu 637
|||
Db 717 CGCTGTGATGTGTGGCTGCTGCTGCAAGCCCTG 746

Search completed: March 1, 2006, 09:18:55
Job time : 7498 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 10:31:11 ; Search time 165 Seconds
(without alignments)
1868.837 Million cell updates/sec

Title: US-10-616-788-2

Sequence: 1 MAPWQLGCVFTVNAALNG.....SCKADICGRSYDELAAVAP 738

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3948	100.0	738	3	US-09-809-567-2
2	3948	100.0	738	4	US-10-216-156-2
3	3948	100.0	738	4	US-10-616-788-2
4	3948	100.0	738	4	US-10-842-006-4
5	3918	99.2	739	3	US-09-912-157-8
6	3918	99.2	739	4	US-10-717-282-8
7	3908	99.0	739	5	US-10-842-006-2
8	3908	99.0	739	5	US-10-608-449-2
9	3901	98.8	753	3	US-09-912-157-2
10	3901	98.8	753	4	US-10-717-282-2
11	3891	98.6	753	3	US-09-912-157-5
12	3891	98.6	753	4	US-10-717-282-5
13	3835.5	97.2	738	3	US-09-863-818A-10
14	3835.5	97.2	738	4	US-10-749-144-10
15	3835.5	97.2	738	5	US-10-924-667-10
16	3706	93.9	728	4	US-10-104-047-3399
17	3681.5	93.2	728	3	US-09-874-503-18
18	3681.5	93.2	728	3	US-09-816-744-18
19	3681.5	93.2	728	3	US-09-747-259-18
20	3681.5	93.2	728	3	US-09-908-827-18
21	3681.5	93.2	728	4	US-10-000-157-18
22	3681.5	93.2	728	4	US-10-410-927-18
23	3681.5	93.2	728	4	US-10-410-374-18
24	3681.5	93.2	728	4	US-10-410-552-18
25	3681.5	93.2	728	4	US-10-458-442-18
26	3681.5	93.2	728	4	US-10-408-385-18
27	3382	85.7	739	3	US-09-912-157-12

28	3382	85.7	739	4	US-10-717-282-12	Sequence 12, Appl
29	3164	80.1	595	5	US-10-477-714-16	Sequence 16, Appl
30	3158	80.0	595	4	US-10-608-449-4	Sequence 4, Appl
31	2701.5	68.4	554	4	US-10-343-348-16	Sequence 16, Appl
32	1333	33.8	296	4	US-09-616-788-19	Sequence 19, Appl
33	315	8.0	810	3	US-09-809-567-3	Sequence 3, Appl
34	315	8.0	810	4	US-10-216-156-3	Sequence 3, Appl
35	315	8.0	810	4	US-10-616-788-3	Sequence 3, Appl
36	315	8.0	866	3	US-09-778-971-9	Sequence 9, Appl
37	315	8.0	866	4	US-10-033-522-1	Sequence 1, Appl
38	315	8.0	866	4	US-10-207-655-107	Sequence 107, App
39	315	8.0	866	4	US-10-742-161-10	Sequence 10, Appl
40	315	8.0	866	4	US-10-742-372-10	Sequence 10, Appl
41	315	8.0	866	4	US-10-646-308-4	Sequence 4, Appl
42	315	8.0	866	5	US-10-918-084-1	Sequence 1, Appl
43	315	8.0	866	6	US-11-128-403-9	Sequence 5, Appl
44	298	7.5	864	4	US-10-742-161-2	Sequence 2, Appl
45	298	7.5	864	4	US-10-742-372-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1									
US-09-809-567-2									
Sequence 2, Application US/09809567									
Patent No. US20020045213A1									
GENERAL INFORMATION:									
APPLICANT: Jing, Shuguan									
TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof									
FILE REFERENCE: 01017/36916A									
CURRENT APPLICATION NUMBER: US/09/809,567									
CURRENT FILING DATE: 2001-03-15									
PRIOR APPLICATION NUMBER: 09/724,460									
PRIOR FILING DATE: 2000-11-28									
PRIOR APPLICATION NUMBER: 60/189,816									
PRIOR FILING DATE: 2000-03-16									
NUMBER OF SEQ ID NOS: 17									
SOFTWARE: PatentIn Ver. 2.0									
SEQ ID NO 2									
LENGTH: 738									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-809-567-2									
Query Match									
Best Local Similarity 100.0%; Score 3948; DB 3; Length 738;									
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MAPWQLGCVFTVNAALNGSOLAAGSGRAGVDTGMRGVGPASRNSGLNITTFKX	60						
DB	1	MAPWQLGCVFTVNAALNGSOLAAGSGRAGVDTGMRGVGPASRNSGLNITTFKX	60						
QY	61	DNCTTLYNVGKRVADANNTITSOYACHDOVAVITLMSGALGIFLNGFRITBELKS	120						
DB	61	DNCTTLYNVGKRVADANNTITSOYACHDOVAVITLMSGALGIFLNGFRITBELKS	120						
QY	121	EGRQCOQLIKPKQKLNSSFKRTGMSQPLNKKFETDFVKVVPSSIKNSNHPFF	180						
DB	121	EGRQCOQLIKPKQKLNSSFKRTGMSQPLNKKFETDFVKVVPSSIKNSNHPFF	180						
QY	181	RTRACDLILQPNLACKPFWKPRNLTISQHGSDMOVSPHAPNNGFRFFLYLKXKHG	240						
DB	181	RTRACDLILQPNLACKPFWKPRNLTISQHGSDMOVSPHAPNNGFRFFLYLKXKHG	240						
QY	241	PPFRKCKOEQTETTSCLQNVSPEDYIIEVDNTNTRKVMHVALKXVSPMAGPIRA	300						
DB	241	PPFRKCKOEQTETTSCLQNVSPEDYIIEVDNTNTRKVMHVALKXVSPMAGPIRA	300						
QY	301	MAITVPLVVISAPATLFTVMCRKKQOENIYSHLDESSSSSTYTAALPRERLAPRKVEL	360						
DB	301	MAITVPLVVISAPATLFTVMCRKKQOENIYSHLDESSSSSTYTAALPRERLAPRKVEL	360						

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QY 361 CYSSKQGNMNMVQCFAYFLQDFCGCEVALDLMEDFSLCREGQREWVIOKIHESQFIIV 420
DB 361 |-----|-----|-----|-----|-----|-----|-----|-----|
QY 421 VCSKGMKYPVDDKKNYKHKGGGSGKGEFLVAVASIAEKLROAKOSSAALSKEFLAVVF 480
DB 421 |-----|-----|-----|-----|-----|-----|-----|-----|
QY 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGR 540
DB 481 |-----|-----|-----|-----|-----|-----|-----|-----|
QY 541 SLVVAICNNHQFTIDEBEDWFEKQFVPHPPPLRYREPVLEKFPDGLVNDVMCKPGESD 600
DB 541 |-----|-----|-----|-----|-----|-----|-----|-----|
QY 601 FCILKVEAPVLGATGPADSGHESQHGGILDQGEARPALDGSAAIOPPLHTTVKAGSPSDMPR 660
DB 601 |-----|-----|-----|-----|-----|-----|-----|-----|
QY 661 DSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGIGBEEPPALPSKLLSSGSC 720
DB 661 |-----|-----|-----|-----|-----|-----|-----|-----|
QY 721 KADLCGRSYTDELHAAVAP 738
DB 721 |-----|-----|-----|-----|-----|-----|-----|-----|
KADLCGRSYTDELHAAVAP 738

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RESULT 2
US-10-216-156-2
; Sequence 2, Application US/10216156
; Publication No. US20030099980A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shugian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/10/216,156
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US/09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-156-2

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Query Match 100.0%; Score 3948; DB 4; Length 738;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPWQLCSVFTVNAACLNQSOLAIVAAGSGRAMGVDTGCMRGVGPASRNSGLYNITFKY 60
DB 1 |-----|-----|-----|-----|-----|-----|-----|-----|
MAPWQLCSVFTVNAACLNQSOLAIVAAGSGRAMGVDTGCMRGVGPASRNSGLYNITFKY 60
QY 61 DNTCTTLNPNVGGKIVADANITISQYACHDQVAVTILMSGALGIEFLKGFVILBELKS 120
DB 61 |-----|-----|-----|-----|-----|-----|-----|-----|
DNTCTTLNPNVGGKIVADANITISQYACHDQVAVTILMSGALGIEFLKGFVILBELKS 120
QY 121 EGRQCOQLILKDBKOLNSSPKRTGMSQPLANKFETDYFVKVVPSPSINKESNYHPFPF 180
DB 121 |-----|-----|-----|-----|-----|-----|-----|-----|
EGRQCOQLILKDBKOLNSSPKRTGMSQPLANKFETDYFVKVVPSPSINKESNYHPFPF 180
QY 181 KTRACQLLLOPDLACKPFWKPRNLINISQHSQMSQFSDHAPNFGRRFFYLHYKLKHG 240
DB 181 |-----|-----|-----|-----|-----|-----|-----|-----|
KTRACQLLLOPDLACKPFWKPRNLINISQHSQMSQFSDHAPNFGRRFFYLHYKLKHG 240

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QY 241 PFKRKTCKOBTETETSCILQNVSPGDYIIELVDDINTTRKVMYALKEVHSPMAGPIRA 300
DB 241 |-----|-----|-----|-----|-----|-----|-----|-----|
PFKRKTCKOBTETETSCILQNVSPGDYIIELVDDINTTRKVMYALKEVHSPMAGPIRA 300
QY 301 MATTVPLVVISAPATLFTWCRKQOENYSHLDESSSSSTYTALPREBLRPRKVL 360
DB 301 |-----|-----|-----|-----|-----|-----|-----|-----|
MATTVPLVVISAPATLFTWCRKQOENYSHLDESSSSSTYTALPREBLRPRKVL 360
QY 361 CYSSKQGNMNMVQCFAYFLQDFCGCEVALDLMEDFSLCREGQREWVIOKIHESQFIIV 420
DB 361 |-----|-----|-----|-----|-----|-----|-----|-----|
CYSSKQGNMNMVQCFAYFLQDFCGCEVALDLMEDFSLCREGQREWVIOKIHESQFIIV 420
QY 421 VCSKGMKYPVDDKKNYKHKGGGSGKGEFLVAVASIAEKLROAKOSSAALSKEFLAVVF 480
DB 421 |-----|-----|-----|-----|-----|-----|-----|-----|
VCSKGMKYPVDDKKNYKHKGGGSGKGEFLVAVASIAEKLROAKOSSAALSKEFLAVVF 480
QY 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGR 540
DB 481 |-----|-----|-----|-----|-----|-----|-----|-----|
DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGR 540
QY 541 SLVVAICNNHQFTIDEBEDWFEKQFVPHPPPLRYREPVLEKFPDGLVNDVMCKPGESD 600
DB 541 |-----|-----|-----|-----|-----|-----|-----|-----|
SLVVAICNNHQFTIDEBEDWFEKQFVPHPPPLRYREPVLEKFPDGLVNDVMCKPGESD 600
QY 601 FCILKVEAPVLGATGPADSGHESQHGGILDQGEARPALDGSAAIOPPLHTTVKAGSPSDMPR 660
DB 601 |-----|-----|-----|-----|-----|-----|-----|-----|
FCILKVEAPVLGATGPADSGHESQHGGILDQGEARPALDGSAAIOPPLHTTVKAGSPSDMPR 660
QY 661 DSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGIGBEEPPALPSKLLSSGSC 720
DB 661 |-----|-----|-----|-----|-----|-----|-----|-----|
DSGIYDSSVPSSELSLPLMEGLSTDQETSSLTESVSSSGIGBEEPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAAVAP 738
DB 721 |-----|-----|-----|-----|-----|-----|-----|-----|
KADLCGRSYTDELHAAVAP 738

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RESULT 3
US-10-616-788-2
; Sequence 2, Application US/10616788
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shugian
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/39525
; CURRENT APPLICATION NUMBER: US/10/616,788
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-788-2

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Query Match 100.0%; Score 3948; DB 4; Length 738;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPWQLCSVFTVNAACLNQSOLAIVAAGSGRAMGVDTGCMRGVGPASRNSGLYNITFKY 60
DB 1 |-----|-----|-----|-----|-----|-----|-----|-----|
MAPWQLCSVFTVNAACLNQSOLAIVAAGSGRAMGVDTGCMRGVGPASRNSGLYNITFKY 60
QY 61 DNTCTTLNPNVGGKIVADANITISQYACHDQVAVTILMSGALGIEFLKGFVILBELKS 120
DB 61 |-----|-----|-----|-----|-----|-----|-----|-----|
DNTCTTLNPNVGGKIVADANITISQYACHDQVAVTILMSGALGIEFLKGFVILBELKS 120

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QY 121 EGRQCOOLIKDPKOLNSPFRKTMESOPFLANKFETDVFVKVPPSPINKESNYHPFF 180
DB 121 EGRQCOOLIKDPKOLNSPFRKTMESOPFLANKFETDVFVKVPPSPINKESNYHPFF 180
QY 181 RTACDILLQPDNLACKPFKPRNLINISQHSQDMQVSPDAPNFGFRFYLYKLGHEG 240
DB 181 RTACDILLQPDNLACKPFKPRNLINISQHSQDMQVSPDAPNFGFRFYLYKLGHEG 240
QY 241 PFRKCTCKOQOTETTSTCLQONVSPGDYIIELVDDNTTRKVMHYALKPHSPWAGPIRA 300
DB 241 PFRKCTCKOQOTETTSTCLQONVSPGDYIIELVDDNTTRKVMHYALKPHSPWAGPIRA 300
QY 301 MATTVPLVVISAPATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
DB 301 MATTVPLVVISAPATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
QY 361 CYSKQGNHNMVVOCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQPIIV 420
DB 361 CYSKQGNHNMVVOCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQPIIV 420
QY 421 VCSKMKKTFYVDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKFLAVYF 480
DB 421 VCSKMKKTFYVDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKFLAVYF 480
QY 481 DYSCEGDVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSRNRYFRSKSGR 540
DB 481 DYSCEGDVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSRNRYFRSKSGR 540
QY 541 SLVVAICNMHQFIDEBPDWFEKQFVFPHPPLRYRBPVLEKFPDGLVINDVMCKPGBESD 600
DB 541 SLVVAICNMHQFIDEBPDWFEKQFVFPHPPLRYRBPVLEKFPDGLVINDVMCKPGBESD 600
QY 601 FCLKEAPVLTGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPSPMDPR 660
DB 601 FCLKEAPVLTGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPSPMDPR 660
QY 661 DSGIYSSVPSSELSPLMEGLSTDQETSTLRESVSSSGLGEEBPPALPSKLLSSGSC 720
DB 661 DSGIYSSVPSSELSPLMEGLSTDQETSTLRESVSSSGLGEEBPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAAP 738
DB 721 KADLCGRSYTDELHAAP 738

RESULT 4

US-10-842-006-4
; Sequence 4, Application US/10842006
; Publication No. US2004023104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SBF Molecule and Uses
; FILE REFERENCE: MP103-071P1RM
; CURRENT APPLICATION NUMBER: US/10/842, 006
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-842-006-4

Query Match 100.0%; Score 3948; DB 5; Length 739;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFMLQCSVFYFNACLNGSOLAVAGSGRAMGVDTGMRGVGAPSRNSGLYNTFFKY 60
DB 1 MAFMLQCSVFYFNACLNGSOLAVAGSGRAMGVDTGMRGVGAPSRNSGLYNTFFKY 60

QY 61 DNCTTYLNPVKGKVIADAQNTTISOYACHDOVAVTILMSGALGIEFLKGFVILEELKS 120
DB 61 DNCTTYLNPVKGKVIADAQNTTISOYACHDOVAVTILMSGALGIEFLKGFVILEELKS 120
QY 121 EGRQCOOLIKDPKOLNSPFRKTMESOPFLANKFETDVFVKVPPSPINKESNYHPFF 180
DB 121 EGRQCOOLIKDPKOLNSPFRKTMESOPFLANKFETDVFVKVPPSPINKESNYHPFF 180
QY 181 RTACDILLQPDNLACKPFKPRNLINISQHSQDMQVSPDAPNFGFRFYLYKLGHEG 240
DB 181 RTACDILLQPDNLACKPFKPRNLINISQHSQDMQVSPDAPNFGFRFYLYKLGHEG 240
QY 241 PFRKCTCKOQOTETTSTCLQONVSPGDYIIELVDDNTTRKVMHYALKPHSPWAGPIRA 300
DB 241 PFRKCTCKOQOTETTSTCLQONVSPGDYIIELVDDNTTRKVMHYALKPHSPWAGPIRA 300
QY 301 MATTVPLVVISAPATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
DB 301 MATTVPLVVISAPATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
QY 361 CYSKQGNHNMVVOCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQPIIV 420
DB 361 CYSKQGNHNMVVOCFAYFLQDFCGCEVALDLMEDFSLCREGOREWVIOKIHESQPIIV 420
QY 421 VCSKMKKTFYVDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKFLAVYF 480
DB 421 VCSKMKKTFYVDKKNYKKGSGSGKGEFLVAVSAIAEKLROAKOSSAALSKFLAVYF 480
QY 481 DYSCEGDVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSRNRYFRSKSGR 540
DB 481 DYSCEGDVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSRNRYFRSKSGR 540
QY 541 SLVVAICNMHQFIDEBPDWFEKQFVFPHPPLRYRBPVLEKFPDGLVINDVMCKPGBESD 600
DB 541 SLVVAICNMHQFIDEBPDWFEKQFVFPHPPLRYRBPVLEKFPDGLVINDVMCKPGBESD 600
QY 601 FCLKEAPVLTGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPSPMDPR 660
DB 601 FCLKEAPVLTGATGPADSOHESQHGGLDQGEARPALDGSAAALQPLHTYKAGSPSPMDPR 660
QY 661 DSGIYSSVPSSELSPLMEGLSTDQETSTLRESVSSSGLGEEBPPALPSKLLSSGSC 720
DB 661 DSGIYSSVPSSELSPLMEGLSTDQETSTLRESVSSSGLGEEBPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAAP 738
DB 721 KADLCGRSYTDELHAAP 738

RESULT 5

US-09-912-157-8
; Sequence 8, Application US/09912157
; Patent No. US28020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-157-8

Query Match 99.2%; Score 3918; DB 3; Length 739;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MAFWLOLCVFTVNAACNGSOLAAGSGRAMGVDTGMRGVGPASRNSGLYNITFKY 60
DB 1 MAFWLOLCVFTVNAACNGSOLAAGSGRAMGVDTGMRGVGPASRNSGLYNITFKY 60
QY 61 DICTTYLANPVGKVIADAOQNTTISQYACHDQVAVTILMSGALGIEFLKGFVILEELKS 120
DB 61 DICTTYLANPVGKVIADAOQNTTISQYACHDQVAVTILMSGALGIEFLKGFVILEELKS 120
QY 121 EGRQCOQLIKDKPKOLNSFFKRTGMSQFPLMKKEFTDYFVYVPPPSIKNSNHYHPPF 180
DB 121 EGRQCOQLIKDKPKOLNSFFKRTGMSQFPLMKKEFTDYFVYVPPPSIKNSNHYHPPF 180
QY 181 RTACDILLQPDNLACKPFWKPRNLNISQHSQDMQVSPDHA PHNFGFRFFYLHYKLKHG 240
DB 181 RTACDILLQPDNLACKPFWKPRNLNISQHSQDMQVSPDHA PHNFGFRFFYLHYKLKHG 240
QY 241 PFRKRTCKEQTTETTSCLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA 300
DB 241 PFRKRTCKEQTTETTSCLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA 300
QY 301 MATTVPLVVISAPATLFTWCRKQOENIYSHLDESSSSSTYTALPRERLRPRKRVFL 360
DB 301 MATTVPLVVISAPATLFTWCRKQOENIYSHLDESSSSSTYTALPRERLRPRKRVFL 360
QY 361 CYSKQGMKYFVDKKNYGHKGSGSGKGEFLVAVSAIAEKLRQAKQSSAALSKFLAVYF 480
DB 361 CYSKQGMKYFVDKKNYGHKGSGSGKGEFLVAVSAIAEKLRQAKQSSAALSKFLAVYF 480
QY 421 VCSKGMKYFVDKKNYGHKGSGSGKGEFLVAVSAIAEKLRQAKQSSAALSKFLAVYF 480
DB 421 VCSKGMKYFVDKKNYGHKGSGSGKGEFLVAVSAIAEKLRQAKQSSAALSKFLAVYF 480
QY 481 DVSCEBDVGIIDLSKTKRYLMDNLPOLCSHLHSRHDGLQEPQHTQGSRRNYFRKSGR 540
DB 481 DVSCEBDVGIIDLSKTKRYLMDNLPOLCSHLHSRHDGLQEPQHTQGSRRNYFRKSGR 540
QY 541 SLVVAICNMHQFIDEPRDFEKOFPFHPPLRYREPVLEKDFSGVLNDVMCKPESD 600
DB 541 SLVVAICNMHQFIDEPRDFEKOFPFHPPLRYREPVLEKDFSGVLNDVMCKPESD 600
QY 601 FCUKVEAPVLTGATGPADSGHESQHGLDQGEARPALDGSAAALQPLHTVKAGSPSDMPR 660
DB 601 FCUKVEAPVLTGATGPADSGHESQHGLDQGEARPALDGSAAALQPLHTVKAGSPSDMPR 660
QY 661 DSGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSGLGEERPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSGLGEERPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAYAP 738
DB 721 KADLCGRSYTDELHAYAP 738

RESULT 6
US-10-717-282-8
; Sequence 8, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Priesnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717,282
; CURRENT FILING DATE: 2003-11-19
; PRIOR APPLICATION NUMBER: US/09/912,157
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PaacSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 739
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-717-282-8
Query Match 99.2%; Score 3918; DB 4; Length 739;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAFWLOLCVFTVNAACNGSOLAAGSGRAMGVDTGMRGVGPASRNSGLYNITFKY 60
DB 1 MAFWLOLCVFTVNAACNGSOLAAGSGRAMGVDTGMRGVGPASRNSGLYNITFKY 60
QY 61 DICTTYLANPVGKVIADAOQNTTISQYACHDQVAVTILMSGALGIEFLKGFVILEELKS 120
DB 61 DICTTYLANPVGKVIADAOQNTTISQYACHDQVAVTILMSGALGIEFLKGFVILEELKS 120
QY 121 EGRQCOQLIKDKPKOLNSFFKRTGMSQFPLMKKEFTDYFVYVPPPSIKNSNHYHPPF 180
DB 121 EGRQCOQLIKDKPKOLNSFFKRTGMSQFPLMKKEFTDYFVYVPPPSIKNSNHYHPPF 180
QY 181 RTACDILLQPDNLACKPFWKPRNLNISQHSQDMQVSPDHA PHNFGFRFFYLHYKLKHG 240
DB 181 RTACDILLQPDNLACKPFWKPRNLNISQHSQDMQVSPDHA PHNFGFRFFYLHYKLKHG 240
QY 241 PFRKRTCKEQTTETTSCLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA 300
DB 241 PFRKRTCKEQTTETTSCLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA 300
QY 301 MATTVPLVVISAPATLFTWCRKQOENIYSHLDESSSSSTYTALPRERLRPRKRVFL 360
DB 301 MATTVPLVVISAPATLFTWCRKQOENIYSHLDESSSSSTYTALPRERLRPRKRVFL 360
QY 361 CYSKQGMKYFVDKKNYGHKGSGSGKGEFLVAVSAIAEKLRQAKQSSAALSKFLAVYF 480
DB 361 CYSKQGMKYFVDKKNYGHKGSGSGKGEFLVAVSAIAEKLRQAKQSSAALSKFLAVYF 480
QY 421 VCSKGMKYFVDKKNYGHKGSGSGKGEFLVAVSAIAEKLRQAKQSSAALSKFLAVYF 480
DB 421 VCSKGMKYFVDKKNYGHKGSGSGKGEFLVAVSAIAEKLRQAKQSSAALSKFLAVYF 480
QY 481 DVSCEBDVGIIDLSKTKRYLMDNLPOLCSHLHSRHDGLQEPQHTQGSRRNYFRKSGR 540
DB 481 DVSCEBDVGIIDLSKTKRYLMDNLPOLCSHLHSRHDGLQEPQHTQGSRRNYFRKSGR 540
QY 541 SLVVAICNMHQFIDEPRDFEKOFPFHPPLRYREPVLEKDFSGVLNDVMCKPESD 600
DB 541 SLVVAICNMHQFIDEPRDFEKOFPFHPPLRYREPVLEKDFSGVLNDVMCKPESD 600
QY 601 FCUKVEAPVLTGATGPADSGHESQHGLDQGEARPALDGSAAALQPLHTVKAGSPSDMPR 660
DB 601 FCUKVEAPVLTGATGPADSGHESQHGLDQGEARPALDGSAAALQPLHTVKAGSPSDMPR 660
QY 661 DSGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSGLGEERPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSGLGEERPPALPSKLLSSGSC 720
QY 721 KADLCGRSYTDELHAYAP 738
DB 721 KADLCGRSYTDELHAYAP 738

RESULT 7
US-10-842-006-2
; Sequence 2, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; APPLICANT: Therefor
; TITLE OF INVENTION: A Novel Human SEF Molecule and Uses
; FILE REFERENCE: MP103-07191PM
; CURRENT APPLICATION NUMBER: US/10/842,006
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; PRIOR FILING DATE: 2003-05-08
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NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PaacSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 739
 TYPE: PR
 ORGANISM: Homo Sapiens
 US-10-842-006-2

Query Match 99.0%; Score 3908; DB 5; Length 739;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 732; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAMWLOICSVFTFVNAACINSGQLAAAGSGGRAGVDTCCMRGVGPASRNSGLNITPKY 60
DB 1 MAMWLOICSVFTFVNAACINSGQLAAAGSGGRAGVDTCCMRGVGPASRNSGLNITPKY 60
QY 61 DNCCTYANPVGKRVIAADQNTTISQYACHQVAVTILMSFGALGIEFLKGFVILELKS 120
DB 61 DNCCTYANPVGKRVIAADQNTTISQYACHQVAVTILMSFGALGIEFLKGFVILELKS 120
QY 121 EGRQCOOLIKDPKOLNSFKRTGMSQPLNKKFETDYFVKVPPPSIKNESNYHPPFF 180
DB 121 EGRQCOOLIKDPKOLNSFKRTGMSQPLNKKFETDYFVKVPPPSIKNESNYHPPFF 180
QY 181 RTBACDILLQPDNLACRPFKPRNLNISOHSDMVSFDHAPNFGFRFFYLHYKLHGE 240
DB 181 RTBACDILLQPDNLACRPFKPRNLNISOHSDMVSFDHAPNFGFRFFYLHYKLHGE 240
QY 241 PPRKCTCKOQTETTSCLQNVSPGDIIELVDDNTTRKVMHYALKPVHSPAGPIRA 300
DB 241 PPRKCTCKOQTETTSCLQNVSPGDIIELVDDNTTRKVMHYALKPVHSPAGPIRA 300
QY 301 MATVPLVVISAPATLFTWCRKQOENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
DB 301 MATVPLVVISAPATLFTWCRKQOENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
QY 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDPSLCREGREWVIOKIHESQPIIV 420
DB 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDPSLCREGREWVIOKIHESQPIIV 420
QY 421 VCSKGMKTFYDKKQYKHKGGSGSGKGLFLVAVSAIAEKLRAKQSSSALSKFLAVYF 480
DB 421 VCSKGMKTFYDKKQYKHKGGSGSGKGLFLVAVSAIAEKLRAKQSSSALSKFLAVYF 480
QY 481 DYCCEGVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGR 540
DB 481 DYCCEGVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGR 540
QY 541 SLVYALCNMHQFIIDEBPDMFEKQFVPHPPPLRYREPVLEKFDGSLVANDVMCKPGBESD 600
DB 541 SLVYALCNMHQFIIDEBPDMFEKQFVPHPPPLRYREPVLEKFDGSLVANDVMCKPGBESD 600
QY 601 FCILKVEAPVIGAGPAPDSOHSHQHGGLDQGEARPALDGSALQPLLHTYKASPSMPR 660
DB 601 FCILKVEAPVIGAGPAPDSOHSHQHGGLDQGEARPALDGSALQPLLHTYKASPSMPR 660
QY 661 DSGIYSSVPSSELPLMEGLSTDQETETSLTESVSSSGGLGEBEPALPSKLSSGSC 720
DB 661 DSGIYSSVPSSELPLMEGLSTDQETETSLTESVSSSGGLGEBEPALPSKLSSGSC 720
QY 721 KADIGCRSYTDELHAAP 738
DB 721 KADIGCRSYTDELHAAP 738

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RESULT 8
 US-10-608-449-2
 Sequence 2, Application US/10608449
 Publication No. US20040265834A1
 GENERAL INFORMATION:
 APPLICANT: Tsinghua University
 TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
 FILE REFERENCE: 12003269C-US

CURRENT APPLICATION NUMBER: US/10/608,449
 CURRENT FILING DATE: 2003-06-30
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 739
 TYPE: PR
 ORGANISM: Homo sapiens
 US-10-608-449-2

Query Match 99.0%; Score 3908; DB 5; Length 739;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 732; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MAMWLOICSVFTFVNAACINSGQLAAAGSGGRAGVDTCCMRGVGPASRNSGLNITPKY 60
DB 1 MAMWLOICSVFTFVNAACINSGQLAAAGSGGRAGVDTCCMRGVGPASRNSGLNITPKY 60
QY 61 DNCCTYANPVGKRVIAADQNTTISQYACHQVAVTILMSFGALGIEFLKGFVILELKS 120
DB 61 DNCCTYANPVGKRVIAADQNTTISQYACHQVAVTILMSFGALGIEFLKGFVILELKS 120
QY 121 EGRQCOOLIKDPKOLNSFKRTGMSQPLNKKFETDYFVKVPPPSIKNESNYHPPFF 180
DB 121 EGRQCOOLIKDPKOLNSFKRTGMSQPLNKKFETDYFVKVPPPSIKNESNYHPPFF 180
QY 181 RTBACDILLQPDNLACRPFKPRNLNISOHSDMVSFDHAPNFGFRFFYLHYKLHGE 240
DB 181 RTBACDILLQPDNLACRPFKPRNLNISOHSDMVSFDHAPNFGFRFFYLHYKLHGE 240
QY 241 PPRKCTCKOQTETTSCLQNVSPGDIIELVDDNTTRKVMHYALKPVHSPAGPIRA 300
DB 241 PPRKCTCKOQTETTSCLQNVSPGDIIELVDDNTTRKVMHYALKPVHSPAGPIRA 300
QY 301 MATVPLVVISAPATLFTWCRKQOENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
DB 301 MATVPLVVISAPATLFTWCRKQOENIYSHLDESSSESTYTAALPRELRPRPKVFL 360
QY 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDPSLCREGREWVIOKIHESQPIIV 420
DB 361 CYSSKQGNMNVVQCFAYFLQDFCGCEVALDLMEDPSLCREGREWVIOKIHESQPIIV 420
QY 421 VCSKGMKTFYDKKQYKHKGGSGSGKGLFLVAVSAIAEKLRAKQSSSALSKFLAVYF 480
DB 421 VCSKGMKTFYDKKQYKHKGGSGSGKGLFLVAVSAIAEKLRAKQSSSALSKFLAVYF 480
QY 481 DYCCEGVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGR 540
DB 481 DYCCEGVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGQHTROGSRNRYFRSKSGR 540
QY 541 SLVYALCNMHQFIIDEBPDMFEKQFVPHPPPLRYREPVLEKFDGSLVANDVMCKPGBESD 600
DB 541 SLVYALCNMHQFIIDEBPDMFEKQFVPHPPPLRYREPVLEKFDGSLVANDVMCKPGBESD 600
QY 601 FCILKVEAPVIGAGPAPDSOHSHQHGGLDQGEARPALDGSALQPLLHTYKASPSMPR 660
DB 601 FCILKVEAPVIGAGPAPDSOHSHQHGGLDQGEARPALDGSALQPLLHTYKASPSMPR 660
QY 661 DSGIYSSVPSSELPLMEGLSTDQETETSLTESVSSSGGLGEBEPALPSKLSSGSC 720
DB 661 DSGIYSSVPSSELPLMEGLSTDQETETSLTESVSSSGGLGEBEPALPSKLSSGSC 720
QY 721 KADIGCRSYTDELHAAP 738
DB 721 KADIGCRSYTDELHAAP 738

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RESULT 9
 US-09-912-157-2
 Sequence 2, Application US/09912157
 Patent No. US20020165348A1
 GENERAL INFORMATION:
 APPLICANT: Presnell, Scott R.

APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/09/912.157
CURRENT FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 753
TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-157-2

Query Match 98.8%; Score 3901; DB 3; Length 753;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWQLCSVFPTVNACLNGSQLAAVAGSGSGRAMGVDTGMR-----GVGP 46
DB 1 MAPWQLCSVFPTVNACLNGSQLAAVAGSGSGRAGADTCGMRKKAARPRLCVANGVGP 60
QY 47 ASNSGLNITTKYNDCTTYLNPVGKRVADADONITISQYACHDQYAVTILMSPGALGIE 106
DB 61 ASNSGLNITTKYNDCTTYLNPVGKRVADADONITISQYACHDQYAVTILMSPGALGIE 120
QY 107 FLKGFVILIELKESGROCOQLIKDPKQNSFKRTGMSOPFLMKKETDYFVAVVP 166
DB 121 FLKGFVILIELKESGROCOQLIKDPKQNSFKRTGMSOPFLMKKETDYFVAVVP 180
QY 167 PSIKESNHPFPFRTACDLILQPDNLACKPFWKPRNLNISQHSQDMQVSPDHAHPNFG 226
DB 181 PSIKESNHPFPFRTACDLILQPDNLACKPFWKPRNLNISQHSQDMQVSPDHAHPNFG 240
QY 227 FRFFLYHLKHEGPPKRTCKOBTETTSCILQNSGDIYIELVDNTTRKMYHA 286
DB 241 FRFFLYHLKHEGPPKRTCKOBTETTSCILQNSGDIYIELVDNTTRKMYHA 300
QY 287 LKRVHSPMAGPIRAVAITVPLVISAFAITLFTWCRKQOENIYSHLDESSSSTYTAA 346
DB 301 LKRVHSPMAGPIRAVAITVPLVISAFAITLFTWCRKQOENIYSHLDESSSSTYTAA 360
QY 347 LPRERLRPRPKVFLCYSSKDGQNMHVQCFAFYLDPCGCEVALDLMEDFSLCREGORE 406
DB 361 LPRERLRPRPKVFLCYSSKDGQNMHVQCFAFYLDPCGCEVALDLMEDFSLCREGORE 420
QY 407 WYIOKIHESQFIIVVCSKMKYFVDKKNYKHGGSGSGKGLFLVAVSAIAEKLRQAKQ 466
DB 421 WYIOKIHESQFIIVVCSKMKYFVDKKNYKHGGSGSGKGLFLVAVSAIAEKLRQAKQ 480
QY 467 SSSAALSKFIAYVFDYSCGSDVPGIILSTKYRLMDNLPOLGSHLSRHDGLQEPGOHTR 526
DB 481 SSSAALSKFIAYVFDYSCGSDVPGIILSTKYRLMDNLPOLGSHLSRHDGLQEPGOHTR 540
QY 527 QGSRNRYFPSKSGRSIYVAICNMHQFIDEEPDMFEKQFVFPFHPPLRYRPEVLEKDSGL 586
DB 541 QGSRNRYFPSKSGRSIYVAICNMHQFIDEEPDMFEKQFVFPFHPPLRYRPEVLEKDSGL 600
QY 587 VLVNDVCKCPGSDPFLCKYEAAPVLAGTGPADSOHESQHGLDQDGEARPALDGSALQPL 646
DB 601 VLVNDVCKCPGSDPFLCKYEAAPVLAGTGPADSOHESQHGLDQDGEARPALDGSALQPL 660
QY 647 LHTVYKAGSPDMRDSGIYDSSVPSSELSTPLMEGSTQOTETSTLTSVSSSSGLGEEB 706
DB 661 LHTVYKAGSPDMRDSGIYDSSVPSSELSTPLMEGSTQOTETSTLTSVSSSSGLGEEB 720
QY 707 PPALPSKLLSSGSKADLCGRSYTDELHNAVAP 738
DB 721 PPALPSKLLSSGSKADLCGRSYTDELHNAVAP 752

RESULT 10
US-10-717-282-2

Sequence 2, Application US/10717282
Publication No. US2004007052A1
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.
APPLICANT: Kuestner, Rolf E.
APPLICANT: Gao, Zeren
TITLE OF INVENTION: Human Cytokine Receptor
FILE REFERENCE: 00-49
CURRENT APPLICATION NUMBER: US/10/717,282
CURRENT FILING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US/09/912,157
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 753
TYPE: PRT
ORGANISM: Homo sapiens
US-10-717-282-2

Query Match 98.8%; Score 3901; DB 4; Length 753;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

QY 1 MAPWQLCSVFPTVNACLNGSQLAAVAGSGSGRAMGVDTGMR-----GVGP 46
DB 1 MAPWQLCSVFPTVNACLNGSQLAAVAGSGSGRAGADTCGMRKKAARPRLCVANGVGP 60
QY 47 ASNSGLNITTKYNDCTTYLNPVGKRVADADONITISQYACHDQYAVTILMSPGALGIE 106
DB 61 ASNSGLNITTKYNDCTTYLNPVGKRVADADONITISQYACHDQYAVTILMSPGALGIE 120
QY 107 FLKGFVILIELKESGROCOQLIKDPKQNSFKRTGMSOPFLMKKETDYFVAVVP 166
DB 121 FLKGFVILIELKESGROCOQLIKDPKQNSFKRTGMSOPFLMKKETDYFVAVVP 180
QY 167 PSIKESNHPFPFRTACDLILQPDNLACKPFWKPRNLNISQHSQDMQVSPDHAHPNFG 226
DB 181 PSIKESNHPFPFRTACDLILQPDNLACKPFWKPRNLNISQHSQDMQVSPDHAHPNFG 240
QY 227 FRFFLYHLKHEGPPKRTCKOBTETTSCILQNSGDIYIELVDNTTRKMYHA 286
DB 241 FRFFLYHLKHEGPPKRTCKOBTETTSCILQNSGDIYIELVDNTTRKMYHA 300
QY 287 LKRVHSPMAGPIRAVAITVPLVISAFAITLFTWCRKQOENIYSHLDESSSSTYTAA 346
DB 301 LKRVHSPMAGPIRAVAITVPLVISAFAITLFTWCRKQOENIYSHLDESSSSTYTAA 360
QY 347 LPRERLRPRPKVFLCYSSKDGQNMHVQCFAFYLDPCGCEVALDLMEDFSLCREGORE 406
DB 361 LPRERLRPRPKVFLCYSSKDGQNMHVQCFAFYLDPCGCEVALDLMEDFSLCREGORE 420
QY 407 WYIOKIHESQFIIVVCSKMKYFVDKKNYKHGGSGSGKGLFLVAVSAIAEKLRQAKQ 466
DB 421 WYIOKIHESQFIIVVCSKMKYFVDKKNYKHGGSGSGKGLFLVAVSAIAEKLRQAKQ 480
QY 467 SSSAALSKFIAYVFDYSCGSDVPGIILSTKYRLMDNLPOLGSHLSRHDGLQEPGOHTR 526
DB 481 SSSAALSKFIAYVFDYSCGSDVPGIILSTKYRLMDNLPOLGSHLSRHDGLQEPGOHTR 540
QY 527 QGSRNRYFPSKSGRSIYVAICNMHQFIDEEPDMFEKQFVFPFHPPLRYRPEVLEKDSGL 586
DB 541 QGSRNRYFPSKSGRSIYVAICNMHQFIDEEPDMFEKQFVFPFHPPLRYRPEVLEKDSGL 600
QY 587 VLVNDVCKCPGSDPFLCKYEAAPVLAGTGPADSOHESQHGLDQDGEARPALDGSALQPL 646
DB 601 VLVNDVCKCPGSDPFLCKYEAAPVLAGTGPADSOHESQHGLDQDGEARPALDGSALQPL 660
QY 647 LHTVYKAGSPDMRDSGIYDSSVPSSELSTPLMEGSTQOTETSTLTSVSSSSGLGEEB 706
DB 661 LHTVYKAGSPDMRDSGIYDSSVPSSELSTPLMEGSTQOTETSTLTSVSSSSGLGEEB 720
QY 707 PPALPSKLLSSGSKADLCGRSYTDELHNAVAP 738

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Db 721 PPALPSKLLSSGSCKADLCGRSTYDELHAAVAP 752
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RESULT 11
US-09-912-157-5
; Sequence 5, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912.157
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-912-157-5

Query Match 98.6%; Score 3891; DB 3; Length 753;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 732; Conservative 1; Mismatches 5; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFPTVNACLNGSOLAAGSGRAMGVDTGMR-----GVGP 46
Db 1 MAPWLQCSVFPTVNACLNGSOLAAGSGRAMGVDTGMRKKAARPRLCVANGVGP 60
Qy 47 ASRNSGLVNTFFKYDCTTYLNPVKGVIADAOINITISQYACHDQVAVITLMSPGALGIR 106
Db 61 ASRNSGLVNTFFKYDCTTYLNPVKGVIADAOINITISQYACHDQVAVITLMSPGALGIR 120
Qy 107 FLKGFVILBELSEBROCOQLIKDPKOLNSFKRTGMSOPFLMKKEFTDYFVGVVPP 166
Db 121 FLKGFVILBELSEBROCOQLIKDPKOLNSFKRTGMSOPFLMKKEFTDYFVGVVPP 180
Qy 167 PSIKNSNTHPFFFRTRACDLLOPDLACKPMPKPRNLNISQHSDMQVSPHAPHNFG 226
Db 181 PSIKNSNTHPFFFRTRACDLLOPDLACKPMPKPRNLNISQHSDMQVSPHAPHNFG 240
Qy 227 FRFFYLHYLKHGPPKRTCKOQETETTSCLQNVSPGDYIIELVDTNTTRKVMHYA 286
Db 241 FRFFYLHYLKHGPPKRTCKOQETETTSCLQNVSPGDYIIELVDTNTTRKVMHYA 300
Qy 287 LKRVHSPMAGPIRAVAITVPLVVISAPATLFTVMCKKQOENYSHLDESSSSSTYTA 346
Db 301 LKRVHSPMAGPIRAVAITVPLVVISAPATLFTVMCKKQOENYSHLDESSSSSTYTA 360
Qy 347 LPERLRPRPKVFLCYSSKDGONHNVOCFAFLDOPGCEVALDLMEDFSLCREGORE 406
Db 361 LPERLRPRPKVFLCYSSKDGONHNVOCFAFLDOPGCEVALDLMEDFSLCREGORE 420
Qy 407 WYIOLKHSQPIIIVVCSKGMKTFVDKKNYKHGSGSGKGLFLVAVSAIAEKLQAAQ 466
Db 421 WYIOLKHSQPIIIVVCSKGMKTFVDKKNYKHGSGSGKGLFLVAVSAIAEKLQAAQ 480
Qy 467 SSSAALSKPIAYFYDSCGDVPGIIDLSTKRLMDNLPOLCSHLHSRDHGLQEPQOHR 526
Db 481 SSSAALSKPIAYFYDSCGDVPGIIDLSTKRLMDNLPOLCSHLHSRDHGLQEPQOHR 540
Qy 527 QGSRNRYFPSKSGRSLYVAICNMHOFIDEEPDMFEKQFVFPHPPLRYRBPVLEKFDGSL 586
Db 541 QGSRNRYFPSKSGRSLYVAICNMHOFIDEEPDMFEKQFVFPHPPLRYRBPVLEKFDGSL 600
Qy 587 VLNDVNCCKPESDFCLKYEAPVLTGAPADSQHESQHGSLDQGEARPALDGSAAALQPL 646
Db 601 VLNDVNCCKPESDFCLKYEAPVLTGAPADSQHESQHGSLDQGEARPALDGSAAALQPL 660
Qy 647 LHTVKAQSPBDMRDSGITDSSVPSSELPLMEGLSTQDTETTSILTESVSSSGIGEEZ 706
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Db 661 LHTVKAQSPBDMRDSGITDSSVPSSELPLMEGLSTQDTETTSILTESVSSSGIGEEZ 720
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RESULT 12
US-10-717-282-5
; Sequence 5, Application US/10717282
; Publication No. US20040077052A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/10/717.282
; PRIOR FILING DATE: 2003-11-19
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 753
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-717-282-5

Query Match 98.6%; Score 3891; DB 4; Length 753;
Best Local Similarity 97.3%; Pred. No. 0;
Matches 732; Conservative 1; Mismatches 5; Indels 14; Gaps 1;

Qy 1 MAPWLQCSVFPTVNACLNGSOLAAGSGRAMGVDTGMR-----GVGP 46
Db 1 MAPWLQCSVFPTVNACLNGSOLAAGSGRAMGVDTGMRKKAARPRLCVANGVGP 60
Qy 47 ASRNSGLVNTFFKYDCTTYLNPVKGVIADAOINITISQYACHDQVAVITLMSPGALGIR 106
Db 61 ASRNSGLVNTFFKYDCTTYLNPVKGVIADAOINITISQYACHDQVAVITLMSPGALGIR 120
Qy 107 FLKGFVILBELSEBROCOQLIKDPKOLNSFKRTGMSOPFLMKKEFTDYFVGVVPP 166
Db 121 FLKGFVILBELSEBROCOQLIKDPKOLNSFKRTGMSOPFLMKKEFTDYFVGVVPP 180
Qy 167 PSIKNSNTHPFFFRTRACDLLOPDLACKPMPKPRNLNISQHSDMQVSPHAPHNFG 226
Db 181 PSIKNSNTHPFFFRTRACDLLOPDLACKPMPKPRNLNISQHSDMQVSPHAPHNFG 240
Qy 227 FRFFYLHYLKHGPPKRTCKOQETETTSCLQNVSPGDYIIELVDTNTTRKVMHYA 286
Db 241 FRFFYLHYLKHGPPKRTCKOQETETTSCLQNVSPGDYIIELVDTNTTRKVMHYA 300
Qy 287 LKRVHSPMAGPIRAVAITVPLVVISAPATLFTVMCKKQOENYSHLDESSSSSTYTA 346
Db 301 LKRVHSPMAGPIRAVAITVPLVVISAPATLFTVMCKKQOENYSHLDESSSSSTYTA 360
Qy 347 LPERLRPRPKVFLCYSSKDGONHNVOCFAFLDOPGCEVALDLMEDFSLCREGORE 406
Db 361 LPERLRPRPKVFLCYSSKDGONHNVOCFAFLDOPGCEVALDLMEDFSLCREGORE 420
Qy 407 WYIOLKHSQPIIIVVCSKGMKTFVDKKNYKHGSGSGKGLFLVAVSAIAEKLQAAQ 466
Db 421 WYIOLKHSQPIIIVVCSKGMKTFVDKKNYKHGSGSGKGLFLVAVSAIAEKLQAAQ 480
Qy 467 SSSAALSKPIAYFYDSCGDVPGIIDLSTKRLMDNLPOLCSHLHSRDHGLQEPQOHR 526
Db 481 SSSAALSKPIAYFYDSCGDVPGIIDLSTKRLMDNLPOLCSHLHSRDHGLQEPQOHR 540
Qy 527 QGSRNRYFPSKSGRSLYVAICNMHOFIDEEPDMFEKQFVFPHPPLRYRBPVLEKFDGSL 586
Db 541 QGSRNRYFPSKSGRSLYVAICNMHOFIDEEPDMFEKQFVFPHPPLRYRBPVLEKFDGSL 600
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QY 587 VLVNDVCKPESDPCFKVAPVLTGATGPADSGHESQHGGLDQDGEARPALDSSAALQPL 646
DB 601 VLVNDVCKPESDPCFKVAPVLTGATGPADSGHESQHGGLDQDGEARPALDSSAALQPL 660
QY 647 LHTVKAQSPDMRDSGIDYSSVPSSELSPLMEGLSTDQETSSLTESVSSSGIGEEB 706
DB 661 LHTVKAQSPDMRDSGIDYSSVPSSELSPLMEGLSTDQETSSLTESVSSSGIGEEB 720
QY 707 PPLPSPKLLSSGCKADLCGRSTYDELHAAVAP 738
DB 721 PPLPSPKLLSSGCKADLCGRSTYDELHAAVAP 752

RESULT 13
US-09-863-818A-10

/ Sequence 10, Application US/09863818A
/ Publication No. US20030092881A1
/ GENERAL INFORMATION:
/ APPLICANT: Gorman, Daniel M.
/ TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
/ FILE REFERENCE: DX01170K
/ CURRENT APPLICATION NUMBER: US/09/863, 818A
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/206, 862
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 10
/ LENGTH: 738
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (18)..(18)
/ OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
/ NAME/KEY: misc_feature
/ LOCATION: (26)..(26)
/ OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
/ NAME/KEY: misc_feature
/ LOCATION: (109)..(109)
/ OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
/ NAME/KEY: misc_feature
/ LOCATION: (120)..(120)
/ OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
/ NAME/KEY: misc_feature
/ LOCATION: (134)..(134)
/ OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
/ NAME/KEY: misc_feature
/ LOCATION: (8)..(8)
/ OTHER INFORMATION: unknown amino
/ NAME/KEY: misc_feature
/ LOCATION: (144)..(144)
/ OTHER INFORMATION: unknown amino
/ NAME/KEY: misc_feature
/ LOCATION: (170)..(170)
/ OTHER INFORMATION: unknown amino
/ NAME/KEY: misc_feature
/ LOCATION: (194)..(194)
/ OTHER INFORMATION: unknown amino
/ NAME/KEY: misc_feature
/ LOCATION: (442)..(442)
/ OTHER INFORMATION: unknown amino
/ NAME/KEY: misc_feature
/ LOCATION: (475)..(475)
/ OTHER INFORMATION: unknown amino
/ NAME/KEY: misc_feature
/ LOCATION: (519)..(519)
/ OTHER INFORMATION: unknown amino
/ US-09-863-818A-10

Query Match 97.2%; Score 3835.5; DB 3; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;

Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;
QY 1 MAPWLOLGVFFTVNACLNQSLAVAGSGRAMGVDTQGWGVGPASRNSGLYNTTPKY 60
DB 1 MAPWLOLGVFFTVNACLNQSLAVAGSGRAMGVDTQGWGVGPASRNSGLYNTTPKY 60
QY 61 DICTTYLNVGKGVADANITISQYACHDQAVITLMSGALGIEFLGFFVILELKS 120
DB 61 DICTTYLNVGKGVADANITISQYACHDQAVITLMSGALGIEFLGFFVILELKS 120
QY 121 EGRQCOQLIKDPKQINSFKRTGMSOPFLMKPFTDYFKVVPSPSJKNSNTHPEFF 180
DB 121 EGRQCOQLIKDPKQINSFKRTGMSOPFLMKPFTDYFKVVPSPSJKNSNTHPEFF 179
QY 181 RTKACDLLOPNLACKPFWKPRNLNISOHSGDMOVSPPHAPNRSFPPYLYLKHKG 240
DB 181 RTKACDLLOPNLACKPFWKPRNLNISOHSGDMOVSPPHAPNRSFPPYLYLKHKG 239
QY 241 PFKRTCKQEQETTESCLQNVSPDYIIEVDNTTRKMYHALKPVHSPMAGPIRA 300
DB 241 PFKRTCKQEQETTESCLQNVSPDYIIEVDNTTRKMYHALKPVHSPMAGPIRA 299
QY 301 MAITVPLVISAFAITFTWCRKQOENIYSHLDESSSTYTAALPRELRPRPKVL 360
DB 301 MAITVPLVISAFAITFTWCRKQOENIYSHLDESSSTYTAALPRELRPRPKVL 359
QY 361 CYSSKQGNHNVVQCFAYFLDPCGCEVALDMEFSLCRBQREWVLOKHESQFLIV 420
DB 361 CYSSKQGNHNVVQCFAYFLDPCGCEVALDMEFSLCRBQREWVLOKHESQFLIV 419
QY 421 VCSKGMKVFVDKKNYHKGKGRSGKGBELFVAVSAIAKELQAKQSSAALSKPIAVYF 480
DB 421 VCSKGMKVFVDKKNYHKGKGRSGKGBELFVAVSAIAKELQAKQSSAALSKPIAVYF 479
QY 481 DYCSEGDVGIILDKTKYLMNLPQLCSHLHSRDHGLQEPQHTROGSRNYPFSKGR 540
DB 481 DYCSEGDVGIILDKTKYLMNLPQLCSHLHSRDHGLQEPQHTROGSRNYPFSKGR 539
QY 541 SIYVACNMHOFIDEPDMEKQFVPPHPRRYRPEVLEKDSGLVNDVCKPESD 600
DB 541 SIYVACNMHOFIDEPDMEKQFVPPHPRRYRPEVLEKDSGLVNDVCKPESD 599
QY 601 PCLKVEAPVLTGATGPADSGHESQHGGLDQDGEARPALDSSAALQPLLHTVKAQSPDMR 660
DB 601 PCLKVEAPVLTGATGPADSGHESQHGGLDQDGEARPALDSSAALQPLLHTVKAQSPDMR 659
QY 661 DSGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSGIGEEBPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVPSSELSPLMEGLSTDQETSSLTESVSSSGIGEEBPPALPSKLLSSGSC 719
QY 721 KADLCGRSTYDELHAAVAP 738
DB 721 KADLCGRSTYDELHAAVAP 737

RESULT 14
US-10-749-144-10

/ Sequence 10, Application US/10749144
/ Publication No. US20040197306A1
/ GENERAL INFORMATION:
/ APPLICANT: Gorman, Daniel M.
/ TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
/ FILE REFERENCE: DX01170K1
/ CURRENT APPLICATION NUMBER: US/10/749, 144
/ PRIOR FILING DATE: 2003-12-29
/ PRIOR APPLICATION NUMBER: US 60/206, 862
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 10
/ LENGTH: 738
/ TYPE: PRT
/ ORGANISM: Homo sapiens

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FEATURE:
NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.
FEATURE:
NAME/KEY: misc feature
LOCATION: (26)..(26)
OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.
FEATURE:
NAME/KEY: misc feature
LOCATION: (109)..(109)
OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.
FEATURE:
NAME/KEY: misc feature
LOCATION: (120)..(120)
OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (134)..(134)
OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
US-10-749-144-10

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Query Match      97.2%; Score 3835.5; DB 4; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

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QY 1 MAPWLOCSVFTVNAALNGSQLAAAGSGRAWGVDTCCRGVGPASRNSGLYNTTFKY 60
DB 1 MAPWLOCSVFTVNAALNGSQLAAAGSGRAWGVDTCCRGVGPASRNSGLYNTTFKY 60
QY 61 DNCCTYINPVGKVIADANQITTSQVACHQVAAITLMSRPAIGIEFLKGRVLEELKS 120
DB 61 DNCCTYINPVGKVIADANQITTSQVACHQVAAITLMSRPAIGIEFLKGRVLEELKS 120
QY 121 EGRQCOQLIKDPRKQNLSSFKRTGMSQPLANKFETDYFKVVPFSIKNESYHPPFF 180
DB 121 EGRQCOQLIKDPRKQNLSSFKRTGMSQPLANKFETDYFKVVPFSIKNESYHPPFF 180
QY 121 EGRQCOQLIKDPRKQNLSSFKRTGMSQPLANKFETDYFKVVPFSIKNESYHPPFF 179
DB 121 EGRQCOQLIKDPRKQNLSSFKRTGMSQPLANKFETDYFKVVPFSIKNESYHPPFF 179
QY 181 RTBACDILLQPDNLACRPFMKPRNLINISQHGSDQVSPDHAHNFGFRFYLYKLNREG 240
DB 181 RTBACDILLQPDNLACRPFMKPRNLINISQHGSDQVSPDHAHNFGFRFYLYKLNREG 240
QY 241 PFRKRTCKOQTETTSCLLQNSRQYIIEVDVTTTKVWYALKPVPSPAGTIRA 300
DB 241 PFRKRTCKOQTETTSCLLQNSRQYIIEVDVTTTKVWYALKPVPSPAGTIRA 300
QY 240 PFRKRTCKOQTETTSCLLQNSRQYIIEVDVTTTKVWYALKPVPSPAGTIRA 299
DB 240 PFRKRTCKOQTETTSCLLQNSRQYIIEVDVTTTKVWYALKPVPSPAGTIRA 299
QY 301 MATVPLVIVSAFATLFTVWCRKQKQENIYSHLDESSSTYTAALPRELRPRPVFL 360
DB 301 MATVPLVIVSAFATLFTVWCRKQKQENIYSHLDESSSTYTAALPRELRPRPVFL 360
QY 361 CYSSKQGNMNVVOCFAVFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQPIIV 420
DB 361 CYSSKQGNMNVVOCFAVFLQDFCGCEVALDLWEDFSLCREGQREWVIOKIHESQPIIV 420
QY 421 VCSKGMKTFYDKKRYKRGSGSGKQELFLVAVSAIAEKLRAKQKSSAALSTFIAYVF 480
DB 421 VCSKGMKTFYDKKRYKRGSGSGKQELFLVAVSAIAEKLRAKQKSSAALSTFIAYVF 480
QY 481 DYCCEGDPVPIGLDSTKYRLMDNLPCLSHLSHDHGLQEPGQHTRGSSRRNFRSSGR 540
DB 481 DYCCEGDPVPIGLDSTKYRLMDNLPCLSHLSHDHGLQEPGQHTRGSSRRNFRSSGR 540
QY 541 SLVVAICNMHQFIIDEDPWEKQFVPPHPPRLRYREPLKFKFSGVLANDVMCKPGESED 600
DB 541 SLVVAICNMHQFIIDEDPWEKQFVPPHPPRLRYREPLKFKFSGVLANDVMCKPGESED 600
QY 601 FCLKVEAPVLDGAPADSGHSHGGLDQGEARPAIDGSAALQPLATHTYKAGSPSPMPR 660
DB 601 FCLKVEAPVLDGAPADSGHSHGGLDQGEARPAIDGSAALQPLATHTYKAGSPSPMPR 660
QY 661 DSGIYDSSVSSSLPLMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSSGSC 720
DB 661 DSGIYDSSVSSSLPLMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSSGSC 720

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QY 721 KADIGCRSYTDEHAAVAP 738
DB 720 KADIGCRSYTDEHAAVAP 737

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RESULT 15

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US-10-924-667-10
Sequence 10, Application US/10924667
Publication No. US2005009145A1
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS, RELATED REAGENTS AND
METHODS
FILE REFERENCES: DX01170K
CURRENT APPLICATION NUMBER: US/10/924,667
CURRENT FILING DATE: 2004-08-23
PRIOR APPLICATION NUMBER: US/09/863,818
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,862
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 738
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (18)..(18)
OTHER INFORMATION: The 'Xaa' at location 18 stands for Gln, Arg, Pro, or
Leu.
FEATURE:
NAME/KEY: misc feature
LOCATION: (26)..(26)
OTHER INFORMATION: The 'Xaa' at location 26 stands for Lys, Arg, Thr, or
Met.
FEATURE:
NAME/KEY: misc feature
LOCATION: (109)..(109)
OTHER INFORMATION: The 'Xaa' at location 109 stands for Ser, Gly, Arg, or
Cys.
FEATURE:
NAME/KEY: misc feature
LOCATION: (120)..(120)
OTHER INFORMATION: The 'Xaa' at location 120 stands for Ile, Val, Leu, or
Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (134)..(134)
OTHER INFORMATION: The 'Xaa' at location 134 stands for Leu, or Phe.
FEATURE:
NAME/KEY: misc feature
LOCATION: (144)..(144)
OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEY: misc feature
LOCATION: (145)..(145)
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NAME/KEY: misc feature
LOCATION: (170)..(170)
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NAME/KEY: misc feature
LOCATION: (194)..(194)
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NAME/KEY: misc feature
LOCATION: (442)..(442)
OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEY: misc feature

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LOCATION: (475)..(475)
OTHER INFORMATION: unknown amino
FEATURE:
NAME/KEY: misc_feature
LOCATION: (519)..(519)
OTHER INFORMATION: unknown amino
US-10-924-667-10

Query Match 97.2%; Score 3835.5; DB 5; Length 738;

Best Local Similarity 97.8%; Pred. No. 0;

Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;

QY	1	MAPWLQCSVFVTNACINSQLAVAAGSGRAMGVDTGMRGVPASRNSGLYNITPKY	60
DB	1	MAPWLQCSVFVTNACINSQLAVAAGSGRAMGVDTGMRGVPASRNSGLYNITPKY	60
QY	61	DNCTTYLNPVGKVIADAQNIITISQYACHDQVAVTILMSPALGIEFLKGFVILELKS	120
DB	61	DNCTTYLNPVGKVIADAQNIITISQYACHDQVAVTILMSPALGIEFLKGFVILELKS	120
QY	121	EGRQCOQLIKDKQKLNSSFKRTGMSQPLMKFFETDYFVKVPPPSIKNSNTHPPF	180
DB	121	EGRQCOQLIKDKQKLNSSFKRTGMSQPLMKFFETDYFVKVPPPSIKNSNTHPPF	179
QY	181	RTACDLILQPDNLACPFKPRNLNISQSGDMQVSFDHAPNPFGRFYLYKLKHEG	240
DB	180	RTACDLILQPDNLACPFKPRNLNISQSGDMQVSFDHAPNPFGRFYLYKLKHEG	239
QY	241	PFRRKTCBOQTETTSCLLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA	300
DB	240	PFRRKTCBOQTETTSCLLQNVSPGDYIIELVDTNTTRKVMHYALKPVHSPMAGPIRA	299
QY	301	MATTVPLVVISAPATLFTWCRKQOENITSHLDEESSESTYTAALPRRLRPRPVFL	360
DB	300	VALTPLVVISAPATLFTWCRKQOENITSHLDEESSESTYTAALPRRLRPRPVFL	359
QY	361	CYSSKQGNMNVVOCFAVFLQFCGCEVALDLMEDEPSLCREGOREWVIOKIHESQFIY	420
DB	360	CYSSKQGNMNVVOCFAVFLQFCGCEVALDLMEDEPSLCREGOREWVIOKIHESQFIY	419
QY	421	VCSKGMKYPVDKKNYKHGGGSGSGKGEFLVAVSAIAEKLROAKOSSNALSKEFLAVYF	480
DB	420	VCSKGMKYPVDKKNYKHGGGSGSGKGEFLVAVSAIAEKLROAKOSSNALSKEFLAVYF	479
QY	481	DVSCBGDVPGLILSTKYRLMDNLPOLCSHLHRDHGLOPQHTROGSRNRYFRSKSGR	540
DB	480	DVSCBGDVPGLILSTKYRLMDNLPOLCSHLHRDHGLOPQHTROGSRNRYFRSKSGR	539
QY	541	SLYVALCNMHQFIDEBDPWFQFVPPHPPRLRYREPVLEKPDGLVANDVCKPGPESD	600
DB	540	SLYVALCNMHQFIDEBDPWFQFVPPHPPRLRYREPVLEKPDGLVANDVCKPGPESD	599
QY	601	FCLKVEAPVLGATPADSQHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSDMPR	660
DB	600	FCLKVEAPVLGATPADSQHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSDMPR	659
QY	661	DSGIYSSVSSSLSLPMEGLSTDQETSSLTESVSSSGLGEEPPALPSKLSSGSC	720
DB	660	DSGIYSSVSSSLSLPMEGLSTDQETSSLTESVSSSGLGEEPPALPSKLSSGSC	719
QY	721	KADLGCRSYTDELHAAVAP 738	
DB	720	KADLGCRSYTDELHAAVAP 737	

Search completed: March 1, 2006, 10:34:42
Job time : 169 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:32:17 ; Search time 21 Seconds

(without alignments)
701.013 Million cell updates/sec

Title: US-10-616-788-2

Sequence: 1 MAPWOLCSEVFVTVNACNG.....SCKADGCSYDDELAAVAP 738

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 133702 seqs, 19947517 residues

Total number of hits satisfying chosen parameters: 133702

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA New:

1: /cgn2_6/prodaca/1/pubpaa/US06_NEW_PUB pep:.*
2: /cgn2_6/prodaca/1/pubpaa/US06_NEW_PUB pep:.*
3: /cgn2_6/prodaca/1/pubpaa/US07_NEW_PUB pep:.*
4: /cgn2_6/prodaca/1/pubpaa/PCF_NEW_PUB pep:.*
5: /cgn2_6/prodaca/1/pubpaa/US09_NEW_PUB pep:.*
6: /cgn2_6/prodaca/1/pubpaa/US10_NEW_PUB pep:.*
7: /cgn2_6/prodaca/1/pubpaa/US11_NEW_PUB pep:.*
8: /cgn2_6/prodaca/1/pubpaa/US60_NEW_PUB pep:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3706	93.9	728	US-11-072-512-3399	Sequence 3399, Ap
2	134.5	3.4	385	US-09-978-560A-438	Sequence 438, App
3	134.5	3.4	502	US-10-063-703-158	Sequence 158, App
4	134.5	3.4	502	US-11-102-240-158	Sequence 158, App
5	112.5	2.8	730	US-10-821-234-1019	Sequence 1019, Ap
6	103.5	2.6	998	US-10-510-524-1	Sequence 1, Appli
7	99.5	2.5	1273	US-11-181-330-8	Sequence 8, Appli
8	98.5	2.5	998	US-11-203-251A-88	Sequence 88, Appl
9	98.5	2.5	2343	US-10-330-773-904	Sequence 904, Appl
10	98	2.5	984	US-11-113-424-60	Sequence 60, Appl
11	97	2.5	2890	US-11-115-639-31	Sequence 31, Appl
12	97	2.5	2890	US-11-115-639-32	Sequence 32, Appl
13	97	2.5	2890	US-11-115-639-33	Sequence 33, Appl
14	95	2.4	984	US-11-203-251A-85	Sequence 85, Appl
15	95	2.4	2098	US-10-055-877-253	Sequence 253, App
16	94	2.4	903	US-11-072-512-2951	Sequence 2951, Ap
17	92	2.3	1130	US-11-086-482-1	Sequence 1, Appli
18	92	2.3	1130	US-11-192-341-23	Sequence 23, Appl
19	91.5	2.3	347	US-11-118-122-2	Sequence 2, Appli
20	91.5	2.3	575	US-11-150-533-5	Sequence 5, Appli
21	91.5	2.3	688	US-11-150-533-10	Sequence 10, Appl
22	91.5	2.3	705	US-10-063-703-162	Sequence 162, App
23	91.5	2.3	705	US-11-102-240-162	Sequence 162, App
24	91.5	2.3	705	US-11-150-533-11	Sequence 11, Appl
25	91.5	2.3	791	US-11-072-512-3296	Sequence 3296, Ap

26	91	2.3	2326	US-11-126-313-37	Sequence 37, Appl
27	91	2.3	2811	US-10-877-346-27	Sequence 27, Appl
28	91	2.3	5405	US-11-108-172-1116	Sequence 1116, Ap
29	90.5	2.3	901	US-11-072-512-2920	Sequence 2920, Ap
30	90.5	2.3	1055	US-11-169-041-155	Sequence 155, App
31	90.5	2.3	1055	US-11-072-175-139	Sequence 139, App
32	90.5	2.3	1055	US-11-203-251A-86	Sequence 86, Appl
33	90.5	2.3	2314	US-11-097-728-2	Sequence 2, Appli
34	90.5	2.3	2353	US-11-097-728-6	Sequence 6, Appli
35	90.5	2.3	2641	US-10-877-346-63	Sequence 63, Appl
36	90	2.3	987	US-10-770-726-61	Sequence 61, Appl
37	90	2.3	987	US-11-203-251A-87	Sequence 87, Appl
38	89.5	2.3	509	US-11-072-512-2072	Sequence 2072, Ap
39	89.5	2.3	1346	US-11-060-005-2	Sequence 2, Appli
40	89	2.3	625	US-10-131-826A-70	Sequence 70, Appl
41	89	2.3	625	US-10-973-115B-70	Sequence 70, Appl
42	89	2.3	979	US-10-636-320-6	Sequence 6, Appli
43	88.5	2.2	871	US-10-933-025-3	Sequence 3, Appli
44	88.5	2.2	8746	US-11-098-686-10232	Sequence 10232, A
45	87.5	2.2	867	US-10-131-826A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-11-072-512-3399
; Sequence 3399, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKI, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCES: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3399
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3399
Query Match 93.9%; Score 3706; DB 7; Length 728;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 694; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 41 MRGVGASRNSGLNYITFKYDCTTYLNPVGKRVADAQNTTISQYACHDOVAVTLLMSP 100
Db 30 MGVGASRNSGLNYITFKYDCTTYLNPVGKRVADAQNTTISQYACHDOVAVTLLMSP 89
QY 101 GAGTIFLKGFRVILELSEBGRQCOQLIKDPKQJLNSFKRGMSQPLMKFETDYR 160

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Db 90 GAGIEPLKGFVYLLELKESEGRQCOQLILKDPKQLNSFKRTGMEQPLINKKFFETDYF 149
Qy 161 VKVPPPSINSENNYHFFRRTRACDILLDPDNLACPFKPPRINTLSQSGSMQVSFDH 220
Db 150 VKVPPPSINSENNYHFFRRTRACDILLDPDNLACPFKPPRINTLSQSGSMQVSFDH 209
Qy 221 APNPFGRFFYLKLGHEGPPFKRTCKOEQTETTSCLLQNVSPGDYIELVDNTTTR 280
Db 210 APNPFGRFFYLKLGHEGPPFKRTCKOEQTETTSCLLQNVSPGDYIELVDNTTTR 269
Qy 281 KVMHYALKPVHSPWAGIRAMAITVPLVISAFAITFTVNCRRKQOENIYSHLDESSSES 340
Db 270 KVMHYALKPVHSPWAGIRAMAITVPLVISAFAITFTVNCRRKQOENIYSHLDESSSES 329
Qy 341 STYTALPRLPRPRVFLCYSSKQGNMNVVOCAYVLOPCCGEVALDLMEDPSLC 400
Db 330 STYTALPRLPRPRVFLCYSSKQGNMNVVOCAYVLOPCCGEVALDLMEDPSLC 389
Qy 401 REGQREWVIOKIHESQFIIVCSKGMKYFVDKKNYKKGSGSGKGLFLVAVSAIAEK 460
Db 390 REGQREWVIOKIHESQFIIVCSKGMKYFVDKKNYKKGSGSGKGLFLVAVSAIAEK 449
Qy 461 LRQAKOSSSAALSKEFLAVFDYSCGDPGILDLSTYRLMDNLPOLCSHLSDRDLQOE 520
Db 450 LRQAKOSSSAALSKEFLAVFDYSCGDPGILDLSTYRLMDNLPOLCSHLSDRDLQOE 509
Qy 521 PGQHTQGSRRNFRSSGSLVYALICNMHQFIIDEEPDEKQFVPHPPPLRYREVL 580
Db 510 PGQHTQGSRRNFRSSGSLVYALICNMHQFIIDEEPDEKQFVPHPPPLRYREVL 569
Qy 581 KFPDGLVNDVMCKPESDFCLKEAPVIGATGPADSOHESOHGGLDQGEARPALDGS 640
Db 570 KFPDGLVNDVMCKPESDFCLKEAPVIGATGPADSOHESOHGGLDQGEARPALDGS 629
Qy 641 AALQPLHTYKAGSPDSMDPSDGIYDSVPSSELSPLMEGLSTDQETSSLTRESVSSSS 700
Db 630 AALQPLHTYKAGSPDSMDPSDGIYDSVPSSELSPLMEGLSTDQETSSLTRESVSSSS 689
Qy 701 GLGEEBPALPSKLLSSGSKADLGCSTYDELHNAVAP 738
Db 690 GLGEEBPALPSKLLSSGSKADLGCSTYDELHNAVAP 727

RESULT 2
US-09-978-360A-438
; Sequence 438, Application US/09978360A
; Publication No. US2006009633A9
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste Dumas Milne
; APPLICANT: Bouguetel, Lydie
; APPLICANT: Jobert, Severin
; APPLICANT: Clusel, Catherine
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with signal Peptides
; FILE REFERENCE: 56, US4, CIP
; CURRENT APPLICATION NUMBER: US/09/978,360A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: US 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: US 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: US 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 60/099,273
; PRIOR FILING DATE: -09-04
; PRIOR APPLICATION NUMBER: US 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 09/215,435

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; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: PCT/1B98/02122
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: US 09/247,155
; PRIOR FILING DATE: 1999-02-09
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 810
; SOFTWARE: Patent .pm
; SEQ ID NO 438
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -184...-1
US-09-978-360A-438

Query Match 3.4%; Score 134.5; DB 5; Length 385;
Best Local Similarity 20.1%; Pred. No. 0.00024;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;

Qy 204 NNTISQSGDMQVSF-----DHAPNFGFRFFYLHYKLKHEGPPFKRTCK----- 247
Db 26 NANNMEDGSMGVSNTFTSPGCLDH-----IMKYK-----KKCVAGSLMDPN 66
Qy 248 -----KQOTR---TTSCLQNVSPGDYIELVDNTTTRKVMHYALKPVHSPWAGPIR 299
Db 67 TRACKNEBTEVNFPTTTL-----GNRYMALIQHSTI-----IGFQVPEPHQKOT 114
Qy 300 AMAITVPLVISAFAITL-----FTVNCRRKQOENIYSHLDESSSES 341
Db 115 RASVVIPTVGDSEGAIVQLTPFPPTGSDICRHKKVTVLC---PQGVPPPLDNNKSKG 171
Qy 342 TYTAL-----PRELR-----PRKYFLCYSSKQGNMNV 372
Db 172 GMLPILLSLVAIYVYLVAGIYIMMRHERIKTSTSTTLPLPIKVLVYPSIEICFH-- 229
Qy 373 VVQCFAYFLDPCGCEVALDLMEDPSLCREGQREWVIOKIHESQFIIVCSKGMKYFVDK 432
Db 230 TICYTEFLQNHCRSEVILEKQKKIAMEGVOMLATQKAAADKVVFLISNDVNSVCG 289
Qy 433 KNYKHKGGSGSGKGLFLVAVSAIAEKLRQAKOSSSAALSKEFLAVFDYSCGDPGIL 492
Db 290 TCGSKSGSPSENSQ--DLFPLAFNLFCSDLR-----SQHLHYKVVVYFREDTQKDYNAL 343
Qy 493 DLSTYRLMDNLPOLCSHL 511
Db 344 SVCPKTHLMKDATAFCAEL 362

RESULT 3
US-10-063-703-158
; Sequence 158, Application US/10063703
; Publication No. US2006008901A1
; GENERAL INFORMATION:
; APPLICANT: Baton, Dan L.
; APPLICANT: Pilvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austen L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William J.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,703
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: - See Palm or file wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 158
; LENGTH: 502

```

TYPE: PRT
ORGANISM: Homo Sapien
US-10-063-703-158

Query Match 3.4%; Score 134.5; DB 6; Length 502;
Best Local Similarity 20.1%; Pred. No. 0.00036;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;

QY 204 NUNISQSGDMQVSF-----DHAPHNFGRRFFLYHKLKHEGPFKKTCT----- 247
DB 143 NANNNEGSPMSVNFSPGCLD-----IMKYK-----KKCVKAGSLMDPN 183
QY 248 -----KOEOTE---TTSCLQNVSPGDYIIEVDNTTRKVMHAKLVHPHMACPIR 299
DB 184 ITACKKNEEVEVNFPTTLP-----GNRYMALIOHSTI-----IGFSQVFEHPQKQT 231
QY 300 AMATVPLVVISAFATL-----FTVMCRKKQENIYSHLDEBSESS 341
DB 232 RASVVIPTGDSGATVQLTPYPTGSDCI RHKGTVLC---PQTGVPPFLDNKSKPG 288
QY 342 TYTAA-----PRELR-----PRPKVFLCYSSKQGNHNM 372
DB 289 GMLPILLSLVATVWLVAGIYLMHMERIKKTSFTTLLPPIKLVVYPSICFHH-- 346
QY 373 VVOCFAVFLDPGCEVALDLMEDFSLCRGQREWVIOKIHESQFIIVVCSKMKYVDK 432
DB 347 TICFTEFLQNHCRSEVILEKQKKIAEMGPVOMLATOQKADKVFLSLNDVNSVCDG 406
QY 433 KNYKHGGGSGSGELFLVAVSAIAEKLQAKOSSAALSKFIAYFDYSCGDPVGL 492
DB 407 TCGKSESPSENSQ-DLPLAFNLFCSDLR-----SQIHAKVYVVFREIDTDVYNAL 460
QY 493 DLSTKRLMDNLPOLCSHL 511
DB 461 SVCPRKHLMDATAFCAEL 479

RESULT 4

US-11-102-240-158
Sequence 158, Application US/11102240
Publication No. US20050260647A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
FILE REFERENCE: P3230R1C106C
CURRENT APPLICATION NUMBER: US/11/102,240
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 10/063662
PRIOR FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/170262
PRIOR FILING DATE: 199-12-09
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 158
LENGTH: 502
TYPE: PRT
ORGANISM: Homo Sapien
US-11-102-240-158

Query Match 3.4%; Score 134.5; DB 7; Length 502;
Best Local Similarity 20.1%; Pred. No. 0.00036;
Matches 76; Conservative 49; Mismatches 141; Indels 113; Gaps 14;
QY 204 NUNISQSGDMQVSF-----DHAPHNFGRRFFLYHKLKHEGPFKKTCT----- 247

DB 143 NANNNEGSPMSVNFSPGCLD-----IMKYK-----KKCVKAGSLMDPN 183
QY 248 -----KOEOTE---TTSCLQNVSPGDYIIEVDNTTRKVMHAKLVHPHMACPIR 299
DB 184 ITACKKNEEVEVNFPTTLP-----GNRYMALIOHSTI-----IGFSQVFEHPQKQT 231
QY 300 AMATVPLVVISAFATL-----FTVMCRKKQENIYSHLDEBSESS 341
DB 232 RASVVIPTGDSGATVQLTPYPTGSDCI RHKGTVLC---PQTGVPPFLDNKSKPG 288
QY 342 TYTAA-----PRELR-----PRPKVFLCYSSKQGNHNM 372
DB 289 GMLPILLSLVATVWLVAGIYLMHMERIKKTSFTTLLPPIKLVVYPSICFHH-- 346
QY 373 VVOCFAVFLDPGCEVALDLMEDFSLCRGQREWVIOKIHESQFIIVVCSKMKYVDK 432
DB 347 TICFTEFLQNHCRSEVILEKQKKIAEMGPVOMLATOQKADKVFLSLNDVNSVCDG 406
QY 433 KNYKHGGGSGSGELFLVAVSAIAEKLQAKOSSAALSKFIAYFDYSCGDPVGL 492
DB 407 TCGKSESPSENSQ-DLPLAFNLFCSDLR-----SQIHAKVYVVFREIDTDVYNAL 460
QY 493 DLSTKRLMDNLPOLCSHL 511
DB 461 SVCPRKHLMDATAFCAEL 479

RESULT 5

US-10-821-234-1019
Sequence 1019, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Seache-Crain, Birgit
APPLICANT: Andarmant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methode for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes Version 1.0
SEQ ID NO 1019
LENGTH: 730
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-1019

Query Match 2.8%; Score 112.5; DB 6; Length 730;
Best Local Similarity 19.7%; Pred. No. 0.066;
Matches 144; Conservative 80; Mismatches 261; Indels 247; Gaps 33;

QY 153 MKETIYPAKVVPSPISKNSNHPFRTRACDLLOP----- 192
DB 88 LKTEBDY-----IPYPSV-----HEVLGRGEPPLILPQFGVWEGTNEHTISIPETE 137
QY 193 -----NLACKP-----FMKPRNUNISQSGDMQVSFDHAPHNFGRRFFLYHKLK 235
DB 138 PLOSPPTKVLGNPFAIRYKHFLOGKEHN-----YSLDTA-----LGHVFSIKYD 186
QY 236 L-----KHEGPFKKTCKOBTETTSCLQNVSPGDYIIEVDNTTRKVMHAKLVH 291
DB 187 VIDQEHRLRLATKCRTHDVIPISCLTFPVPVQMAKLVCDVAVDR-----FYPVL 240
QY 292 SPWAGPIRMAATVPLVVIS-----AFATLFTVMCRKKQENIYSHLDEBSESSSTYTAALP 348
DB 241 YPVAAS---RLIVTFDEHVISNNPKFGVITYOKLGQTSSEB-----LFTSWESAPVFEFLR 292
QY 349 RERLRPRPKVFLCYSSKQGNHNMVVOCAVFLDPGCEVALDLM-----DFSICR--- 401
DB 293 -----FLGQKTK-----LQDFKGRGGLDVTHGQGTESVVCNPR 327

QY 402 -----EGOREMVIQKIHESQFIIVVCSKGMKYFYDK-----KNYK 436
| : : : : :
DB 328 NKEIMFHVSTKLPYTESDQAOLQKRIHNDIVAV-----VFQDETPVPVPMIASNFL 381
| : : : : :
QY 437 H-----KGGGSGSGKGLFLVAVSAIAE-----KLQAKOSSAALSKEPIA 477
| : : : : :
DB 382 HAVVVAOAEGG---PDGPLYKVSVTARDVPPFGPPLPDPAVFRKGPFOEFLTLIN 438
| : : : : :
QY 478 VYFDYGC-BEVDVCGILDSTKRYLMONTLPOLCSHLHRD-HGLQEPQHRQSSRRRYF- 534
| : : : : :
DB 439 A--EVACYKAEKPAKLEERTALLETLYEEL-HHSQSMWGLGDEDKENNSGGGGFF 495
| : : : : :
QY 535 -----RSKSGRSL-----YVAIQMHOIFDEBPWFPE---KQFVFPHPPLR 573
| : : : : :
DB 496 ESKFVIRSRQSDMDAMGLSNKKPNVSTSHSGSFANNDPLAKAGISILIVGKSTRK 555
| : : : : :
QY 574 YREPVLEKFDPSGLVLDVMCKPGEPSDFCLKVEAPVLGATGPADSOHESGHGLDQGEA 633
| : : : : :
DB 556 KSGPFSGRSSAIGIENI-----QEVQKRSPPAQKTP-DSGHVSGEPKSE----- 602
| : : : : :
QY 634 RPLDGSALQPLHTYKAGSPSDMPRDSGIYSSVSSLS-----LPLMEGLSTDQTE 688
| : : : : :
DB 603 ---NSSTGSPMPPTKNAETPAQRAEALXDFSRSSSSASFPASVETEEDVDEDTG 658
| : : : : :
QY 689 TSS-----LTESVSSSG-----LGEPEPPALPSKL 714
| : : : : :
DB 659 LBSVSSSGTPHKRDSPTYSTWLEDVSYTTSGSSPGFSRPHPDAGLGDPAPEIKIQL 718
| : : : : :
QY 715 LSSGSCKADLGC 726
| : : : : :
DB 719 EASEQHMPQLGC 730

RESULT 6
US-10-510-524-1
; Sequence 1, Application US/10510524
; Publication No. US20050260209A1
; GENERAL INFORMATION:
; APPLICANT: BOYD, ROBERT S
; APPLICANT: FLETCHER, GRAHAM C
; APPLICANT: HUDSON, LYNDSEY J
; APPLICANT: PATEL, SONAL
; APPLICANT: TERRETT, JONATHAN A
; TITLE OF INVENTION: AN EPHRIN-B RECEPTOR PROTEIN INVOLVED IN CARCINOMA
; FILE REFERENCE: 2543-1-037PCT/US
; CURRENT APPLICATION NUMBER: US/10/510,524
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: GB0208089.3
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-524-1

Query Match 2.6%; Score 103.5; DB 6; Length 998;
Best Local Similarity 18.8%; Pred. No. 0.71;
Matches 148; Conservative 119; Mismatches 293; Indels 229; Gaps 39;

QY 42 RGVGPASRNSGLNITFKYN-----CTTYLNPVGHVADADQNTISYACHDQAVY 95
| : : : : :
DB 309 RITSPPASISICTGNNFPRADSDASACTVPSR-PRGVISNV-----NETSIL 356
| : : : : :
QY 96 ILWS-EGALGIEFLKGRVILIELKSEG-----RQCQOLILKPKQLNSFKTGMESQP 149
| : : : : :
DB 357 LEWSEPRDLGVRDLDLVNYICKCHGAGSASACRCDNDVEFPRQLGSEPRVHTS--- 413
| : : : : :
QY 150 FLNMKEETDVFVAVPPPSIKNSNVHPFFRTACDLLQIDPNLACKCPKPRNINISQ 209
| : : : : :
DB 414 --HLLAHTRYTFEVQAVNVGSGKSLPBRVAAVNITTNQAAPSEV-----PTLRHLS 464
| : : : : :
Query Match 2.5%; Score 99.5; DB 7; Length 1273;
Best Local Similarity 18.5%; Pred. No. 2.4;
Matches 143; Conservative 92; Mismatches 214; Indels 323; Gaps 36;

QY 210 HSGDMOVSPDHAIPHNGFPFYLYHKLKHEGPF-KKTKCKOBQTTETTSCLIONVSP-GD 267
| : : : : :
DB 465 SSSSLTSLNAPPERPBG---VILDIEMKY---PEKSEGLASTVTSQMSNVOLDGLRPPDR 518
| : : : : :
QY 268 YIIELVDDNTTRTKVMHYA-LKPVH---SPWAGPIRAMAITVPLVISAFTL----- 316
| : : : : :
DB 519 YVVQV-----RARTVAGQYGRPAFEFTTSBRSGAQLOQLPLIVGSATAGLVFVA 573
| : : : : :
QY 317 ---FTWCKKQOENIYSHLDESSSSSTYTALPREKRPRPKYPLCTSSSDGQNNMV 373
| : : : : :
DB 574 VVVIATVCLARKQRH-----GSDSEYTEKL-QQYLAPEMKYIIDPFYEDPN--EA 620
| : : : : :
QY 374 VOCFAFFLQDFC-GCEVALDLMEFSLCREGOREWVIQKIHESQFIIVVCSKGMKYFYDK 432
| : : : : :
DB 621 VKEFAEIVDSVCKIIEVVGAGEFGEVCR----- 649
| : : : : :
QY 433 KNYKKGGRSGSGKGLFLVAVSAI---AEKLQAKOSSAALSKEPIAVYFDYSCGDV 488
| : : : : :
DB 650 -----GRLKQPGREVF-VAIKTLKVGYTERQRDRDIFSEASIMQOF-----DH 691
| : : : : :
QY 489 PGILDS---TKR-----LMDNLPOLCSHLHSRDHGLQEPQHT----- 525
| : : : : :
DB 692 PNIRLEGVVTGSRPVMILTFEMENC-ALDSFLRLND-----GQFTVIQLVGMRLGIAA 744
| : : : : :
QY 526 ---ROGSRMY-FRSKSGRELAV---AIC-----NMHOIFDEBPWFPEKQFVFPHP- 570
| : : : : :
DB 745 GMYLSBNMYVYRDLAARNILVNSNLVCKVSDPGLSRFLIEDPS-----DPTYSSSLGG 798
| : : : : :
QY 571 --PLRYREP--VLEKFD-----GLVLDVMCKPGEPSDFCLKVEAPVLGATGPADS 618
| : : : : :
DB 799 KIPIRWTAPEALAYRKFTSASDVMSGYIMMEVMS-----YGERPYMD 842
| : : : : :
QY 619 QHESQHGILDQGEARPALDGSALQPLHTYKAGSPSDMPRDSGIYDS----- 667
| : : : : :
DB 843 SNQDVINAVEODYRLPEPPDCPTALHQLMLDCVADRNLRPFESQIVNTLDKLIRNAASL 902
| : : : : :
QY 668 ---SVPSSELSPLMEGLSTDQETSSLTESVSSSGSGEPEPPALPSKLSSGSKADL 724
| : : : : :
DB 903 KYIASQSGMSQPLDRYTPDYTTFTTVGMDALIK-MGRYK-----BSFVAGAFASFDL 956
| : : : : :
QY 725 GCRSYTDEL 733
| : : : : :
DB 957 VAQMTAEDL 965

RESULT 7
US-11-181-330-8
; Sequence 8, Application US/1181330
; Publication No. US20060035283A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S MEDICAL CENTER CORPORATION
; TITLE OF INVENTION: NEUROPROTECTIVE THERAPEUTICS AND ASSAYS FOR IDENTIFYING
; FILE REFERENCE: CMA-3.25
; CURRENT APPLICATION NUMBER: US/11/181,330
; PRIOR FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: PCT/US04/01209
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/440,679
; PRIOR FILING DATE: 2003-01-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 1273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-181-330-8

Query Match 2.5%; Score 99.5; DB 7; Length 1273;
Best Local Similarity 18.5%; Pred. No. 2.4;
Matches 143; Conservative 92; Mismatches 214; Indels 323; Gaps 36;

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QY 112 RVILIELKSEGRCCOOL-ILKD-----PKOLNSFKRTGME-----SQPLNKKPFIDYFVK 162
DB 243 QVPSHLEBAEAEVYQOHLILNNPRLRLRAASAKKPPITHDVDSIFLMS--ETIMFLH 300
QY 163 VWPSPISXNENYHPPFRTACDILLQPNLACKPWPCKRNINISQ-----HGSDMQVS 217
DB 301 QIFVQGLKARISWPLVLADLFDILLP-----MNTYGEFPRNHQYSQI- 346
QY 218 FDHAPNPFGRFRLYAKLKHGEPFKKTKQEQOTTETTSCLLONNSPGDYII--ELVD 274
DB 347 LAMCKORRDKLKHKEAKPD-----C-BERTLETPLTYPMFOIP-RYIILHMLLA 397
QY 275 DT---NTRKVMHYALPVHSPMAGPIRAMAIVPLVISAAPALPFWCKRKOQENIYS 331
DB 398 HTHHEVERNSLDYA-----KSKLELSR 421
QY 332 HLDSESSSTYTAALPRERLPRPKVFLCYSSKQGNHNVVOCFAVPLQDPGCEVAL 391
DB 422 IMDEVESETENIKNLAIERM-----IIE-----GCEILL 451
QY 392 DLWEDF-----SLRCQOREWVIOKIHESQFIIVCSKM 426
DB 452 DTSQTFRQOGLIQVPMSEKGIKTRGRLSGLKGEGRQCFLEPSK-----LIICTRGS 506
QY 427 --KYPVDKKNY-----KHKGG-----RSGKGEFLVA 453
DB 507 GGLHLTKNGVISLIDCTLLEBPSTEEAKSGODIDLDFKIGVBPCKSPPTVLVA 566
QY 454 VSAIAELRQAKOSSAALSKFIANVPDYSCEGDPILDLSTYKRLMDNLPOLCSHLHS 513
DB 567 SS-----ROKKAAMTSDISQVD--NIRCNGLMNAFENGSKV-----TYPMOI----- 608
QY 514 RDHGOEPGHTQGSRRNYFRSKGSRSLVYALCNMHQFIDEBPWEKQFVPPHPLR 573
DB 609 -----KRTREGTEAEM--SRSDASY-----CDVDVIRFSKTMNSCKVQIR 649
QY 574 YR--EPVLEK-----PDSGLVLDVMCKPGESDCLKVEAPVL 610
DB 650 YASVERLELRLTLRPLSLIDPLNTFLHSYRVFTTAYVLDKL-----ITIKKPI- 699
QY 611 GATGPADSQHSQHGLDQGEARPA-----LDGSALQPLHTVAKGSPSPDRDS 662
DB 700 -----SAIPAMWLSLELLFPASGONKLLY-----GEPKSPRAT 734
QY 663 GIYDSSVPS-----ELSLPLMEG-----LST 684
DB 735 RKFSPPPLSITKTSRSPRRKLSINIPITGKALDLALASCNNGYTSWYASMSPSK 794
QY 685 DQETESLTSVSSSGGLGEE-----EPPLPSTGLSSGCKADLGRSTTD 731
DB 795 ATLDTSKLYVSSSFTWKIPDEGDTTPKPDPSALSKOSS-----EVSMBESD 843

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; ORGANISM: Homo sapiens
US-11-203-251A-88
Query Match 2.5%; Score 98.5; DB 7; Length 998;
Best Local Similarity 18.6%; Pred. No. 2;
Matches 147; Conservative 121; Mismatches 292; Indels 229; Gaps 39;

QY 42 RGVGPASRNSGLYNIFKDN-----CTTYLNPVKHVAADANNTISQYACHDOVAVT 95
DB 309 RTTSPASICTCHNNYFRADSDSADSACTVPSR-PBGVLSNV-----NETSLI 356
QY 96 ILMS-PGALGIEFLKGFVRLIEELKSEG-----ROCCOOLIKDPKOLNSFKRTGMSQP 149
DB 357 LEMSEPRDLGGRDILLNYICKKHGAGASACRSDDNVEFPRQGLTERRVHIS--- 413
QY 150 FLNKKFETDYFVKVPPSPISXNENYHPPFRTACDILLQPNLACKPWPCKRNINISQ 209
DB 414 --HLAHTRYTFEVOAVNGVSGSKPLPPRYAAVNITTNQAPSEV-----PILRLHSS 464
QY 210 HGSDMQVSPHAPNPGFRFVLYHKLKHGEP-KRKTCKQBOTTTETTSCLLONVSP-GD 267
DB 465 SGSSLTLSWAPPRPNP-----VILDYEMKY--FEKSEGLASTVTSQWNSVOLGLRDPAR 518
QY 268 YIIELVDDTNTKRWNYA--LKPVH-----SPWAGPIRAMAIVPLVISAAPAL- 316
DB 519 YVQV-----PANTVAGYGYSRPAEFTTSEKSGAQOQOPLIVGSATAGLVFVA 573
QY 317 ---FTWCKRKOQENIYSHLDESSSSTYTAALPRERLPRPKVFLCYSSKQGNHNV 373
DB 574 VVVAIVYCLRKQH-----GSDSEYTEKL-QOYIAPGMKVYIDPETYDDPN--EA 620
QY 374 VOCFAYFLDQFC-GCEVALDLMEDFSLCREGQREWVIOKIHESQFIIVCSKMKRYVDK 432
DB 621 VREFAKRIDVSCYKIEVIVGAGEFGEVCR----- 649
QY 433 KNYKHGGKSGKGEFLVAVSAI--AEKLRQAKOSSAALSKFIANVPDYSCEGDV 488
DB 650 -----GRLKQPRRREV-VAITTLKGYTERORRDLFSLASITMGQF-----DH 691
QY 489 PGILDLSS--TKYR-----LMDNLPOLCSHLSDHGOEPGQHT----- 525
DB 692 PNIRLEGVYTKSRPMLILFERFENC-ALDSFLRLND-----GQFVILVGLMGLGIAA 744
QY 526 --RQSGRRNY-FRSGKGRSLYV--AIC-----NMHOFIDEBPWEKQFVPPHPP 570
DB 745 GMKYLEMNYVHDLARNILVNSNLVKVSDGRLFRFLEDDPS-----DPTYSILG 798
QY 571 --PLRYREP--VLEKPS-----GIYLDVMCKPGESDCLKVEAPVLGATPADS 618
DB 799 KIRIRWTAPALAYRKFTSASDVMSYGIWMEVMS-----YGBRPYWDW 842
QY 619 QHESQHGGLDQGEARPALDGSALQPLHTVAKGSPSPDRSGIYDS----- 667
DB 843 SNQDVINAYEQDRRLRPPMDCFALHQMLDCVVRBNLRPKSQVINTLTKLIRNAASL 902
QY 668 ---SVPSSELISLPLMEGLSTQETSSLTESVSSSGGLGEEPPALPSKILSSGCKADL 724
DB 903 KYIASAQSGMSQPLDLRTVDPYTTFTVGMIDLAIK-MGRYK-----ESFVSGAFSFDL 956
QY 725 GCRSYDEL 733
DB 957 VAOQTAEDL 965

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RESULT 8
US-11-203-251A-88
; Sequence 88; Application US/11203251A
; Publication No. US20060039904A1
; GENERAL INFORMATION:
; APPLICANT: MedImmune Inc.
; TITLE OF INVENTION: EPH RECEPTOR P-2 VARIANTS WITH ENHANCED ANTIBODY DEPENDENT
; FILE REFERENCE: A6702US
; CURRENT APPLICATION NUMBER: US/11/203,251A
; PRIOR FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: 60/601,634
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: 60/608,852
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 88
; LENGTH: 998
; TYPE: PRT

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RESULT 9
US-10-330-773-904
; Sequence 904; Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300

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;; CURRENT APPLICATION NUMBER: US/10/330,773
;; CURRENT FILING DATE: 2002-12-27
;; NUMBER OF SEQ ID NOS: 981
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 904
;; LENGTH: 2343
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-10-330-773-904

Query Match 2.5%; Score 98.5; DB 6; Length 2343;
Best Local Similarity 27.1%; Pred. No. 7.3;
Matches 29; Conservative 18; Mismatches 43; Indels 17; Gaps 4;

QY 606 EAPVLGATGPADSHQSGHGLDODGEA---RPALDGSALOPLHTVTKAGSPSDMDRDS 662
DB 715 EPPAFSGPSEFAHNPPLGSTSPAFASKASPSLEPSTFOP--RTPKGAGSSEPK-- 770

QY 663 GIYDSVPSSELSLPLMEGLSTDQETSLTESVSSSGLEBEPRA 709
DB 771 ---ERRTMSKEISV-----IHTSFEKSDPEEGSGLEBEPRA 807

RESULT 10
US-11-113-424-60
; Sequence 60, Application US/11/113,424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; PRIOR FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-113-424-60

Query Match 2.5%; Score 98; DB 7; Length 984;
Best Local Similarity 17.7%; Pred. No. 2.2;
Matches 117; Conservative 86; Mismatches 201; Indels 256; Gaps 32;

QY 185 CDLLPPDNLACPFMKPRNLNISQHSQMDQVSPDHAHNGFRFFYLAKLKHGEPFKR 244
DB 373 CD-----DNE-----FVPRQLGLTECVSISSLMAHTPYTFDQAI---NGVSKSPFP 420
QY 245 KTKGKQOTETTSCLQNVSPGDIYIELVDVDTNTRKVMY---ALKPVSPAPGPIRAM 301
DB 421 QHVSVAITTNQA-----PSTVPIHQVSAITMSITLSNPPQEPQ 461
QY 302 AITVPLVISAFTLFTVMCKRKQENIYSHLDESESSSTYPAALPRELRP----- 354

DB 462 GILDEYI-----RYEKEHNEFNSSNARSQNTARI--DGLRGMVYVQ 505
QY 355 -RPKFLCYSSKDGQNHMNVQCFAYFLQDFGCEVALDMEDFSICRGOREMVIQKH 413
DB 506 VRAKTVAGYGFSGK-----MCFQTLTDD-----DYKSELREQPLIASSAAGV---- 551
QY 414 ESQFII-----VCSGK-----GMKYFVDKKNYK----- 436
DB 552 ---FVVSLVAISIVCSRKQAVSKAAYSDKLQHYSTGRGSPGKKIYIDPFYEDPNEAYR 608
QY 437 -----HKGGRSGKRELVLVVASA-----AEYLROAKGS 467
DB 609 BFAKEIDVSPVKIEEYVIGAGEEYVYKRLKLPGRKEIY-VAIKTKAGYSEKQRPDLS 667
QY 468 SSAAISKPIAVVYFDYSCBGVFGIIDLs---TKYR-----LMDVLPOLCSHLSRDHG 517
DB 668 EASIMQF-----DHENIILLEGVTKSRVMTITERMEN-GALDSFLROND-- 713
QY 518 LQEPGQHT-----RQGRNRY-FRSKSGRLVY---AICNMHQF----- 552
DB 714 ---GGFTYIQLVGMRLGIAQMKYLSMNYYHRDLAANILVNSVLCKVSDPFGLSRYL 769
QY 553 IDEEPPWFEKQVFPFHP-----PLRYRP---VLEKFS-----GLVLDNVCKKG 596
DB 770 QDTSDD-----PRTYSLGSKI PVKWTAPFAIAYRKFTSADVWSYGIWMEVWS--- 819
QY 597 PESDPLKTVAPVLGATGPADSHQSGHGLDODGEARPALGSAALOPLHTVTKAGSPS 656
DB 820 -----FGRPYWDSNODVINAIEDRLPPEMDCPALHQMLMDCKQKDN 866
QY 657 DNEPDSGIYD-----SSVPSSELSLPLMEGLSTDQETSLTESVSS 698
DB 867 SRPRFAELIVNTLDMKMRNPASLKTVAITIVAVSQ-----PLDRSIDPFAFTVDWLGA 922

RESULT 11
US-11-115-639-31
; Sequence 31, Application US/11/115,639
; Publication No. US2005028242A1
; GENERAL INFORMATION:
; APPLICANT: Rothelein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: Macneil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-31

Query Match 2.5%; Score 97; DB 7; Length 2890;
Best Local Similarity 18.6%; Pred. No. 14;
Matches 110; Conservative 68; Mismatches 162; Indels 250; Gaps 26;

QY 45 GPASRNSGLYNT-----FRYDNCITYLNPVGKHIADAQNTITSQY----- 86
DB 2304 GTASRSQDREIIVASKEGFRFYNLTYNKEGKNIIARRNASILVVEPKIAPFDGL 2363
QY 87 ---ACHDQAVNTI-----LMSPGALGIEFLKGF 111
DB 2364 RIETVYEEVVASVKNQDQAKVLRSDIVKPSLAVGCGKIGKAYLLPYAAGSHKVGCG 2423
QY 112 RV--ILBE---LKSQRQCQQLLK--DPKQINSFKRGMESOPFLNKK-FETDYFVAV 163


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Db 2424 STADIIQEGMNVNRI.PYASELLVKNONDPIDQDVAKKGVLYVLEANHLERTGICK 2483
Qy 164 VPPPSIK-----NESNYHPFFRTACDILL-----QPNLACKP----- 198
Db 2484 GDMVSEKGL.FAVIADNGREARH---YIAROSEIILIDNSVSTNSVSKPTTNTFKTI 2540
Qy 199 -FWKPNLNISQHGSDMOVSPDHAPNFGFRFFLYHLKHKHGPFRKTC----- 247
Db 2541 ATMDPNTPII-----ADFGKKG.FVDVIAGTV 2569
Qy 248 --KOEQTETTSCLLONVSPGDYIIEVDNTTRKVMHYAL.KPVHSPMAGPIRAMAITY 305
Db 2570 AEREDENTGITSLVNDYIPSGYKPSL.FLE-GANGEMRYFLEPKTS----- 2615
Qy 306 PLVVISAPATLFTVMCRKQOENIYSHLDESESSSTYALPR-----ERLPRPKVFL 360
Db 2616 --IAISDSSV-----EQAEVLAKIPKATVKSNDITGCLPRVSELFEARKPKKQDVA 2665
Qy 361 CVSSKDGQNMNVOC.FAYFLQDFCGCEVALDLMEDPSLCRGQREWVLOKIHESQFIY 420
Db 2666 ILSEVDG-----IVSFG-----KPIINKKHITV 2688
Qy 421 VCSKG--MKYFVDK-----KNYKHKGQ-----RSGKGL.FLVAVS--- 455
Db 2689 TSKDGRSMDYFVDKQKQILVHADFEVHAGEAMTDVSISSHDILRISGEKELYKYIVSEVQ 2748
Qy 456 -----AIAXK-----LRQAKQSSAALSKEFIAYFPDYSGEDV 488
Db 2749 QYRRQGVSIADKHIEIIVSQMLRQVRIIDSGD-SKEI-----EGDL 2789
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RESULT 12

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US-11-115-639-32
; Sequence 32, Application US/11115639
; Publication No. US2005028242A1
; GENERAL INFORMATION:
; APPLICANT: Rochelein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: Macneil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-32
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Query Match 2.5%; Score 97; DB 7; Length 2890;

Best Local Similarity 18.6%; Pred. No. 14;

Matches 110; Conservative 68; Mismatches 162; Indels 250; Gaps 26;

```
Qy 45 GPASRNSGLYNIT-----FKYDNCCTTYLNPVGKVIADQNTTISQY----- 86
Db 2304 GTRNSQDEREIVASKEGFVRFNLTNTYKESKNIIANRRNASILVVEPKIKAPDGL 2363
Qy 87 ---ACHDOVAVTI-----LMSGALGIEFLKGF 111
Db 2364 RIETVVEEVVSVKNGDQAKFVLRSDDIVKPSLAVGSGKIEGKYLLPYASGHKVKHG 2423
Qy 112 RV--IIEE--LKSEGRQCOOLIK--DPKQUNSSFKRTGMSQPLNKK--PFTDVFVY 163
Db 2424 STADIIQEGMNVNRI.PYASELLVKNONDPIDQDVAKKGVLYVLEANHLERTGICK 2483
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Qy 164 VPPPSIK-----NESNYHPFFRTACDILL-----QPNLACKP----- 198
Db 2484 GDMVSEKGL.FAVIADNGREARH---YIAROSEIILIDNSVSTNSVSKPTTNTFKTI 2540
Qy 199 -FWKPNLNISQHGSDMOVSPDHAPNFGFRFFLYHLKHKHGPFRKTC----- 247
Db 2541 ATMDPNTPII-----ADFGKKG.FVDVIAGTV 2569
Qy 248 --KOEQTETTSCLLONVSPGDYIIEVDNTTRKVMHYAL.KPVHSPMAGPIRAMAITY 305
Db 2570 AEREDENTGITSLVNDYIPSGYKPSL.FLE-GANGEMRYFLEPKTS----- 2615
Qy 306 PLVVISAPATLFTVMCRKQOENIYSHLDESESSSTYALPR-----ERLPRPKVFL 360
Db 2616 --IAISDSSV-----EQAEVLAKIPKATVKSNDITGCLPRVSELFEARKPKKQDVA 2665
Qy 361 CVSSKDGQNMNVOC.FAYFLQDFCGCEVALDLMEDPSLCRGQREWVLOKIHESQFIY 420
Db 2666 ILSEVDG-----IVSFG-----KPIINKKHITV 2688
Qy 421 VCSKG--MKYFVDK-----KNYKHKGQ-----RSGKGL.FLVAVS--- 455
Db 2689 TSKDGRSMDYFVDKQKQILVHADFEVHAGEAMTDVSISSHDILRISGEKELYKYIVSEVQ 2748
Qy 456 -----AIAXK-----LRQAKQSSAALSKEFIAYFPDYSGEDV 488
Db 2749 QYRRQGVSIADKHIEIIVSQMLRQVRIIDSGD-SKEI-----EGDL 2789
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RESULT 13

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US-11-115-639-33
; Sequence 33, Application US/11115639
; Publication No. US2005028242A1
; GENERAL INFORMATION:
; APPLICANT: Rochelein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: Macneil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-33
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Query Match 2.5%; Score 97; DB 7; Length 2890;

Best Local Similarity 18.6%; Pred. No. 14;

Matches 110; Conservative 68; Mismatches 162; Indels 250; Gaps 26;

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Qy 45 GPASRNSGLYNIT-----FKYDNCCTTYLNPVGKVIADQNTTISQY----- 86
Db 2304 GTRNSQDEREIVASKEGFVRFNLTNTYKESKNIIANRRNASILVVEPKIKAPDGL 2363
Qy 87 ---ACHDOVAVTI-----LMSGALGIEFLKGF 111
Db 2364 RIETVVEEVVSVKNGDQAKFVLRSDDIVKPSLAVGSGKIEGKYLLPYASGHKVKHG 2423
Qy 112 RV--IIEE--LKSEGRQCOOLIK--DPKQUNSSFKRTGMSQPLNKK--PFTDVFVY 163
Db 2424 STADIIQEGMNVNRI.PYASELLVKNONDPIDQDVAKKGVLYVLEANHLERTGICK 2483
Qy 164 VPPPSIK-----NESNYHPFFRTACDILL-----QPNLACKP----- 198
Db 2484 GDMVSEKGL.FAVIADNGREARH---YIAROSEIILIDNSVSTNSVSKPTTNTFKTI 2540
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QY 199 -FWKPRNLNISOHGSMDQVSPDHAHNFGRFFPYLHKLKHEGPPKRTK----- 247
DB 2541 ATWDPFYNTPII-----ADFGKVGFDVVIAGVT 2669
QY 248 --KOEOTETSTCLLQNVSPGDIYIELVDYTTTRKMYHALKPVHSPMAGPIRAMAIY 305
DB 2570 AAEKEDNTGITSIVVNDYIPSGYKPSLFE-GANGEMRFFLEPKTS----- 2615
QY 306 PLVVISAPATLFTVMCRKKQOENIYSHLDESESSSTYTAALPR-----ERLAPRPVFL 360
DB 2616 --IAIDGSSV-----EQAEVLAKIPATYKSRDITGGLRVSLEFAPKPKEDVA 2665
QY 361 CYSSKQGNHNVQCFAYFLQDFCGCEVALDLMEFSLCREGOREWVIOKIHESQFIY 420
DB 2666 ILSEVDG-----IVSFG-----KPIINKKHIIY 2688
QY 421 VCSKG--MKYFDK-----KNYHKGCG-----RSGKGEFLVAVS--- 455
DB 2689 TSKDGRSMDFYVDKQQLVHADEPVHAGEAMTDGVLSHDILRISGEKELYKYIVSEVQ 2748
QY 456 -----AIAEK-----LROAKQSSSALSKFIANYFDYSGEDV 488
DB 2749 QYTRGCVSTADKHIEIIVSQMLRQVRIIDSD-SKFI-----BGDL 2789

RESULT 14

US-11-203-251A-85
; Sequence 85, Application US/11203251A
; Publication No. US2006003904A1
; GENERAL INFORMATION:
; APPLICANT: Medimmune Inc.
; TITLE OF INVENTION: EPH RECEPTOR FC VARIANTS WITH ENHANCED ANTIBODY DEPENDENT
; TITLE OF INVENTION: CELL-MEDIATED CYTOTOXICITY ACTIVITY
; FILE REFERENCE: A6702US
; CURRENT APPLICATION NUMBER: US/11/203, 251A
; CURRENT FILING DATE: 2005-08-15
; PRIOR APPLICATION NUMBER: 60/601,634
; PRIOR FILING DATE: 2004-08-16
; PRIOR APPLICATION NUMBER: 60/608,852
; PRIOR FILING DATE: 2004-09-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 984
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-203-251A-85

Query Match 2.4%; Score 95; DB 7; Length 984;

Best Local Similarity 17.6%; Pred. No. 4.2;
Matches 116; Conservative 87; Mismatches 201; Indels 256; Gaps 32;

QY 185 CDLLQPDNLACKPFKPRNLNISOHGSMDQVSPDHAHNFGRFFPYLHKLKHEGPPK 244
DB 373 CD-----DNVE-----FVPRQLGLTECRVSISSIMATPYFDIOAI---NGVSKSPFP 420
QY 245 KTCCKQOTETSTCLLQNVSPGDIYIELVDYTTTRKMY---ALKPVHSPMAGPIRAM 301
DB 421 QHVSNNITNQAA-----DSTVIMHQSATMKRSTLSLPOPEQPN 461
QY 302 AITVPLVVISAPATLFTVMCRKKQOENIYSHLDESESSSTYTAALPRELRP----- 354
DB 462 GILLDVEI-----RYEKENHEFSSMARSGTNTARI--DGLRGMYYVVG 505
QY 355 -REKVELCYSSKQGNHNVQCFAYFLQDFCGCEVALDLMEFSLCREGOREWVIOKIH 413
DB 506 VVARVTAAGVKGKFGK-----MCFQLTLTD---DYKSELREQPLIAGSAAAGVV----- 551
QY 414 ESQFI-----VCSK-----GKTFYDKKKNY----- 436
DB 552 ---FVSVLVAISIVCSRKAIVSKAVVSDKLQHYSTGRSGPKMKIYIDPFTYEDPNEAVR 608

QY 437 -----HKGGKSGSGKGEFLVAVSAI-----AEKLRQAKOS 467
DB 609 EFAKEIDVSVKIEEYVIGAGEGEEYKGRLLKLPGRKEIY-VAIKTLKAGYSEKQRDFLS 667
QY 468 SGAALSKFIANYFDVSCBEDVPGIILDS---TKYR-----LMDLPLQCSHLSRDRG 517
DB 668 EASIMQF-----DHEPITRLBGVVTKSRVMTITEFEN-GALDSFLROND--- 713
QY 518 LQEPGQHT-----RQSSRRNY-FRSKSGSLYV---AICNMQF----- 552
DB 714 -----GQFTYIQLVGMRLGIAGMKYLAEMNYHRDLAANILVNSLVCKVSPFGLSRYL 769
QY 553 IBEEDPWEKQVPPHPP-----PLRYRP---VLEKFS-----GLVLDNVCCKG 596
DB 770 QDPTSD-----PYTSSLGKIPVMTAPALAVRKFTSADVWSYGIWMEVWS--- 819
QY 597 PESDPLKYEAPVLATGATGADSOHSGHGLDODGAPRALDSALQPLHTVYKAGSPS 656
DB 820 -----FGRFPYWDMSNDVINALQDYLPPPMCCPALHQLMLDCWQXDRN 866
QY 657 DMPRDSGIYD-----SSVPSSELSPLMEGLSTDQETSSLTSESVS 698
DB 867 SRPRRAEIVNTLDMKMTIRNPASLKTVAITRAVDSQ-----PLDORSIPDFTFAFTVDWLSA 922

RESULT 15

US-10-055-877-253
; Sequence 253, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DecistoFaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zethusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patuturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Wolsenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corinne
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Perence
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25

PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 253
LENGTH: 2098
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-055-877-253

Query Match 2.4%; Score 95; DB 6; Length 2098;

Best Local Similarity 21.4%; Pred. No. 13; Matches 101; Conservative 61; Mismatches 189; Indels 122; Gaps 24;

QY 335 EESESSTYALPREELRPKVFILCYSSKDGONHNVVQCFAYFLQDFGCEVALDLW 394
DB 1249 EESLDKTSHSV--RRAR-----YVKNPOAFNNYKVLAEVYQDRA-----LV 1290
QY 395 EDSFLCREGQREWVIOKIHESOPFIIVCSKMKYFYDKNNYKHKGGGSG-----KGE 448
DB 1291 GDFMSRDNVED-----PKVCAKEPKEFVEKLEKPSGGLRNPNIPIPTLQE 1338
QY 449 LF-----LVAVSATAEKLRQAKQSSAALSKFIAYFPDYSCGDVPGILDLSTK----- 497
DB 1339 LFAKYRVLAIGDEKDRKEDELNSVEDIHFLVL-----QNLIGSTLSLSNSQSNCSOS 1392
QY 498 ---YRLMDN-----LPQLCSHLHSRDHGLQEPQHTROGSRN-----YFRSKGR 540
DB 1393 FOIFRLYREERREPVLAFAFECOKRSLVNRVSHS-QGPKKRAVPFVPMSTOLSOSTY 1451
QY 541 SLV-----VAIC-NMHOPID-----EEDWFEKOFPVPHPP-----PLRYR 575
DB 1452 KLFPTWFPPTVCTESQFYDRLRANGILDQPDHPSFMDMSNDPSSDLVAFSLDSPGHC 1511
QY 576 BPVLEKFDGSLVNDVMCKKGPESDFCL--KYEAPVLCATGPADSGHSGHGLDQGE 632
DB 1512 VTALALFSLGLLSVDVRI--PEQIVVDSMSWSESEVMKSLG-----KDGGLDDDE 1560
QY 633 ARPALGSALQPLHTVTKAGSPD---WPRDSGIYDSVPS--SELSPLMEGLSTQ 686
DB 1561 BEDLDGSGTKRQSVR-VKAKQASHTKYTLMR--GYT--TVPGKAVSTRNINPNDISIVNS 1615
QY 687 TETSSLTESVSSSGLEEEPPALPFSKLSSGSCADLIGCRSYTD-ELHAVAP 738
DB 1616 CQVKFRLNTPATHLGPTGTATPLEELQAGPSCLPASFTSLVDPQLHTRCP 1668

Search completed: March 1, 2006, 10:35:08
Job time: 24 secs

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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:30:22 ; Search time 48 Seconds
(Without alignments)

1271.139 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948
Sequence: 1 MAPMTQLGCVFPTVNAACNG.....SCRADGCRSYDELHAAVAP 738

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5.COMB.pep.*
2: /cgn2_6/prodata/1/aa/6.COMB.pep.*
3: /cgn2_6/prodata/1/aa/H.COMB.pep.*
4: /cgn2_6/prodata/1/aa/PCUS.COMB.pep.*
5: /cgn2_6/prodata/1/aa/R2.COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3706	93.9	728	2	US-10-104-047-3399
2	3681.5	93.2	728	2	US-09-747-259-18
3	3681.5	93.2	728	2	US-09-816-744-18
4	315	8.0	866	1	US-08-620-694A-10
5	315	8.0	866	2	US-09-022-255-10
6	315	8.0	866	2	US-09-022-696-10
7	315	8.0	866	2	US-08-978-773-4
8	315	8.0	866	2	US-09-022-253-10
9	315	8.0	866	2	US-09-022-260-10
10	315	8.0	866	2	US-09-022-259-10
11	315	8.0	866	2	US-09-022-257-10
12	315	8.0	866	2	US-09-549-679-10
13	315	8.0	866	2	US-10-033-522-1
14	315	8.0	866	2	US-09-949-002-403
15	315	8.0	876	2	US-09-949-002-412
16	298	7.5	864	1	US-08-620-694A-2
17	298	7.5	864	2	US-09-022-255-2
18	298	7.5	864	2	US-09-022-696-2
19	298	7.5	864	2	US-08-978-773-2
20	298	7.5	864	2	US-09-022-253-2
21	298	7.5	864	2	US-09-022-260-2
22	298	7.5	864	2	US-09-022-259-2
23	298	7.5	864	2	US-09-022-257-2
24	298	7.5	864	2	US-09-549-679-2
25	134.5	3.4	502	2	US-09-599-3608-106
26	134.5	3.4	502	2	US-09-747-259-12
27	134.5	3.4	502	2	US-09-816-744-12

28	134.5	3.4	504	2	US-09-949-016-11658	Sequence 11658, A
29	117.5	3.0	617	2	US-09-188-930-303	Sequence 303, App
30	117.5	3.0	617	2	US-09-312-283C-303	Sequence 303, App
31	116	2.9	552	2	US-09-949-016-8005	Sequence 8005, Ap
32	110.5	2.8	549	2	US-09-949-016-6384	Sequence 6384, Ap
33	106.5	2.7	489	2	US-09-248-796A-25826	Sequence 25826, A
34	105.5	2.7	595	1	US-08-468-036-3	Sequence 3, App1
35	105.5	2.7	595	1	US-08-476-843-3	Sequence 3, App1
36	105.5	2.7	595	1	US-09-538-092-664	Sequence 664, App
37	105	2.7	993	1	US-08-548-143-1	Sequence 1, App1
38	105	2.7	993	1	US-08-571-785-1	Sequence 1, App1
39	105	2.7	993	2	US-09-192-435-1	Sequence 1, App1
40	105	2.7	993	2	US-09-558-340-1	Sequence 1, App1
41	103.5	2.6	998	1	US-08-449-645A-20	Sequence 20, App1
42	103.5	2.6	998	1	US-08-702-367A-20	Sequence 20, App1
43	103.5	2.6	998	4	PCT-US95-04681-20	Sequence 20, App1
44	101	2.6	838	2	US-09-949-016-9916	Sequence 9916, Ap
45	101	2.6	838	2	US-09-949-016-9917	Sequence 9917, Ap

ALIGNMENTS

RESULT 1									
US-10-104-047-3399									
; Sequence 3399, Application US/10104047									
; Patent No. 6943241									
; GENERAL INFORMATION:									
; APPLICANT: HELIX RESEARCH INSTITUTE									
; TITLE OF INVENTION: No. 6943241el full length cDNA									
; FILE REFERENCE: H1-A0105									
; CURRENT APPLICATION NUMBER: US/10/104, 047									
; CURRENT FILING DATE: 2002-03-25									
; PRIOR APPLICATION NUMBER:									
; NUMBER OF SEQ ID NOS: 4096									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 3399									
; LENGTH: 728									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-104-047-3399									
Query Match									
Best Local Similarity 93.9%; Score 3706; DB 2; Length 728;									
Matches 694; Conservativity 2; Mismatches 2; Indels 0; Gaps 0;									
QY	41	WRGVGASRNSGLYNTFRYDNCCTTLNVPYKRVINDAQNITISQYACHDQVAVTILMSP	100						
DB	30	WQGVGASRNSGLYNTFRYDNCCTTLNVPYKRVINDAQNITISQYACHDQVAVTILMSP	89						
QY	101	GALGIEPLKGFVYILELSEBGRCCOQLIKDPKOLNSPFRKTMESOPPLANKFETDYF	160						
DB	90	GAIGIEPLKGFVYILELSEBGRCCOQLIKDPKOLNSPFRKTMESOPPLANKFETDYF	149						
QY	161	VKVVPPPSIKNSNHPFFRTACDLILQPDNLAKPFRKPNLNIISQHSIMQVSFDH	220						
DB	150	VKVVPPPSIKNSNHPFFRTACDLILQPDNLAKPFRKPNLNIISQHSIMQVSFDH	209						
QY	221	APNHPFRFFLYLTKKHGSPFRKTKCKOETETTSCLQNVSPGDYIIEVDNTNTR	280						
DB	210	APNHPFRFFLYLTKKHGSPFRKTKCKOETETTSCLQNVSPGDYIIEVDNTNTR	269						
QY	281	KWGHVYALKVSHSPWAPIRAMATTVPLVVISAFATLFTWCRKQOENIYSHLDESSSES	340						
DB	270	KWGHVYALKVSHSPWAPIRAMATTVPLVVISAFATLFTWCRKQOENIYSHLDESSSES	329						
QY	341	STYTAALPRERLRPREKVFCTISSKQGNHNVVQCFAYFLDPCCEVALDIEDPFLC	400						
DB	330	STYTAALPRERLRPREKVFCTISSKQGNHNVVQCFAYFLDPCCEVALDIEDPFLC	389						
QY	401	REGOREWVIOKHESGFIIVVCSKGMKVFVDKKNNYHGKGGSGSGGELFLVAVSAIAEK	460						

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Db 390 REGQREWVIOKIHESQFIIVVCSKMKYFVDKINVKHKGGRSGSGKELFLVAVSAIAEK 449
QY 461 LRQAKSSSAALSKFLAVYVDYSCGQVPGILDLSTKYRLMDNLPOLCSHLHSRDGLQ 520
Db 450 LRQAKSSSAALSKFLAVYVDYSCGQVPGILDLSTKYRLMDNLPOLCSHLHSRDGLQ 509
QY 521 PGQHTQGSRRNYFRSKSGSLVYALCNMQFTIDEEPWFQKQFVFPHPPLRYREPVLE 580
Db 510 PGQHTQGSRRNYFRSKSGSLVYALCNMQFTIDEEPWFQKQFVFPHPPLRYREPVLE 569
QY 581 KPDSGLVNDVWCKPGPESDFCLKVEAPVLTGATGPADSOHSGHGLDQGEARPALDGS 640
Db 570 KPDSGLVNDVWCKPGPESDFCLKVEAPVLTGATGPADSOHSGHGLDQGEARPALDGS 629
QY 641 AALQPLHTVYKASPSDMPDSDGIYDSVPSSELSPLMEGLSTDQETNSLTESVSSS 700
Db 630 AALQPLHTVYKASPSDMPDSDGIYDSVPSSELSPLMEGLSTDQETNSLTESVSSS 689
QY 701 GLGEEPPALPSKLSGSGCKADLGCRSYTDELHAAVAP 738
Db 690 GLGEEPPALPSKLSGSGCKADLGCRSYTDELHAAVAP 727

RESULT 2
US-09-747-259-18
; Sequence 18, Application US/09747259
; Patent No. 6569645
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Vanlookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Vansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24

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; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 18
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-747-259-18

Query Match 93.2%; Score 3681.5; DB 2; Length 728;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 694; Conservative 2; Mismatches 3; Indels 13; Gaps 1;

QY 40 GWRGVGPASRNSGLVNIYFKYDNCTTYLNPVGKGYADQNITISQYACHDQVAATILMS 99
Db 16 GEOGVGPASRNSGLVNIYFKYDNCTTYLNPVGKGYADQNITISQYACHDQVAATILMS 75
QY 100 PGALGIEFLKGFRRVILIELKSEGRQCOQLIKDPQLNSSFKRTGMEQPLTMKRETDY 159
Db 76 PGALGIEFLKGFRRVILIELKSEGRQCOQLIKDPQLNSSFKRTGMEQPLTMKRETDY 135
QY 160 FYKVVVPSIKNESNHPFFFTTRACDILLQPDNLACRFMPKRYNLNTSQ----- 209
Db 136 FYKVVVPSIKNESNHPFFFTTRACDILLQPDNLACRFMPKRYNLNTSQ----- 195
QY 210 --HGSMDQVSPDHAAPHNGFRFFYLHYLAKHGGPFKRTCKQEQTTETTSCLQNVSPG 266
Db 196 HAPKSGDQVSPDHAAPHNGFRFFYLHYLAKHGGPFKRTCKQEQTTETTSCLQNVSPG 255
QY 267 DYIIELVDNTTRKRVHYALKPVHSPWAGPIRAMAIVPLVISAFAITLFTWCRKKQ 326
Db 256 DYIIELVDNTTRKRVHYALKPVHSPWAGPIRAMAIVPLVISAFAITLFTWCRKKQ 315
QY 327 ENIYSHLDESESSSTYTAALPRELRPRPKVFLCYSSSDQGNHNNVQCFAYFLQDFCG 386
Db 316 ENIYSHLDESESSSTYTAALPRELRPRPKVFLCYSSSDQGNHNNVQCFAYFLQDFCG 375
QY 387 CEVALDLMEFSLCEGQREWVIOKIHESQFIIVVCSKMKYFVDKINVKHKGGRSGSK 446
Db 376 CEVALDLMEFSLCEGQREWVIOKIHESQFIIVVCSKMKYFVDKINVKHKGGRSGSK 435
QY 447 GELFLVAVSAIAEKLRQAKSSSAALSKFLAVYVDYSCGQVPGILDLSTKYRLMDNLQ 506
Db 436 GELFLVAVSAIAEKLRQAKSSSAALSKFLAVYVDYSCGQVPGILDLSTKYRLMDNLQ 495
QY 507 LSHLSRPHGLOEQRQHTROGSRNNYFRSKSGSLVYALCNMQFTIDEEPWFQKQFVP 566
Db 496 LSHLSRPHGLOEQRQHTROGSRNNYFRSKSGSLVYALCNMQFTIDEEPWFQKQFVP 555
QY 567 FHPPLRYREPVLEKPDGLVNDVWCKPGPESDFCLKVEAPVLTGATGPADSOHSGHGL 626
Db 556 FHPPLRYREPVLEKPDGLVNDVWCKPGPESDFCLKVEAPVLTGATGPADSOHSGHGL 615
QY 627 LDQGEARPALDGSAAQLPLHTVYKASPSDMPDSDGIYDSVPSSELSPLMEGLSTDQ 686
Db 616 LDQGEARPALDGSAAQLPLHTVYKASPSDMPDSDGIYDSVPSSELSPLMEGLSTDQ 675
QY 687 TETSSLTESVSSSGIGEEPPALPSKLSGSGCKADLGCRSYTDELHAAVAP 738
Db 676 TETSSLTESVSSSGIGEEPPALPSKLSGSGCKADLGCRSYTDELHAAVAP 727

RESULT 3
US-09-816-744-18
; Sequence 18, Application US/09816744
; Patent No. 6579520
; GENERAL INFORMATION:

```

```

APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth
APPLICANT: Tumaas, Daniel
APPLICANT: Vanlookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yaneura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P2 (US)
CURRENT APPLICATION NUMBER: US/09/816,744
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 39
LENGTH: 728
SEQ ID NO 18
TYPE: PRT
ORGANISM: Homo Sapien
US-09-816-744-18

Query Match          93.2%; Score 3681.5; DB 2; Length 728;
Best Local Similarity 97.5%; Pred. No. 0;
Matches 694; Conservative 2; Mismatches 3; Indels 13; Gaps 1;

QY 40 GMRGVPASNSGLNITFRYDNCCTTLYNPGKHVYADAGNTTISQYACHDQVAVITLMS 99
DB 16 GEGGVGPASNSGLNITFRYDNCCTTLYNPGKHVYADAGNTTISQYACHDQVAVITLMS 75
QY 100 PGALGIEPLKGFVILIEELKSEGRQCOQLIKDPOKOLNSFKXTGMSOPLMKKETDY 159
DB 76 PGALGIEPLKGFVILIEELKSEGRQCOQLIKDPOKOLNSFKXTGMSOPLMKKETDY 135
QY 160 FVAVVPPSIXNSNYHPPFFTRACDLILQPNLACKPMPKRNINISQ----- 209
DB 136 FVAVVPPSIXNSNYHPPFFTRACDLILQPNLACKPMPKRNINISQHGSDMOVSFD 135
QY 210 --HGSDMOVSFDHAPNFGFRFFYLHYLKHGPPKRTCKOQETTTSCILQNVSPG 266
DB 196 HAPHGSDMOVSFDHAPNFGFRFFYLHYLKHGPPKRTCKOQETTTSCILQNVSPG 255
QY 267 DYIIEVDNTTRKVMHYALKPVHSMAGPIRAMAITVPLVVISAPATLFTWCKRQKQ 326
DB 256 DYIIEVDNTTRKVMHYALKPVHSMAGPIRAMAITVPLVVISAPATLFTWCKRQKQ 315
QY 327 ENYSHLDESSSSSTYTALPREBLRPRKPVLCYSSKDGONHNVVOCFAVFLDPCG 386
DB 316 ENYSHLDESSSSSTYTALPREBLRPRKPVLCYSSKDGONHNVVOCFAVFLDPCG 375
QY 387 CEVALDLMEDPSLCRQEGREVIQKIHESQFIIVVCSKMKYFVDDKKNYHKGSGRSGK 446
DB 376 CEVALDLMEDPSLCRQEGREVIQKIHESQFIIVVCSKMKYFVDDKKNYHKGSGRSGK 435
QY 447 GEIPLVAVSAIAKLRQAKOSSAALSKFTAVYFDVSCBEDVNGILDSTKRYLMDLPQ 506
DB 436 GEIPLVAVSAIAKLRQAKOSSAALSKFTAVYFDVSCBEDVNGILDSTKRYLMDLPQ 495
QY 507 LCGHLSRDLGLOPQOHTQGSRRNYFRSKGSLVVALCNHQPIDEPPMPKQFVP 566
DB 496 LCGHLSRDLGLOPQOHTQGSRRNYFRSKGSLVVALCNHQPIDEPPMPKQFVP 555
QY 567 FHPPPLRYRBPVLEKEDSGVLVNDVMCKPGPESDFCLKVAEAPVYGATGAPDSQHSQHG 626
DB 556 FHPPPLRYRBPVLEKEDSGVLVNDVMCKPGPESDFCLKVAEAPVYGATGAPDSQHSQHG 615
QY 627 LDDGGRARPLDSSAALQPLIHTYKAGSPSDMRDSDGITYDSVPSSELSPLMEGLSTQ 686

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DB 616 LDDGGRARPLDSSAALQPLIHTYKAGSPSDMRDSDGITYDSVPSSELSPLMEGLSTQ 675
QY 687 TETTSITSEVSSSGGIEEPPALPSKLLSSGSCAKDLGCRSTYDELHAAVAP 738
DB 676 TETTSITSEVSSSGGIEEPPALPSKLLSSGSCAKDLGCRSTYDELHAAVAP 727

RESULT 4
US-08-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 5869286e1 Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-620-694A-10

Query Match          8.0%; Score 315; DB 1; Length 866;
Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

QY 55 NITFKYDNC--TTYLNPVGHVYADAGNTT-----ISQYACHDQ-----VAVTITLMS 99
DB 49 NCTVKNSTCIDSDSWHP-----RNLTPSSPKDILQIOLHFAHQQDLPFAHIEWT 99
QY 100 -PGALGIEPLKGFVILIEELKSEGRQCOQLIKDPOKOLNSFKXTGMSOPLMKKETDY 158
DB 100 LQTDASILYBEGMELSLVDLQNTLRLCVR--FEPLSKLHHNRKRRFTTSHEV--VDPDQ 156
QY 159 YFVKV--VPPSIXNSNYHPPFFTRACDLILQPNLACK--PMPKRNLT----- 205
DB 157 YEVTVHLPKPIPDGDPNHSKXNPLVDPCEHAKMKVTTQWSSGSLMDP--NIVETTLAAH 215

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QY 206 -----NISQSGDMOVSPDHAPHNFGFFPYLYTKLKHGPFKRTCKOQOTETT 256
DB 216 QLRVSTPLWNESTHYQILTSFPHMENSCEFHMH-HIPAPREBFHQSNTVTLRNK 274
QY 257 SCLQNVSPDYIIEIVDT--NTTRKVMHYALKPHSWAGPIRAMAIVLVISAF 313
DB 275 GGCRRHQVOIQPFSSCLNDCLRHSAIVSCPEMDTPEPIDVPLWVWFYITISILVG 334
QY 314 ATLFVWCKRKKQOENIYSHLDESSSESTYTAALPRELRPRP---KYFLCYSSKXGON 369
DB 335 SYLLIVCMTRLAGES---EKYSDTKYTDGLPAADLPPPLKPRKWIYSA-DHPL 390
QY 370 HNNVQCFAYFLQDPGCEVALDLMEDFSLCSEGOREWV---IQKHESQFIIVCSKG 425
DB 391 YVDVVLKPAQFLITAGTEVALDLLEQAISEAGVMTWVGROKQEWESNKIIVLCNRG 450
QY 426 MKYFVDKKVKHKGCG-----RSGKGEFLVAVSAIAEKLROAKOSSAALSFTFA 477
DB 451 TR---AKQALLGKGPVRLRCDHGKPVGDLFTAAAMMILPDPFKR---PACFGTYVV 501
QY 478 VYF-DYSGEGVPGIIDLSTKYRLMDNLPOLCSHLSRDLGQEPQHTROG--SRNRY 534
DB 502 CYFEVSCDGDVDDLGAAPRYPLMDRFEV--YFRIQDLEMFQPGMRHVGELSGDNYL 559
QY 535 RSKSGSLVVAICNMHQFIDEBPDWPE-----KQVYFPHPPPLRYREPVLEKFDSCI 586
DB 560 RSPGRLQRLAALDRFRDQVRCDFECENLVSADQDAPSLDEEV-FEERPLLP-GTGI 617
QY 587 VANDVCKGPEBDFCLKEAPVLGATGPADSQHSOQ-----624
DB 618 VKRAPLVRE-PGSOACIAID-PLVGBEGGAIVAKLEPHIQPRGAPAPQPLHTLVLAEBG 675
QY 625 -----GGLDDGGEARPDGSAALQPLHTVYKASPSMDRDSGIYSSVSELSL 676
DB 676 ALVAVPEGLADGAIVRLALAGEBACPLSGPGAG-----RNSVLFP--LPVDPEDS 726
QY 677 PLMEGLSTDQTESLTSVSSSGIGEBEPALPSKLSGSCAKDLGC 726
DB 727 PL--GSSTPMASPDLLPEDVR-----EHLGELMLSLFEQSLSGCAQGGC 768

RESULT 5
US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanelow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-255-10

Query Match      8.0%; Score 315; DB 2; Length 866;
Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

QY 55 NITPKYDNC--TTLNPNVGVKVIADAQNT-----ISQYACHDQ-----VAATILMS 99
DB 49 NCTVKNSTCLDSDSWHP-----RNLTPSSPKDLQIQLHFAITQOGLPPVAHIETW 99
QY 100 -PGALGIEBPKGPRVILBELKSEGRCCOOLILKDPKOLNSSFKRTGMSQPLNMKFTD 158
DB 100 LQDTASILYLBGAEISVQLANTNERLCVR--FEPLSKLRHHRNRFTTSHVY-VDPOE 156
QY 159 YFVKV--VFPSIKNESNYHPFFFTACDILLIOPDNLACK--PFWKPRNL-----205
DB 157 YEVTYHHLKPIPDGDPNHQSKNFIPLPDCEHARMKVTPCMSGSSGLMDP-NITVETLEAH 215
QY 206 -----NISQSGDMOVSPDHAPHNFGFFPYLYTKLKHGPFKRTCKOQOTETT 256
DB 216 QLRVSTPLWNESTHYQILTSFPHMENSCEFHMH-HIPAPREBFHQSNTVTLRNK 274
QY 257 SCLQNVSPDYIIEIVDT--NTTRKVMHYALKPHSWAGPIRAMAIVLVISAF 313
DB 275 GGCRRHQVOIQPFSSCLNDCLRHSAIVSCPEMDTPEPIDVPLWVWFYITISILVG 334
QY 314 ATLFVWCKRKKQOENIYSHLDESSSESTYTAALPRELRPRP---KYFLCYSSKXGON 369
DB 335 SYLLIVCMTRLAGES---EKYSDTKYTDGLPAADLPPPLKPRKWIYSA-DHPL 390
QY 370 HNNVQCFAYFLQDPGCEVALDLMEDFSLCSEGOREWV---IQKHESQFIIVCSKG 425
DB 391 YVDVVLKPAQFLITAGTEVALDLLEQAISEAGVMTWVGROKQEWESNKIIVLCNRG 450
QY 426 MKYFVDKKVKHKGCG-----RSGKGEFLVAVSAIAEKLROAKOSSAALSFTFA 477
DB 451 TR---AKQALLGKGPVRLRCDHGKPVGDLFTAAAMMILPDPFKR---PACFGTYVV 501
QY 478 VYF-DYSGEGVPGIIDLSTKYRLMDNLPOLCSHLSRDLGQEPQHTROG--SRNRY 534
DB 502 CYFEVSCDGDVDDLGAAPRYPLMDRFEV--YFRIQDLEMFQPGMRHVGELSGDNYL 559
QY 535 RSKSGSLVVAICNMHQFIDEBPDWPE-----KQVYFPHPPPLRYREPVLEKFDSCI 586
DB 560 RSPGRLQRLAALDRFRDQVRCDFECENLVSADQDAPSLDEEV-FEERPLLP-GTGI 617
QY 587 VANDVCKGPEBDFCLKEAPVLGATGPADSQHSOQ-----624
DB 618 VKRAPLVRE-PGSOACIAID-PLVGBEGGAIVAKLEPHIQPRGAPAPQPLHTLVLAEBG 675
QY 625 -----GGLDDGGEARPDGSAALQPLHTVYKASPSMDRDSGIYSSVSELSL 676
DB 676 ALVAVPEGLADGAIVRLALAGEBACPLSGPGAG-----RNSVLFP--LPVDPEDS 726
QY 677 PLMEGLSTDQTESLTSVSSSGIGEBEPALPSKLSGSCAKDLGC 726
DB 727 PL--GSSTPMASPDLLPEDVR-----EHLGELMLSLFEQSLSGCAQGGC 768

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RESULT 6

US-09-022-696-10
 ; Sequence 10, Application US/09022696
 ; Patent No. 6072037
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Panlow, William
 ; TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immune Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/022,696
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/620,694
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US98/0410,535
 ; FILING DATE: 23 MARCH 1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,695
 ; REFERENCE/DOCKET NUMBER: 2617-B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 866 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-022-696-10

Query Match 8.0%; Score 315; DB 2; Length 866;
 Best Local Similarity 22.9%; Pred. No. 5,7e-24;
 Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;
 55 NIPKYNDC--TYLNPVGVNADANIT-----ISQVACHD---VAVTILNS 99
 49 NCTVKSTCLDDSWIH-----NLTSSPKDLQIQLAHNTQOGLFVVAHLEWT 99
 100 -PGALGIEFLKGRVILELSEKROCOQILKDPKQNSPKRTGMSQPLNMKEETD 158
 100 LQTDASILYEGALSTQLANTNERLCVR--FEFLSKLRHHRMRRTFSHFV--VDPDOE 156
 159 YFVKV--VPPSINKESNYPFPFRTACDLLQPDNLACK---PFWKPRNL----- 205
 157 YETVTHLPRIPIDGDGNHQSKNFLVVDGCHARKVTPPCSGSLMDP--NITVETLEAH 215
 206 -----NISQHSQMVSFDHAPNPFRRFYLLYKAKHSGPFRKATCKQOQTETT 236
 216 QLRVSEFLTWMESTHYQLILTSFPMENHSCFEHNR--HIPAPREBEFROSNVTLTLNLK 274
 257 SCLLQNVSPGDYIIELVDT--NTRKVNHYALKPVHSPWAGPIRMAITVPLVISAF 313
 275 GCCRHOVOQIOPFPSSCLNCLRHSAIVSCPEMDPTPEPIPDYMLVYMTTGISILVVG 334

RESULT 7

US-08-978-773-4
 ; Sequence 4, Application US/08978773
 ; Patent No. 6083906
 ; GENERAL INFORMATION:
 ; APPLICANT: Trout, Anthony
 ; TITLE OF INVENTION: Method of Regulating Nitric Oxide Production
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immune Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple PowerMacintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for PowerMacintosh, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/978,773
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 60/052,525
 ; FILING DATE: 27 NOVEMBER 1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2623-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 866 amino acids
 ; TYPE: amino acid

314 ATLFTWCRKQKQENTYSHDESSSESTYTAALPRELRPR---KVFLCYSSKQGN 369
 335 SVILLIVCMTWRLAGPS---EKYSDDTKYTDGLPAADLIPPLKPKRWITISA-DHPL 390
 370 HANVOCFAFYLDPCGEVALDLMEDFSLCREGSEWV-----IOLHESQFIIVCSKG 425
 391 YDVVLKFAQPLTACTEVALDLLEQALSEAGVMTVGRQKQEWESNSKIIIVLCSRG 450
 426 MKYFVDKKNYKHKGQ-----RSGKGEFLVAVAISAIEKLRQAKQSSAALSKEIA 477
 451 TR-----AKWQALLGRGAPVRLRCDHGKPVGDLFTAAAMNMLIPDKR-----PACFGTYVV 501
 478 VVE-DYSCBGDVPGLIDLSFKYRLMDNLPQLCSHHSRHDGLQEPQHTQG--SRNYP 534
 502 CYSEVSCDGDVDPDLFGAARFPLMDRFESEV--YPRIDLEMPQGMHRYGSLSGNYL 559
 535 RSKGSLVVAICNMQFIDSEPDWFE-----KQFVFFHPPLRYRSPVLEKFPDGL 586
 560 RSPGQQLRALRPRPDWQVRCDFWECENTYASDDQDASLDEEV-FEERPLRP-GTGI 617
 587 VLNDVCKPSPESDPLKYAPVLAGATGPADSQHSQH----- 624
 618 VKQAPLYRE-PGSOACIAD-PLVBEKGAAVAKLEPHLQPRGQAPAPQLHTLVLAEEG 675
 625 -----GLDDGGRAPPLDGSALQPLHTVYKAGSPESMDRDSGIYDSSVPSSEL 676
 677 PLMEGLSTQGTETSSLTSESVSSSGGSEEPPLPKLSSGSCSKADLGC 726
 727 PL--GSSTPMASPDLLPEDVR-----EHLGMLSLFEOSSLSCQAGGC 768

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-978-773-4

Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

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QY 55 NTFPKYDNC--TYLNPVGKHVADQNIT-----ISQVACHQ-----VAATILMS 99
DB 49 NCTVKNSTGLDSSWHP-----RNLTPSSPKDLOQLHFAITQOGLDFPVANHIEWT 99
QY 100 -PGALGIEPLKGFVILBELKSEGRQCOQLIKDPKOLNSSPKRTGMSQPLANKFETD 158
DB 100 LQTDASILYLEGAEISVLQNTNERLCVR--PEFLSKLRHHRMRFTPSHFV-VDPDGE 156
QY 159 YFVKV--VPPSITKESNTHPPFFRTACDLLQPDNLACK--PPWKPRNL----- 205
DB 157 YEVTVNHLKPRIPDDGPNHOSKNFLVPDCEHAKMKVTPCMSSGSLMDP-NITVETLEAH 215
QY 206 -----NISQHSMDQVSFDHAPHNFGFRFYLYKAKHSGPPKRTCKQEOQTETT 256
DB 216 QLRVSTLWNSTHYOILTSFPHMHNHSCFEHMH-HIPARPEEFHQRNVTTLRLNIK 274
QY 257 SCILQNVSPGDYIIEIVDDT--NTTRKVMHYALKPVHSPWAGPIRAMAITYPLVVISAF 313
DB 275 GGCRRHQVOIQPFSSGLNDCLRHSATVSCPEMDTPEPIPDVMPLVVWFITGISILVIG 334
QY 314 ATLFTVMCRKQOENIYSHLDESSBSSTYTAALPRELRPRP---KVFLEYSSKDGON 369
DB 335 SVLLILVCMTWRLAGSGS---EKYSDDTKYTDGLPADLIPPLKPRKWIIVISA-DHPL 390
QY 370 HNNVVOCPAYPLDPCGCEVALDLWEDFSLCREGQREWV---IQKHNSQPLIIVCSKG 425
DB 391 YDVVVKFAPQFLITACGTEVALDLLEBOAISAGVMTWGRQKQEWESNSKTIIVLCSRG 450
QY 426 MKYFYVDKKNYKHKGGG-----RSGSGKGLFLVAVSAIAEKLQAKOSSAALSKFTA 477
DB 451 TR----AKNQALLGRAPVRLRCDHGRKPVGDLLFTAMNMILLPPKFG-----PACFGTYV 501
QY 478 VVF-DVSCGDVPGIIDLSTKRYLMONLPOLCSHLHSRDHLOEPCQHTROG--SRRTNF 534
DB 502 CFSEFVSCGDVVDLFGAARPRYPLMDRFEEV--YFRIQDLEMFQPRMRHVGELSDNYL 559
QY 535 RKSNGSGLYVAICNMHQPIDEEDWPE-----KQFVPHPRPRKRYEPVLEKDSGL 586
DB 560 RSPGGKQLRALDRFRDMQVRCDFECENTYLSADODAPSLDEEV--FEERPLRP-GTGI 617
QY 587 VLNDVWCKECPESDPCIKYEAIVLGATGPAQSQHSQH-----624
DB 618 VKRAPLVRE-PSGQALCLAD-PLVGEEGGAVALKLEPHLOPQGRAPORPLHTVLAAEG 675
QY 625 -----GGLDDGGRPALDGSAAILOPLHTVKAQSPDMPRDSGIYDSSVPSSELSL 676
DB 676 ALVAAVEPGLADGAVALRLALAGEGACPLDGSFGAG-----RNSVLF--LPVDPDS 726
QY 677 PLMEGISTQGTSTSTESVSSSSGIGREPRALPSEKLSGCKADLGC 726
DB 727 PL--GSSTPMASPDLLPEDVR-----EHLEGIMLSLFEQSLSGQAQGGC 768

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RESULT 8
US-09-022-253-10

Sequence 10, Application US/09022253

Patent No. 6096305

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

APPLICANT: Fanele, William

TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

```

/ STREET: 51 University Street
/ CITY: Seattle
/ STATE: WA
/ COUNTRY: USA
/ ZIP: 98101
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: Apple Power Macintosh
/ SOFTWARE: Microsoft Word for Apple, Version 6.0.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/022,253
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US/08/620,694
/ FILING DATE: 21-MARCH-1996
/ APPLICATION NUMBER: USSN 08/538,765
/ FILING DATE: 7 AUGUST 1995
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: USSN 08/410,535
/ FILING DATE: 23 MARCH 1995
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Perkins, Patricia Anne
/ REGISTRATION NUMBER: 34,695
/ REFERENCE/DOCKET NUMBER: 2617-B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 587-0430
/ TELEFAX: (206)
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 866 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-022-253-10

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Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

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QY 55 NTFPKYDNC--TYLNPVGKHVADQNIT-----ISQVACHQ-----VAATILMS 99
DB 49 NCTVKNSTGLDSSWHP-----RNLTPSSPKDLOQLHFAITQOGLDFPVANHIEWT 99
QY 100 -PGALGIEPLKGFVILBELKSEGRQCOQLIKDPKOLNSSPKRTGMSQPLANKFETD 158
DB 100 LQTDASILYLEGAEISVLQNTNERLCVR--PEFLSKLRHHRMRFTPSHFV-VDPDGE 156
QY 159 YFVKV--VPPSITKESNTHPPFFRTACDLLQPDNLACK--PPWKPRNL----- 205
DB 157 YEVTVNHLKPRIPDDGPNHOSKNFLVPDCEHAKMKVTPCMSSGSLMDP-NITVETLEAH 215
QY 206 -----NISQHSMDQVSFDHAPHNFGFRFYLYKAKHSGPPKRTCKQEOQTETT 256
DB 216 QLRVSTLWNSTHYOILTSFPHMHNHSCFEHMH-HIPARPEEFHQRNVTTLRLNIK 274
QY 257 SCILQNVSPGDYIIEIVDDT--NTTRKVMHYALKPVHSPWAGPIRAMAITYPLVVISAF 313
DB 275 GGCRRHQVOIQPFSSGLNDCLRHSATVSCPEMDTPEPIPDVMPLVVWFITGISILVIG 334
QY 314 ATLFTVMCRKQOENIYSHLDESSBSSTYTAALPRELRPRP---KVFLEYSSKDGON 369
DB 335 SVLLILVCMTWRLAGSGS---EKYSDDTKYTDGLPADLIPPLKPRKWIIVISA-DHPL 390
QY 370 HNNVVOCPAYPLDPCGCEVALDLWEDFSLCREGQREWV---IQKHNSQPLIIVCSKG 425
DB 391 YDVVVKFAPQFLITACGTEVALDLLEBOAISAGVMTWGRQKQEWESNSKTIIVLCSRG 450
QY 426 MKYFYVDKKNYKHKGGG-----RSGSGKGLFLVAVSAIAEKLQAKOSSAALSKFTA 477

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Db 451 TR----AKQALLGRGAPVRLCDHGKPVGDLFTAAANNMLPDKFR-----PACFGTYVV 501
 Qy 478 VVF-DYSCGSDVPGIIDLSTKRYLMDNLPOLCSHLSRPHGLQEPQHTROG--SRNRYF 534
 Db 502 CYFSEVSCGDVVDLFGAARPYPLMDRFEV--YFRIQDLEMFPQGMHVGSLSDNYL 559
 Qy 535 RSKSGSLVVAICNMHQFIDEBPWF-----KQVVFHPPPLRYREPVLEKFDGSL 586
 Db 560 RSPGGRQLRALALDRFDWQVRCDFWECENLYSADQDAPSLDEEV-FEFPILPP-GTGI 617
 Qy 587 VLNDVWCKGPPSDFCLKVAPVLTGATGPADSOHSGH-----624
 Db 618 VKRAPIVRS-PGSOACIATD-PLVGEEGGAATAKLEPHLQPRGQAPAPQPLHTLVLAABEG 675
 Qy 625 -----GGLDDGGRPALDGSALQPLHTVKAQSPDMRDSGIYDSSVPSSELSL 676
 Db 676 ALVAAVEPGLADGAAVRLALAGEGACPLGSPGAG-----RNSVLF--LPVDPEDS 726
 Qy 677 PLMEGLSTDQETSTLTSVSSSGLGEERPPALPSKLSGSCAKDLGC 726
 Db 727 PL--GSSTPMASPDLLPEDVR-----EHLGMLSLFQSLSCQAGGC 768

RESULT 9

US-09-022-260-10
 ; Sequence 10, Application US/09022260
 ; Patent No. 6100235
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Fanelow, William
 ; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/022,260
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/620,694
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: USSN 08/410,535
 ; FILING DATE: 23 MARCH 1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia Anne
 ; REGISTRATION NUMBER: 34,695
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 866 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-022-260-10
 Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5,7e-24;
 Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

Qy 55 NTFKYDNC--ITTYLNPVGRNVIADAQNT-----ISQACHQD-----VAATILMS 99
 Db 49 NCTVKNSTCIDSDMHIHP-----RNLTPSPKDLQIQLFHAIHQOQDLFPVAHIEWT 99
 Qy 100 -PGALGIEFLKGRVILIELKSBGRQCOOLIKDPKOLSSFPRTMSQPLNMFEND 158
 Db 100 LQTDASILYLGAEISLVQLNTNERLCVR--FEPLSKLHHHRRKFTSHFV-VPDDE 156
 Qy 159 YFVKV--VPPPSIKESNHPPEFFTRACDLLQPDNLACK--PRMKRNL-----205
 Db 157 YETVTHLKPPIPDGDPNHSKNFLVPDEHARMKYTTQMSGSLMDP-NIVETLEAH 215
 Qy 206 -----NISQSGDMQVSPDHANFGFRPYLHYLKHGPPKRTCKQEQTTETT 256
 Db 216 QLRSFTLWNSTHYQILLTSPFHMHNSCFEIMH-HIPAPREEHORSNTVTLRLNLK 274
 Qy 257 SCLQVNSPGDYIIELVDT--NTTRKVMYALKRVHS PMAGPIAAMITVPLVVISAF 313
 Db 275 GCCRHQVQIQPFSSCLNDCLRHSAIVSCPEMDTPEPIPDYMPLVWYFPGISILVNG 334
 Qy 314 ATLFTVWCKRKOQENIYSHDEESSSESTYTAALPRELRPP-----KYFLCYSSKQGN 369
 Db 335 SVTLIVCTWKLARGS---EKYSDTKYTGDLPAADLIPPLKRYKWIYISA-DHPL 390
 Qy 370 HNNVQCFAYFIODFCGCEVALDLMEDFSLCBGQRENV---IQKHESQPIIVVCSHG 425
 Db 391 YVDVVLKFAQFLLTACGTEVALDLLEEQAISEAGVWTWVGROKQEWESNSKIIVLCRH 450
 Qy 426 MKYFVDKRYKRYKGGG-----RSGKGELFVAVSAIAETLRKAKOSSAALSKEFLA 477
 Db 451 TR----AKQALLGRGAPVRLCDHGKPVGDLFTAAANNMLPDKFR-----PACFGTYVV 501
 Qy 478 VVF-DYSCGSDVPGIIDLSTKRYLMDNLPOLCSHLSRPHGLQEPQHTROG--SRNRYF 534
 Db 502 CYFSEVSCGDVVDLFGAARPYPLMDRFEV--YFRIQDLEMFPQGMHVGSLSDNYL 559
 Qy 535 RSKSGSLVVAICNMHQFIDEBPWF-----KQVVFHPPPLRYREPVLEKFDGSL 586
 Db 560 RSPGGRQLRALALDRFDWQVRCDFWECENLYSADQDAPSLDEEV-FEFPILPP-GTGI 617
 Qy 587 VLNDVWCKGPPSDFCLKVAPVLTGATGPADSOHSGH-----624
 Db 618 VKRAPIVRS-PGSOACIATD-PLVGEEGGAATAKLEPHLQPRGQAPAPQPLHTLVLAABEG 675
 Qy 625 -----GGLDDGGRPALDGSALQPLHTVKAQSPDMRDSGIYDSSVPSSELSL 676
 Db 676 ALVAAVEPGLADGAAVRLALAGEGACPLGSPGAG-----RNSVLF--LPVDPEDS 726
 Qy 677 PLMEGLSTDQETSTLTSVSSSGLGEERPPALPSKLSGSCAKDLGC 726
 Db 727 PL--GSSTPMASPDLLPEDVR-----EHLGMLSLFQSLSCQAGGC 768

RESULT 10

US-09-022-259-10
 ; Sequence 10, Application US/09022259
 ; Patent No. 6191104
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Fanelow, William
 ; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,259
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 866 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-022-259-10
```

Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5,7e-24; Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

```
55 NITPKYDNC--TLYLNPVKGVIADQNT-----ISQYACHDQ-----VAVTILMS 99
49 NCTVKNSTCLDSDWIHP-----RNLTPSSPKDLQIQLHFAHTQOGLDFPVAAHIEWT 99
100 -PGALGIEFLKGRVILBELKSGROCOQILKDPKOLNSSFKRTGMSQPLNMFEND 158
100 LQTDASILYLEGAEISVLQNTNERLCVR--PEFLSKLRHHRMRPTFSHFV-VPDQGE 156
159 YPKYV--VPPPSIKESNTHPPFRTRACDLILQPNLAK--PPKPRNL-----205
157 YEVYVHLRPPIDGDPNHSKNFLVDPCEHAKMKVTPPCSSGSLMDP-NITVETLEAH 215
206 -----NISQSGDMQVSPHAPNFGFRFFYLHYKLKHGSPFRKTCXQEQTEET 256
216 QLRVSTLWNESTHYQLILTSFPHMENHSCFEMNH-HIAPRDEEFGQSNVTLIRNLK 274
257 SCLQNVSPGDYILIEDVT--NTTRKVMYALKPVHSGAPIRAMATVPLVVISAF 313
275 GCCRHQVQIOPFSSCLNDCIRHSATVSCPEMDTPRPIIDVNPVWVYFITSILVVG 334
314 AILPTWCKRKOQENIYSHLDESSSTYTAALPREKLAPR---KVPLCTSSDQGN 359
335 SVILLVCMTRWLAGPSS--EKYSDTKYTTDGLPADLLPPLKPKRKWIIISA-DHPL 390
370 HMMVVCFAFLDPCGCEVALDLMEDFSLCRREGQREWV-----IOKIHESQFIIVCSKG 425
391 YVDVYLKFAQFLITAGTEVALDLLEQALISEAGWMTVGRQKQENVESKIIIVCSRG 450
426 MKYFVNDKYNKHKGG-----RSGKGELFVAVSAIAEKLQAKOSSAALSKEFLA 477
451 TR-----AKQDALGRGARVRLRCDHGRVGDLTFAAMNMILPRPKR-----PACFGYVV 501
478 VVF-DVSCBEDVVGILDLSTKRYLMDNLPOLCSHLSRHDGLDPRGQHTQG--SRRTYF 534
502 CVFSSEVSCDGDVLDLFGAARPRYPLMDRFBEV--YFRLODLEMPQPMHNVGELSDNYL 559
535 RSKSGRSLYVALICNMHQFIDEBPDWPE-----KQFVVFHPPRLRYRPRVLEKFDQGL 586
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DB 560 RSPGGRQLAALDRFRDQVRCPEWPCENLYSADQDAFSLDBEV-FEPELPLP-CTGI 617
QY 587 YLNDWCKRGPSPDFLKYBAVYLQATGPADQSHESQH-----624
DB 618 VKRAPLVRE-PSQACLAID-PLVGEEGGAVAKLEPHIQPGQAPAPQPLHTLVLAEBG 675
QY 625 -----GGLQDQBARPALDGSALQPLHTVYKAGSPSDMPRDSGIYDSSVPSSELSL 676
DB 676 ALVAAVEPPLDGAARVRLALNGEGACPLSSPGAG-----RNSVLF--LPVDPDS 726
QY 677 PLMEGLSTDQETSSVTSVSSSGVGEEREPALPSKLLSSGSCRADLGC 726
DB 727 PL--GSSTWMASSPDLPEDEV-----EHLFGMLSLFQSLSCQAGGSC 768
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RESULT 11
US-09-022-257-10

Sequence 10, Application US/09022257
Patent No. 6197525

GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Apple Operating System 7.5.5

SOFTWARE: Microsoft Word for Apple, Version 6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,257

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/620,694

FILING DATE: 23 MARCH 1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia Anne

REGISTRATION NUMBER: 34,695

REFERENCE/DOCKET NUMBER: 2617-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430

TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 866 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-022-257-10

Query Match 8.0%; Score 315; DB 2; Length 866;

Best Local Similarity 22.9%; Pred. No. 5,7e-24;

Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

```
55 NITPKYDNC--TLYLNPVKGVIADQNT-----ISQYACHDQ-----VAVTILMS 99
49 NCTVKNSTCLDSDWIHP-----RNLTPSSPKDLQIQLHFAHTQOGLDFPVAAHIEWT 99
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100 -PGALGIEPLKGRVILIEELKSGROCOQILKDPKQINSFKRTGMSQPLMKKETD 158
 100 LQTDASILYEGALSTLQNTNRLCVR--FEFLSLKRRHRRWRTFSHFV-VDDQD 156
 159 YFAKV--VPPSINKSNHPPFRTACDILLQPNLACK--PFKPRNL----- 205
 157 YEVVHLKPRIPDGDHOSKNFLVPDCEHAKMTTPCMSSGSLMDP-NIVETLEAH 215
 206 -----NISQSGDMQVSPDAPNPGFRFYLYHKLKHEPFRKTKCKQQTETT 256
 216 QLRVSTLWMESTHYQILTSFPMENHSCFENH-HIPAPREBFHORSVTLTLNLK 274
 257 SCLQNVSPDYIIEVDTF--NTTRKVMHYALKPVHSPWAGIRAMATVPLVISA 313
 275 GCRHQVQIQPFSSCINCLRHSAATVSCPEMPTPEPIDYMLWYPTIGSILLVG 334
 314 ATLFTWCKRKKQENIYSHLDESSSSTYTAALPRELRPR--KVFCLYSSKQGN 369
 335 SVILLIVCMWTRLAGPS--EKYSDTKYTDGLPADLIPPLKPRKWTIYSA-DHPL 390
 370 HMMVOCFAFLDFCCCEVALDLMEDPSLCREGRQEV---IQKHESQFIIVCSKG 425
 391 YDVVILKFAQFLTLACTEVALDLLEQALSEAGVMTWGRQKQEWESKTIIVLCSRG 450
 426 MKTFVDKQNYKHGGG-----RSGKGEFLVAVSAIAEKLROAKQSSAALSKFA 477
 451 TR---AKQALLGRGAPVRLRCDHGKPVGDLFTAAANNMILPDKR-----PACFGTYV 501
 478 VYF-DYSCGDVPGIIDLSTKYRLMDNLPOLCSHLSRDHLOEPOHTRQG--SRNYP 534
 502 CYSEVSCDGDVPLFGAARVPLMDRFEV--YFRIDLEMPQPGMHVGLSGNYL 559
 535 RSKSGRLVAICMHOQFIDEBDFE-----KQVFPHPPLRYRREPVLEKFDGL 586
 560 RSPGRLRALRDLFRDMQRCDFMFCENLYSADDDAPSLDEEV-FEELPLP-GTGI 617
 587 VLVDMVCKPESDFCLKVEAPVLTGATGPADSCHEQH----- 624
 618 VKQAPLVR--PGQACLAID-PLVGEEGAVALLEPHLOPRQAPAPLHTLVLAEEG 675
 625 -----GGLDDGEARPLDGSALLOPLHTVYKSPSDMPDSDGIDYSSVPSLSL 676
 676 ALVAAPVRE-PSQACLAID-PLVGEEGAVALLEPHLOPRQAPAPLHTLVLAEEG 675
 677 PLMEGLSTQDETSSLTESVSSSGLEBEPPLPSKLLSGSCAKDGLG 726
 727 PL--GSSTPMASPDLPEDVR-----EHLGLMLSLFBQSLSCQAGGC 766

RESULT 12
 US-09-549-679-10
 ; Sequence 10, Application US/09549679
 ; Patent No. 6680057
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; Spriggs, Melanie
 ; Fanelow, William
 ; TITLE OF INVENTION: No. 6680057el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: Apple Power Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.5.5
 ; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/549, 679

FILING DATE: 14-Apr-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/620,694
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US98/0410,535
 FILING DATE: 23 MARCH 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Perkins, Patricia Anne
 REGISTRATION NUMBER: 34,695
 REFERENCE/DOCKET NUMBER: 2617-B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206)
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 866 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-549-679-10
 Query Match 8.0%; Score 315; DB 2; Length 866;
 Best Local Similarity 22.9%; Pred. No. 5,7e-24;
 Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;
 55 NITFKYDNC--TYLNPVGKVIADANIT-----ISQVACHQ-----VAVTLMS 99
 49 NCTVNSTGLDSDMHP-----RNLTPSSPKQLQILHFAHQOGLFPVAHIEWT 99
 100 -PGALGIEPLKGRVILIEELKSGROCOQILKDPKQINSFKRTGMSQPLMKKETD 158
 100 LQTDASILYEGALSTLQNTNRLCVR--FEFLSLKRRHRRWRTFSHFV-VDDQD 156
 159 YFAKV--VPPSINKSNHPPFRTACDILLQPNLACK--PFKPRNL----- 205
 157 YEVVHLKPRIPDGDHOSKNFLVPDCEHAKMTTPCMSSGSLMDP-NIVETLEAH 215
 206 -----NISQSGDMQVSPDAPNPGFRFYLYHKLKHEPFRKTKCKQQTETT 256
 216 QLRVSTLWMESTHYQILTSFPMENHSCFENH-HIPAPREBFHORSVTLTLNLK 274
 257 SCLQNVSPDYIIEVDTF--NTTRKVMHYALKPVHSPWAGIRAMATVPLVISA 313
 275 GCRHQVQIQPFSSCINCLRHSAATVSCPEMPTPEPIDYMLWYPTIGSILLVG 334
 314 ATLFTWCKRKKQENIYSHLDESSSSTYTAALPRELRPR--KVFCLYSSKQGN 369
 335 SVILLIVCMWTRLAGPS--EKYSDTKYTDGLPADLIPPLKPRKWTIYSA-DHPL 390
 370 HMMVOCFAFLDFCCCEVALDLMEDPSLCREGRQEV---IQKHESQFIIVCSKG 425
 391 YDVVILKFAQFLTLACTEVALDLLEQALSEAGVMTWGRQKQEWESKTIIVLCSRG 450
 426 MKTFVDKQNYKHGGG-----RSGKGEFLVAVSAIAEKLROAKQSSAALSKFA 477
 451 TR---AKQALLGRGAPVRLRCDHGKPVGDLFTAAANNMILPDKR-----PACFGTYV 501
 478 VYF-DYSCGDVPGIIDLSTKYRLMDNLPOLCSHLSRDHLOEPOHTRQG--SRNYP 534
 502 CYSEVSCDGDVPLFGAARVPLMDRFEV--YFRIDLEMPQPGMHVGLSGNYL 559
 535 RSKSGRLVAICMHOQFIDEBDFE-----KQVFPHPPLRYRREPVLEKFDGL 586
 560 RSPGRLRALRDLFRDMQRCDFMFCENLYSADDDAPSLDEEV-FEELPLP-GTGI 617
 587 VLVDMVCKPESDFCLKVEAPVLTGATGPADSCHEQH----- 624
 618 VKQAPLVR--PSQACLAID-PLVGEEGAVALLEPHLOPRQAPAPLHTLVLAEEG 675
 625 -----GGLDDGEARPLDGSALLOPLHTVYKSPSDMPDSDGIDYSSVPSLSL 676

Db 676 ALVAAVEPGLADGAARLALAGEACPLLSGPGAG-----RNSVLF---LPVDPEDS 726
Qy 677 PLMEGLSTDQETSTLSESVSSSGLEEEPPALPSKLLSSGCKADLGC 726
Db 727 PL--GSSTPMASPDLLPEDVR-----EHLGLMLSLFQSLSCQAQGC 768

RESULT 13
US-10-033-522-1
Sequence 1, Application US/10033522
Patent No. 6793919
GENERAL INFORMATION:
APPLICANT: MOHLER, Kendall M.
TITLE OF INVENTION: Methode for Treating Rheumatoid Arthritis Using IL-17 Antagonists
FILE REFERENCE: 2982-A
CURRENT APPLICATION NUMBER: US/10/033,522
CURRENT FILING DATE: 2001-10-18
PRIOR APPLICATION NUMBER: US 60/241,230
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 866
TYPE: PRT
ORGANISM: Homo sapiens
US-10-033-522-1

Query Match 8.0%; Score 315; DB 2; Length 866;
Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

Qy 55 NTFKYDNC--TTYLNPVGKVIADAQNT-----ISQYACHDQ-----VAVTILMS 99
Db 49 NCTVKNSTLDDSWIHP-----RNLTPSSPKDQIQAHFHTQOQDLFPVANHWT 99
Qy 100 -PGALGIEFLKGFVILIELKSEGRQCOQLIKDPKQLNSFKRTGMSQPLNMKEFTD 158
Db 100 LGTDAIILYEGAEISVLQNTNERLCVR--FEFLSKLHNHRMRFTFSHFV--VDPDQE 156
Qy 159 YFVKV--VPPRSIKNESNHPFFRTFRACDILLQDPNLAK--PPVKPRNL----- 205
Db 157 YEVTYHNLKPRIPDGGPNHOSKNFLVPDCEHAKMKVTPPCMSGSLMDP--NITVETLEAH 215
Qy 206 -----NISOHGSDMOVSFDHAPNFGFRFFLYLHYLKHGEPFKRTCKQEQTTETT 256
Db 216 QLRVSTLWNESTHYQILTSFPHMENHSCFEMH--HTRPREEFHQNSNTLTIRNLK 274
Qy 257 SCLLQNVSPGDYILIELVDLT--NTTRKVMHYALKPVHSPWAGPIRAMAITYPLVVISAF 313
Db 275 GCGRHQVQIQPFSSCLNDCLRHSAIVSCPEMDTPREPIDVMPVWYFITGISILVG 334
Qy 314 ATLFTWCKRKKQOENIYSHLDESSSSTYTAALPRERLRPP--KYFLCYSSKDGON 369
Db 335 SVILLIVCMTWRLAGRGS--EKYSDTKYTDGLPADLIPPLKPKKWIIVISA--DHPL 390
Qy 370 HNNVVOCPAFYLDOPGCEVALDLMEDPSLCREGOREWY-----IOKIHESQFIIVCSKG 425
Db 391 YDVVVLKFAQFLTLTACTEVALDLLEQALISEAGVMTWGRQKQEVESKTIIVLCSRG 450
Qy 426 MKYFVVDKKNYKHKGG-----RSGSGELFLVANVAIAEKLRAQKQSSAALSKFA 477
Db 451 TR-----AKQALLGRAPVRLRCDHGKPVGDLFTAAAMNMLLPDKR-----PACFGTYV 501
Qy 478 VVF--DYSCEGDVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQBPQHTROG--SRRTNF 534
Db 502 CYFSEVSCDGDVLDLFGAARPRYPLMDRFEV--YFRIQDLEMFQPGHMHVGLSGDNYL 559
Qy 535 RKSSEGLVYVYICMHIQFIQDEEPPDWE-----KQFVPHRPPRLRYREPVLEKDPDGL 586
Db 560 RSPGSGHQLRALDRFRDQVRCPDWFECENYLSADDDADSLDEEV--FEERLLRP--GTGI 617
Qy 587 VLNDWCKPQESDPCIKVEAPVLTGATPADSQHESQH----- 624

Db 618 VRRAPLVRE--PSSQACLAID--PLVGEEGAANAKLEPHLQRPQAPRPLHTLVLAERG 675
Qy 625 -----GGLDODGEARPALDGSAALOPLHTTVKAGSPDMPDSGIYDSSPSEL 676
Db 676 ALVAAVEPGLADGAARLALAGEACPLLSGPGAG-----RNSVLF---LPVDPEDS 726
Qy 677 PLMEGLSTDQETSTLSESVSSSGLEEEPPALPSKLLSSGCKADLGC 726
Db 727 PL--GSSTPMASPDLLPEDVR-----EHLGLMLSLFQSLSCQAQGC 768

RESULT 14
US-09-949-002-403
Sequence 403, Application US/09949002
Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMOERPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 403
LENGTH: 866
TYPE: PRT
ORGANISM: Human
US-09-949-002-403

Query Match 8.0%; Score 315; DB 2; Length 866;
Best Local Similarity 22.9%; Pred. No. 5,7e-24;
Matches 176; Conservative 104; Mismatches 342; Indels 148; Gaps 33;

Qy 55 NTFKYDNC--TTYLNPVGKVIADAQNT-----ISQYACHDQ-----VAVTILMS 99
Db 49 NCTVKNSTLDDSWIHP-----RNLTPSSPKDQIQAHFHTQOQDLFPVANHWT 99
Qy 100 -PGALGIEFLKGFVILIELKSEGRQCOQLIKDPKQLNSFKRTGMSQPLNMKEFTD 158
Db 100 LGTDAIILYEGAEISVLQNTNERLCVR--FEFLSKLHNHRMRFTFSHFV--VDPDQE 156
Qy 159 YFVKV--VPPRSIKNESNHPFFRTFRACDILLQDPNLAK--PPVKPRNL----- 205
Db 157 YEVTYHNLKPRIPDGGPNHOSKNFLVPDCEHAKMKVTPPCMSGSLMDP--NITVETLEAH 215
Qy 206 -----NISOHGSDMOVSFDHAPNFGFRFFLYLHYLKHGEPFKRTCKQEQTTETT 256
Db 216 QLRVSTLWNESTHYQILTSFPHMENHSCFEMH--HTRPREEFHQNSNTLTIRNLK 274
Qy 257 SCLLQNVSPGDYILIELVDLT--NTTRKVMHYALKPVHSPWAGPIRAMAITYPLVVISAF 313
Db 275 GCGRHQVQIQPFSSCLNDCLRHSAIVSCPEMDTPREPIDVMPVWYFITGISILVG 334
Qy 314 ATLFTWCKRKKQOENIYSHLDESSSSTYTAALPRERLRPP--KYFLCYSSKDGON 369
Db 335 SVILLIVCMTWRLAGRGS--EKYSDTKYTDGLPADLIPPLKPKKWIIVISA--DHPL 390
Qy 370 HNNVVOCPAFYLDOPGCEVALDLMEDPSLCREGOREWY-----IOKIHESQFIIVCSKG 425
Db 391 YDVVVLKFAQFLTLTACTEVALDLLEQALISEAGVMTWGRQKQEVESKTIIVLCSRG 450
Qy 426 MKYFVVDKKNYKHKGG-----RSGSGELFLVANVAIAEKLRAQKQSSAALSKFA 477
Db 451 TR-----AKQALLGRAPVRLRCDHGKPVGDLFTAAAMNMLLPDKR-----PACFGTYV 501
Qy 478 VVF--DYSCEGDVPGIILDLSTKRYLMDNLPOLCSHLHSRDHGLQBPQHTROG--SRRTNF 534
Db 502 CYFSEVSCDGDVLDLFGAARPRYPLMDRFEV--YFRIQDLEMFQPGHMHVGLSGDNYL 559

QY 535 RSKSGSLVYALICNMHOFIDBPDWFE-----KQFVFPHPPLRYRREPLEKFPDGL 586
 DB 560 RSGGRLRALRDLRFDMQVRCDFMFCENLYSADDDABSLDEEV-FEPLLP-CTGI 617
 QY 587 VLNDVCKPESDFCLKVEAPVLTGATGPADSQHSQH----- 624
 DB 618 VKAPALVRE-PGSQACLAID-PLVGEAGAAVAKLEPHLQPRGQAPAPQPLHTVLAAEG 675
 QY 625 -----GGLDODGARPALDGSALQPLHTVKAASPSDMPDSCGTVSSVPSSEL 676
 DB 676 ALVAABEPGLADGAAVRLALAGEGACPLGSPGAG-----RNSVLF--LPVDEDS 726
 QY 677 PLMEGLSTQDTERSTLTSVSSSGGEBEPALPSKLLSSGCKADLGC 726
 DB 727 PL-GSSTPMASPDLLPEDVR-----EHLEGMLSLFEQSLSCQAQGGC 768

RESULT 15

US-09-949-002-412
 ; Sequence 412, Application US/09949002
 ; Patent No. 690016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
 ; TITLE OF INVENTION: AND USES THEREOF
 ; FILE REFERENCE: C1000790
 ; CURRENT APPLICATION NUMBER: US/09/949, 002
 ; CURRENT FILING DATE: 2000-01-28
 ; PRIOR APPLICATION NUMBER: 60/231,401
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 10823
 ; SOFTWARE: FaecSeq for Windows Version 4.0
 ; SEQ ID NO 412
 ; LENGTH: 876
 ; TYPE: PRF
 ; ORGANISM: Human
 ; US-09-949-002-412

Query Match 8.0%; Score 315; DB 2; Length 876;
 Best Local Similarity 22.9%; Pred. No. 5.8e-24;
 Matches 176; Conservative 105; Mismatches 341; Indels 148; Gaps 33;

QY 55 NITFKTDNC--TYLNPVGKVIADQNIT-----ISQYACHDQ-----VAVTILMS 99
 DB 59 NCTVKNSTCLDDSWHP-----RNLTPSSPKDQLQIHLPAHTQCGDLFPVAHLEWT 109
 QY 100 -PGALGIBPLKGFVILKEELKSGROCOQLILKDPKQINSFKRTGMEQPLMKFETD 158
 DB 110 LQTDASTLYLEGALSVLQANTERLCVR--FEFLSKLRHHRRMRFTFSHFV-VDPOE 166
 QY 159 YFVKV--VPPSIKNESNYPFFRTACDLLQPDNLACK--PFWKPRNL----- 205
 DB 167 YETVNHLPKPIPDGDNHOSKNFLVPDCBAHMKYTPCMSSGSLMDP-NITVETLEAH 225
 QY 206 -----NISQGSMDQVSFDHAPNFGFRFFYLHYKLHSGPFKRTCKOEQTTEY 256
 DB 226 QLRVSFTLMNESHYQILTSFPMENHSCFEHMH-HI PARPEEFQSRNVTLLTNLK 284
 QY 257 SCLQNVSPGDYIIELVDVT--NTRKWHYALKPVHSPWAGIRAMAITVPLVVISAP 313
 DB 285 GCCRHQVQIOPFPSSCLNDCLRHSATVSCPEMDPTPVLTADYMLVWYFYTGISILVG 344
 QY 314 ATFTVWCRKQOENIYSHLDESSBSSTYTAALPRERLRP-----KVELCYSSKQGN 369
 DB 345 SVILLIVCMTRLAGPS---EKSDTKYTDGLPADLIPPLKPRKWIYSA-DHPL 400
 QY 370 HNAVVOCFAYFLDFCCCEVALDLMEDPSLCRSGQREWV---IQKHESQPIIVVCSKG 425
 DB 401 YVDVVLKFAQFLYLACTEVALDLLEQALISEAGVMTVGRKQKQEWESNKKIIVLCSRG 460
 QY 426 MKCFVDDKQNTKHKGG-----RSGKGELFLVAVSAIAEKLROAKOSSSAALSKEIA 477

DB 461 TR-----AKQOALLRGAPVRLRCDHKGKPVGDLFTAAANNMLLPDFKR-----PACFGTYV 511
 QY 478 VYF-DVSCGDVVGILDLSTKRYLMDNLPOLCSHHSRDLGLOBPQHTROG--SRNRYF 534
 DB 512 CYPSEVSCDQDVDFLGAAPRYPLMDRFEBV--YFRIODLEMFQPRMHRVGLSGDNYL 569
 QY 535 RSKSGSLVYALICNMHOFIDBPDWFE-----KQFVFPHPPLRYRREPLEKFPDGL 586
 DB 570 RSPGRLRALRDLRFDMQVRCDFMFCENLYSADDDABSLDEEV-FEPLLP-CTGI 627
 QY 587 VLNDVCKPESDFCLKVEAPVLTGATGPADSQHSQH----- 624
 DB 628 VKAPALVRE-PGSQACLAID-PLVGEAGAAVAKLEPHLQPRGQAPAPQPLHTVLAAEG 685
 QY 625 -----GGLDODGARPALDGSALQPLHTVKAASPSDMPDSCGTVSSVPSSEL 676
 DB 686 ALVAABEPGLADGAAVRLALAGEGACPLGSPGAG-----RNSVLF--LPVDEDS 736
 QY 677 PLMEGLSTQDTERSTLTSVSSSGGEBEPALPSKLLSSGCKADLGC 726
 DB 737 PL-GSSTPMASPDLLPEDVR-----EHLEGMLSLFEQSLSCQAQGGC 778

Search completed: March 1, 2006, 10:32:01
 Job time : 62 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:23:47 ; Search time 90 Seconds
(without alignment)
3602.906 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948
Sequence: 1 MAPWQLGCVFPTVNAACNG.....SCKADLCGRSYDELAAVAP 738

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2004s:*
8: geneseqp2005s:*
9: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3948	100.0	738	4	AAU09904 Human Int
2	3948	100.0	738	8	ADU69244 Human SER
3	3948	99.9	738	4	AAU09953 Human Int
4	3943	99.9	738	4	AAU09954 Human Int
5	3941	99.8	738	4	AAU09951 Human Int
6	3941	99.8	738	4	AAU09952 Human Int
7	3941	99.8	738	4	AAU09956 Human Int
8	3937	99.7	738	4	AAU09957 Human Int
9	3937	99.7	738	4	AAU09955 Human Int
10	3918	99.2	738	5	ABR07628 Human CYC
11	3908	99.0	738	8	ADU69242 Human SER
12	3908	99.0	738	8	ADU69242 Human SER
13	3901	98.8	738	5	ABR07626 Human CYC
14	3891	98.6	738	5	ABR07627 Human CYC
15	3835.5	97.2	738	9	ABR07627 Human CYC
16	3830.5	97.0	738	5	ABR07627 Human CYC
17	3706	93.9	728	5	AAU11355 Human DNA
18	3687	93.4	728	4	AAU10602 Human Int
19	3681.5	93.2	728	4	AAU04958 Human Int
20	3681.5	93.2	728	6	ABU089705 Human Int
21	3681.5	93.2	728	6	ABU089705 Human Int
22	3681.5	93.2	728	6	ADU43241 Human Int
23	3681.5	93.2	728	7	ADU43241 Human Int
24	3681.5	93.2	728	7	ADU43241 Human Int

25	3681.5	93.2	728	7	ADU66909 Human PRO
26	3681.5	93.2	728	7	ADU66909 Human PRO
27	3681.5	93.2	728	7	ADU66909 Human PRO
28	3681.5	93.2	728	7	ADU66909 Human PRO
29	3681.5	93.2	728	8	ADU16689 Human PRO
30	3681.5	93.2	728	8	ADU16689 Human PRO
31	3396.5	86.0	738	5	ADU76588 Human IL-
32	3392	85.7	738	5	ADU76588 Human IL-
33	3164	80.1	595	6	ABR07630 Murine CY
34	3158	80.0	595	4	ABR07630 Murine CY
35	3158	80.0	595	5	ABR07630 Murine CY
36	3158	80.0	595	5	ABR07630 Murine CY
37	2701.5	68.4	554	5	AAU91330 Human nov
38	2665.5	67.5	594	8	ADU21236 Murine in
39	1594	40.4	531	8	ADU21236 Murine in
40	1333	33.8	296	4	AAU10601 Human int
41	377	9.5	69	8	ADU21237 Murine in
42	315	8.0	866	2	AAU04185 Human int
43	315	8.0	866	2	AAU04185 Human int
44	315	8.0	866	2	AAU04185 Human int
45	315	8.0	866	3	AAU97131 Human int

ALIGNMENTS

RESULT 1
AAU09904
ID AAU09904 standard; protein; 738 AA.
XX
AC AAU09904;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Interleukin 17 (hIL-17) receptor like protein.
XX
KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW hepatic; anabolic; anorectic; anti-asthmatic; dermatological; renal; osteopathic;
KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW vascular; cytotoxic; anti-leukemic; anti-infectivity; ophthalmological;
KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW bone disease; vascular disorder; eye disorder; cancer; human.
XX
OS Homo sapiens.
XX
PN MO200168859-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-US008678.
XX
PR 16-MAR-2000; 2000US-0189816P.
XX
PR 28-NOV-2000; 2000US-00724460.
XX
PA (AMGE-) AMGEN INC.
XX
PI Jing S;
XX
DR WPI: 2001-611392/70.
XX
DR N-PSDB; AAS15346.
XX
PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT psoriasis and glaucoma.
XX
PS Claim 2; Page 152-154; 158pp; English.
XX
CC The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anorectic, anorectic, anti-asthmatic, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,

osteopathic, vascular, cyostatic, anti-leukemic, anti-fertility and ophthalmological activities. The IL-17 receptor like nucleic acids and proteins may be used to prevent and treat diseases associated with inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These include, for example immune disorders (e.g. inflammation, diabetes and transplant rejection), infections (e.g. hepatitis and septicemia), weight disorders (e.g. anorexia, cachexia and obesity), neuronal dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy), lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis), bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and breast cancer), reproductive disorders (e.g. infertility and miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The DNA and its complements may also used as diagnostic probes to detect and quantitate the presence of similar nucleic acids in samples and identify patients needing restorative therapy. The IL17rlp may also be used as antigens in the production of antibodies against the proteins and in assays to identify modulators of expression and activity. The anti-IL17rlp antibodies and antagonists may also be used to down regulate expression and activity. This is the amino acid sequence of the human interleukin 17 (IL-17) receptor like protein described in the method of the invention

Sequence 738 AA:

Query Match 100.0%; Score 3948; DB 4; Length 738;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MAEWLQCSVFVTNACLSGSLAAGSGSGRAMGVDTGMRGVGPAISNSGLYNTTFKY 60
1 MAEWLQCSVFVTNACLSGSLAAGSGSGRAMGVDTGMRGVGPAISNSGLYNTTFKY 60
61 DNTCTTLPVYGVKVIADQNITTSQYACHDQVAVTILMSGALGIFELKFRVILELKS 120
61 DNTCTTLPVYGVKVIADQNITTSQYACHDQVAVTILMSGALGIFELKFRVILELKS 120
121 EGRGCGQLIKDKPKOLNSFKRTGMSOPFLNKKFEDYFVKVPPSINSGSNYPFF 180
121 EGRGCGQLIKDKPKOLNSFKRTGMSOPFLNKKFEDYFVKVPPSINSGSNYPFF 180
181 RTFACDLILQPDNLACKPFKPRNLINISQHSQDMQVSFDHAPNPFGRFFLYLTKLKHG 240
181 RTFACDLILQPDNLACKPFKPRNLINISQHSQDMQVSFDHAPNPFGRFFLYLTKLKHG 240
241 PFRRKTCQKOBQTETTSCLIQNSPDGYIIELVDTNTTRKVMHVALKPVHSPWAGPIRA 300
241 PFRRKTCQKOBQTETTSCLIQNSPDGYIIELVDTNTTRKVMHVALKPVHSPWAGPIRA 300
301 MATTVLAVTISAPATLPTWCRKQOENITYSHLDESSSESTYTALPRERLAPRKVPL 360
301 MATTVLAVTISAPATLPTWCRKQOENITYSHLDESSSESTYTALPRERLAPRKVPL 360
361 CYSSKQGNHNVVQCFAYFLQDFCGCEVALDLMEDPSLCREGQRMWVIOKIHESQFIIV 420
361 CYSSKQGNHNVVQCFAYFLQDFCGCEVALDLMEDPSLCREGQRMWVIOKIHESQFIIV 420
421 VCSKGMKTFVDDKNVYHKGKGRSGKGEIPLVAVSAIAEKLRAKQSSSALSKFIAYVF 480
421 VCSKGMKTFVDDKNVYHKGKGRSGKGEIPLVAVSAIAEKLRAKQSSSALSKFIAYVF 480
481 DVSCEBDVGGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGHTQGSRRNFRKSKSR 540
481 DVSCEBDVGGIIDLSTKRYLMDNLPOLCSHLHSRDHGLQEPGHTQGSRRNFRKSKSR 540
541 SLVVAICNMHQFIDEEDPEKQFVFPHPPLKRYREPVLEKFPSGVLVNDVMCKPPESD 600
541 SLVVAICNMHQFIDEEDPEKQFVFPHPPLKRYREPVLEKFPSGVLVNDVMCKPPESD 600
601 FCILKVAAPVLTGATGAPDSQHSQHGSLDQGEARPALDGSAAQPLILHTVTKAGSPSDMR 660
601 FCILKVAAPVLTGATGAPDSQHSQHGSLDQGEARPALDGSAAQPLILHTVTKAGSPSDMR 660

661 DSGYDSSVPSSELSPLMEGLSTDOTETSSTESVSSSGGGBEPALPSKLSSGSC 720
661 DSGYDSSVPSSELSPLMEGLSTDOTETSSTESVSSSGGGBEPALPSKLSSGSC 720
721 KADLCGRSTYDMLHAVAP 738
721 KADLCGRSTYDMLHAVAP 738
RESULT 2
ADU69244
ADU69244 standard; protein; 739 AA.
ADU69244;
10-FEB-2005 (first entry)
Human SEF amino acid variant SEQ ID NO:4.
fibroblast growth factor; SEF; similar expression of RGF genes; cyostatic; cardiovascular-gen.; antiarteriosclerotic; cardiant; vasotropic; hypotensive; nephrotropic; gene therapy; diagnosis; prognosis; proliferative disorders; cardiovascular disorders; renal disease; glomerular disease.
Homo sapiens.
US2004235104-A1.
25-NOV-2004.
07-MAY-2004; 2004US-00842006.
08-MAY-2003; 2003US-0469522P.
(MILL-) MILLENNIUM PHARM INC.
Yang R;
WPI; 2004-821320/81.
N-PSDB; ADU69243.
New isolated SEF nucleic acid and polypeptide, useful for monitoring, treating, or diagnosing proliferative and/or differentiative disorders, e.g. ovarian cancer, breast cancer, or cardiovascular disorder including arteriosclerosis.
Disclosure; SEQ ID NO 4; 46pp; English.
The invention relates to a novel isolated SEF (similar expression of RGF genes) nucleic acid molecule (I). An SEF of the invention has cyostatic, cardiovascular-gen., antiarteriosclerotic, cardiant, vasotropic, hypotensive, and nephrotropic activity, and may have a use in gene therapy. The SEF nucleic acids and polypeptides can be used for diagnostic assays, prognostic assays, and monitoring clinical trials. They can also be used for treating a subject at risk of or susceptible to a disorder or having a disorder associated with aberrant or unwanted SEF expression or activity. The SEF molecules can also be used for monitoring, treating, or diagnosing proliferative and/or differentiative disorders, e.g. ovarian cancer, breast cancer, colon cancer, prostatic cancer, RGF related disorder, cardiovascular disorder including arteriosclerosis, coronary artery disease, ischemia, reperfusion injury, restenosis, arterial inflammation, hypertension, endothelial disorders, and a kidney disorder, e.g. glomerulonephritis, vascular neuropathy, renal failure, or glomerular disease. The SEF molecules can also be used as markers of disorders or disease states, as markers for precursors of disease states, as markers for predisposition of disease states, as markers of drug activity, or as markers of the pharmacogenomic profile of a subject. The present sequence represents a variant of the SEF amino acid shown in ADU69242.
Sequence 739 AA;

Query Match 100.0%; Score 3948; DB 8; Length 739;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPWLOLCVFFPTVNAACLSGSLAAGGSGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60
 DB 1 MAPWLOLCVFFPTVNAACLSGSLAAGGSGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60
 QY 61 DICTTYLNPVGKXIVADANITTSQYACHDQVAVTILMSFGALGIEFLKGFVILELKS 120
 DB 61 DICTTYLNPVGKXIVADANITTSQYACHDQVAVTILMSFGALGIEFLKGFVILELKS 120
 QY 121 EGRQCOQLIKDKQOLNSSPKRTGMSQPLANKPFEDYVAVVPPPSINSENYHPFR 180
 DB 121 EGRQCOQLIKDKQOLNSSPKRTGMSQPLANKPFEDYVAVVPPPSINSENYHPFR 180
 QY 181 RTRACDLLOPDLACKPFKPRNLNISOHSDMOVSFDHAPNFGFRPYLYLHYKLKHEG 240
 DB 181 RTRACDLLOPDLACKPFKPRNLNISOHSDMOVSFDHAPNFGFRPYLYLHYKLKHEG 240
 QY 241 PFRKRTCKOQTTETTSCLQNVSPGDYIIEVDNTTRKVMHYALKPVHSPWAGPIRA 300
 DB 241 PFRKRTCKOQTTETTSCLQNVSPGDYIIEVDNTTRKVMHYALKPVHSPWAGPIRA 300
 QY 301 MATTVLVVISAATLFTWCRKKQOENYSHLDESSSESTYTAALPRERLAPRKVFL 360
 DB 301 MATTVLVVISAATLFTWCRKKQOENYSHLDESSSESTYTAALPRERLAPRKVFL 360
 QY 361 CVSSKQGNHNVVQCEVAFLODFCGCEVALDMEBPSLCREGOREVNIQKHESQFIY 420
 DB 361 CVSSKQGNHNVVQCEVAFLODFCGCEVALDMEBPSLCREGOREVNIQKHESQFIY 420
 QY 421 VCSKGMKYFVKKXNYKHGGSGSGKGEPLVAVSAIAEKLROAKOSSNALSKFIAYVF 480
 DB 421 VCSKGMKYFVKKXNYKHGGSGSGKGEPLVAVSAIAEKLROAKOSSNALSKFIAYVF 480
 QY 481 DVSCEGDVPGIIDLSTKRYLMDNLPOLCSHLSRDHGLQEPGCHTRQGSRRNFRSKSGR 540
 DB 481 DVSCEGDVPGIIDLSTKRYLMDNLPOLCSHLSRDHGLQEPGCHTRQGSRRNFRSKSGR 540
 QY 541 SLVVAICNMHOFIDEBPDEKOFVPRPPLRYRBPVLEKPSGLVNDVMCKPGESP 600
 DB 541 SLVVAICNMHOFIDEBPDEKOFVPRPPLRYRBPVLEKPSGLVNDVMCKPGESP 600
 QY 601 FCILKVEAPVLGATPADSOHESQHGILDQGEARPALDGSALQPLIHTYKASPSDMPR 660
 DB 601 FCILKVEAPVLGATPADSOHESQHGILDQGEARPALDGSALQPLIHTYKASPSDMPR 660
 QY 661 DSGIYDSSVPSSELSPLMEGLSTQETTSSTRESVSSSGLGEDEPPALPSKLSSGSC 720
 DB 661 DSGIYDSSVPSSELSPLMEGLSTQETTSSTRESVSSSGLGEDEPPALPSKLSSGSC 720
 QY 721 KADLGRSYTDELHAAVAP 738
 DB 721 KADLGRSYTDELHAAVAP 738

RESULT 3
 AAU09953
 ID AAU09953 standard; protein; 738 AA.
 AC AAU09953;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (hIL-17) receptor like protein substitution #3.
 XX
 KW Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytotoxic; anti-leukemic; anti-fertility; ophthalmological;

KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW
 XX
 OS Homo sapiens.
 OS Synthetic.
 PH Key Location/Qualifiers
 FT Misc-difference 353 /label= Ser, Thr, Ala, Cys
 PN W0200168859-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US008678.
 XX
 PR 16-MAR-2000; 2000US-0189816P.
 PR 28-NOV-2000; 2000US-00724460.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Jing S;
 XX
 DR WPI, 2001-611392/70.
 XX
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 PS Claim 20; Page; 158pp; English.

CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anorectic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytotoxic, anti-leukemic, anti-fertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17R1p) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17R1p may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17R1p antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to
 CC information given in claim 20
 CC
 XX
 SQ Sequence 738 AA;

Query Match 99.9%; Score 3944; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPWLOLCVFFPTVNAACLSGSLAAGGSGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60
 DB 1 MAPWLOLCVFFPTVNAACLSGSLAAGGSGRAMGVDTGCMRGVGPASRNSGLYNITPKY 60
 QY 61 DICTTYLNPVGKXIVADANITTSQYACHDQVAVTILMSFGALGIEFLKGFVILELKS 120

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Db      61 DNGCTTYLNPVGGKVIADAGNITISQVACHDQVAVTILMSGALGIEFLKFRVILEELKS 120
Qy      121 EGRQCCOQLIKDPKOLNSFKRTGMSQPLANKKEFDYFVKVPPPSIKNSNYHPFF 180
Db      121 EGRQCCOQLIKDPKOLNSFKRTGMSQPLANKKEFDYFVKVPPPSIKNSNYHPFF 180
Qy      181 RTRACDLLLPDNLACKPFWKPRNLNISQHSQDMQVSFDHAPNFGFRFYLYLKLKHEG 240
Db      181 RTRACDLLLPDNLACKPFWKPRNLNISQHSQDMQVSFDHAPNFGFRFYLYLKLKHEG 240
Qy      241 PFRKRTCKOBQTTETTSCLLQNVSPGDIYIELVDVTNTRKVMHYALKPVHSPWAGPIRA 300
Db      241 PFRKRTCKOBQTTETTSCLLQNVSPGDIYIELVDVTNTRKVMHYALKPVHSPWAGPIRA 300
Qy      301 MATTVPLVVISAPATLFTWVCRKKQENITSHDESSSESTYTAALPRRLAPRRVPL 360
Db      301 MATTVPLVVISAPATLFTWVCRKKQENITSHDESSSESTYTAALPRRLAPRRVPL 360
Qy      361 CVSSKQGNHNVVQCEPAFLQDFCGCEVALDLMEDPSLCRQOREWVIOKHESQPIIV 420
Db      361 CVSSKQGNHNVVQCEPAFLQDFCGCEVALDLMEDPSLCRQOREWVIOKHESQPIIV 420
Qy      421 VCSKGMKYFVDKXNYKHGGSGSGKGEFLVAVSAIAEKLRQAKOSSNALSKFTAVYF 480
Db      421 VCSKGMKYFVDKXNYKHGGSGSGKGEFLVAVSAIAEKLRQAKOSSNALSKFTAVYF 480
Qy      481 DVSCEBDVNGIIDLSTKRYLMDNLPOLCSHLHSRDHQLQDPGQHTQSGSRNFRKSGSR 540
Db      481 DVSCEBDVNGIIDLSTKRYLMDNLPOLCSHLHSRDHQLQDPGQHTQSGSRNFRKSGSR 540
Qy      541 SLVVALCNMHQFIDEEPDMFEKQFVPPHPLRYREPVLEKSPGLVNDVMCKCPGESP 600
Db      541 SLVVALCNMHQFIDEEPDMFEKQFVPPHPLRYREPVLEKSPGLVNDVMCKCPGESP 600
Qy      601 FCLKAVAPVLTGATGPADSGHESQHGILQDGEARPALDGSALQPLHTYKAGSPSDMPR 660
Db      601 FCLKAVAPVLTGATGPADSGHESQHGILQDGEARPALDGSALQPLHTYKAGSPSDMPR 660
Qy      661 DSGIYSSVPSSELSLPMEGSLTDQETSTLTRESVSSSGGLGEEPPALPSLTLSSGSC 720
Db      661 DSGIYSSVPSSELSLPMEGSLTDQETSTLTRESVSSSGGLGEEPPALPSLTLSSGSC 720
Qy      721 KADLCGRSYTDELHAAVAP 738
Db      721 KADLCGRSYTDELHAAVAP 738

RESULT 4
AAU09954
ID      AAU09954 standard; protein; 738 AA.
AC      AAU09954;
XX
XX
DT      14-FEB-2002 (first entry)
XX
DE      Human Interleukin 17 (hIL-17) receptor like protein substitution #4.
XX
XX      Interleukin 17; hIL-17 receptor like protein; immunomodulatory;
KW      anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
KW      hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
KW      anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
KW      vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
KW      hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
KW      bone disease; vascular disorder; eye disorder; cancer; human; mutant;
KW      muten.
XX
XX      Homo sapiens.
OS      Synthetic.
XX
XX      Key Location/Qualifiers
XX      Misc-difference 374
XX      FT /label=Val, Ile, Met, Leu, Phe, Ala, Nle
XX      , FT

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XX      MO200168859-A2.
PN      20-SEP-2001.
XX
XX      15-MAR-2001; 2001MO-US008678.
PF
XX
XX      16-MAR-2000; 2000US-0189816P.
PR      28-NOV-2000; 2000US-00724460.
XX
XX      (AMGE-) AMGEN INC.
PA
XX      Jing S;
XX
XX      MPI; 2001-611392/70.
DR
XX
XX      Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT      for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT      psoriasis and glaucoma.
XX
XX      Claim 21; Page: 158pp; English.
PS
XX
XX      The invention describes novel nucleic acids encoding interleukin (IL) 17
CC      receptor like polypeptides useful as vaccines and in gene therapy. These
CC      have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC      immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC      anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC      osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
CC      ophthalmological activities. The IL-17 receptor like nucleic acids and
CC      proteins may be used to prevent and treat diseases associated with
CC      inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
CC      include, for example immune disorders (e.g. inflammation, diabetes and
CC      transplant rejection), infections (e.g. hepatitis and septicemia),
CC      weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC      dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC      lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC      (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC      bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC      (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
CC      breast cancer), reproductive disorders (e.g. infertility and
CC      miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC      DNA and its complements may also be used as diagnostic probes to detect and
CC      quantitate the presence of similar nucleic acids in samples and identify
CC      patients needing restorative therapy. The IL17rp may also be used as
CC      antigens in the production of antibodies against the proteins and in
CC      assays to identify modulators of expression and activity. The anti-
CC      IL17rp antibodies and antagonists may also be used to down regulate
CC      expression and activity. Note: This sequence is not given in the
CC      specification but is based on the human interleukin 17 (IL-17) receptor
CC      like protein sequence (AAU09904) and has been created according to
CC      information given in claim 21
XX
XX      Sequence 738 AA:
SQ
XX
XX      Query Match      99.9%; Score 3943; DB 4; Length 738;
XX      Best local Similarity 99.9%; Pred. No. 0;
XX      Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 241 PFRKRTCKQEQTTETTSCLLQNVSPGDYIIELVDPNTTRKVMHYALKPVHSPWAPPIRA 300
 DB 241 PFRKRTCKQEQTTETTSCLLQNVSPGDYIIELVDPNTTRKVMHYALKPVHSPWAPPIRA 300
 QY 301 MAITVPLVVISAPATLFTVMCRKQOENIYSHLDESSSSSTYTAALPRERLPRPKVFL 360
 DB 301 MAITVPLVVISAPATLFTVMCRKQOENIYSHLDESSSSSTYTAALPRERLPRPKVFL 360
 QY 361 CYSSKDGQNMNMNVVOCFAVFLADPCGCEVALDLMEDFSLCRGQREWVIQKIHESQFIIV 420
 DB 361 CYSSKDGQNMNMNVVOCFAVFLADPCGCEVALDLMEDFSLCRGQREWVIQKIHESQFIIV 420
 QY 421 VCSKGMKTPYDKNYKHKGGKGGSSGKGEFLVAVSAIAETLRQAKOSSSALSKFTAVYF 480
 DB 421 VCSKGMKTPYDKNYKHKGGKGGSSGKGEFLVAVSAIAETLRQAKOSSSALSKFTAVYF 480
 QY 481 DVSCEGDVPGIIDLSTKRYLMDNLPLQCSHLHSRDHGLQBPQHTQGSRRNYFRSKSGR 540
 DB 481 DVSCEGDVPGIIDLSTKRYLMDNLPLQCSHLHSRDHGLQBPQHTQGSRRNYFRSKSGR 540
 QY 541 SLVVAICNMHQFIDEBPDMFEKQFVPPHPPPLRYRBPVLKEDSGVLNDVMCKPGPESD 600
 DB 541 SLVVAICNMHQFIDEBPDMFEKQFVPPHPPPLRYRBPVLKEDSGVLNDVMCKPGPESD 600
 QY 601 PCLKVAAPVLGATGPADSOHESGHGGLDQDGEARPALDGSALQPLHTYKASBPDMR 660
 DB 601 PCLKVAAPVLGATGPADSOHESGHGGLDQDGEARPALDGSALQPLHTYKASBPDMR 660
 QY 661 DSGITVSSVPSSESLPLMEGLSTDOTETSSLTRESVSSSGLGEEPPPALPSKLSSGSC 720
 DB 661 DSGITVSSVPSSESLPLMEGLSTDOTETSSLTRESVSSSGLGEEPPPALPSKLSSGSC 720
 QY 721 KADLCGRSYTDLHAHAVP 738
 DB 721 KADLCGRSYTDLHAHAVP 738

RESULT 5
 AAU09951
 ID AAU09951 standard; protein; 738 AA.

AC AAU09951;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (IL-17) receptor like protein substitution #1.

XX Interleukin 17, IL-17 receptor like protein; immunomodulatory;
 XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 XX hepatic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 XX vascular; cytotoxic; anti-leukemic; anti-fertility; ophthalmological;
 XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers
 XX Misc-difference 45 /label= Gly, Pro or Ala

PN MO200168859-A2.

PD 20-SEP-2001.

PF 15-MAR-2001; 2001MO-US008678.

PR 16-MAR-2000; 2000US-0189816P.

PR 28-NOV-2000; 2000US-00724460.

PA (AMGE-) AMGEN INC.
 XX Jing S;
 XX WPI; 2001-611392/70.
 DR Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 XX Claim 18; Page; 158pp; English.
 XX
 PS The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytotoxic, anti-leukemic, anti-fertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17R) expression. These
 CC include, for example, immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis, cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17R may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17R antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to
 CC information given in claim 18
 XX
 SQ Sequence 738 AA;
 Query Match 99.8%; Score 3941; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAPWQLGCVFTVNAACNGSQLAAVAGSGGAAWGVTDTGGMGVGASRRSGIYNTTFK 60
 DB 1 MAPWQLGCVFTVNAACNGSQLAAVAGSGGAAWGVTDTGGMGVGASRRSGIYNTTFK 60
 QY 61 DNGCTTLNVGKRVADAQNIITISOYACHDOYAVTILMSGALGIFLKGFRVILELKS 120
 DB 61 DNGCTTLNVGKRVADAQNIITISOYACHDOYAVTILMSGALGIFLKGFRVILELKS 120
 QY 61 DNGCTTLNVGKRVADAQNIITISOYACHDOYAVTILMSGALGIFLKGFRVILELKS 120
 DB 61 DNGCTTLNVGKRVADAQNIITISOYACHDOYAVTILMSGALGIFLKGFRVILELKS 120
 QY 121 EGRQCCQLILKDPKQINSFPRKTMESQPLNKKPEPTDYFVXVVPSPISKNSVYHPFF 180
 DB 121 EGRQCCQLILKDPKQINSFPRKTMESQPLNKKPEPTDYFVXVVPSPISKNSVYHPFF 180
 QY 181 RTKACDLILQPDNLACKPFWKPRNLTISOHSDMOVSPHAHNFRRFFLYLTKLKHG 240
 DB 181 RTKACDLILQPDNLACKPFWKPRNLTISOHSDMOVSPHAHNFRRFFLYLTKLKHG 240
 QY 241 PFRKRTCKQEQTTETTSCLLQNVSPGDYIIELVDPNTTRKVMHYALKPVHSPWAPPIRA 300
 DB 241 PFRKRTCKQEQTTETTSCLLQNVSPGDYIIELVDPNTTRKVMHYALKPVHSPWAPPIRA 300
 QY 301 MAITVPLVVISAPATLFTVMCRKQOENIYSHLDESSSSSTYTAALPRERLPRPKVFL 360
 DB 301 MAITVPLVVISAPATLFTVMCRKQOENIYSHLDESSSSSTYTAALPRERLPRPKVFL 360
 QY 361 CYSSKDGQNMNMNVVOCFAVFLADPCGCEVALDLMEDFSLCRGQREWVIQKIHESQFIIV 420


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Db 361 CYSSKDGQNHMNVVOCFAFYFLQFCGCEVALDLMBDFSLCREGQREWVIOKIHESQFIIV 420
Qy 421 VCSKGMKTFVDKKNYKHKGGRSGSGKGLFLVAVSAIAEKLROAKOSSSALSKFIAYVF 480
Db 422 VCSKGMKTFVDKKNYKHKGGRSGSGKGLFLVAVSAIAEKLROAKOSSSALSKFIAYVF 480
Qy 481 DVSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
Db 481 DVSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
Qy 541 SLTVAICNMHQFIIDBEPDMEKQFVPPHPPPLRYREPVLEKPDGSLVLDVWCKPSPESD 600
Db 541 SLTVAICNMHQFIIDBEPDMEKQFVPPHPPPLRYREPVLEKPDGSLVLDVWCKPSPESD 600
Qy 601 FCLKVAAPVLGATGPADSGHESGHGGLDQGEARPALDGSAAQPLIHTYKAGSPSDMR 660
Db 601 FCLKVAAPVLGATGPADSGHESGHGGLDQGEARPALDGSAAQPLIHTYKAGSPSDMR 660
Qy 661 DSGIYDSSVPSSRLSLPLMEGLSTDOTETSLTESVSSSGGLGEEPPALPSKLSSGSC 720
Db 661 DSGIYDSSVPSSRLSLPLMEGLSTDOTETSLTESVSSSGGLGEEPPALPSKLSSGSC 720
Qy 721 KADLCGRSYTDEIHAHAVAP 738
Db 721 KADLCGRSYTDEIHAHAVAP 738

```

RESULT 6
AAU09952
ID AAU09952 standard; protein; 738 AA.

AC AAU09952;

DT 14-FEB-2002 (first entry)

DE Human Interleukin 17 (IL-17) receptor like protein substitution #2.

XX Interleukin 17, IL-17 receptor like protein; immunomodulatory;
XX anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
XX hepatic; anabolic; anti-asthmatic; dermatological; renal; osteopathic;
XX anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
XX vascular; cytotoxic; anti-leukemic; anti-fertility; ophthalmological;
XX hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
XX bone disease; vascular disorder; eye disorder; cancer; human; mutant;
XX mucin.

OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FT Misc-difference 227 /label= Phe, Leu, Val, Ile, Ala, Tyr
XX

PN WO200168859-A2.

PD 20-SEP-2001.

PF 15-MAR-2001; 2001WO-US008678.

PR 16-MAR-2000; 2000US-0189816P.

PR 28-NOV-2000; 2000US-00724460.

XX (AMGE-) AMGEN INC.

PI Jing S;

DR MPI; 2001-611392/70.

XX Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
PT psoriasis and glaucoma.
XX

PS Claim 19; Page; 158pp; English.

XX The invention describes novel nucleic acids encoding interleukin (IL) 17
CC receptor like polypeptides useful as vaccines and in gene therapy. These
CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
CC osteopathic, vascular, cytotoxic, anti-leukemic, anti-fertility and
CC ophthalmological activities. The IL-17 receptor like nucleic acids and
CC proteins may be used to prevent and treat diseases associated with
CC inappropriate IL-17 receptor like polypeptide (IL17R) expression. These
CC include, for example immune disorders (e.g. inflammation, diabetes and
CC transplant rejection), infections (e.g. hepatitis and septicemia),
CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC bone diseases (e.g. osteoporosis and hypercalcemia), vascular disorders
CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
CC breast cancer), reproductive disorders (e.g. infertility and
CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC DNA and its complements may also be used as diagnostic probes to detect and
CC quantitate the presence of similar nucleic acids in samples and identify
CC patients needing restorative therapy. The IL17R may also be used as
CC antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of expression and activity. The anti-
CC IL17R antibodies and antagonists may also be used to down regulate
CC expression and activity. Note: This sequence is not given in the
CC specification but is based on the human interleukin 17 (IL-17) receptor
CC like protein sequence (AAU09904) and has been created according to
CC information given in claim 19
XX

SQ Sequence 738 AA;

Query Match 99.8%; Score 3941; DB 4; Length 738;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 MAPWLOLSVPTTNAACINGSLAAGSGGAWGVDCGRGVGPASRNSGLNTTFY 60
Db 1 MAPWLOLSVPTTNAACINGSLAAGSGGAWGVDCGRGVGPASRNSGLNTTFY 60
Qy 61 DNCTTYLNPVGHVADANITISQYACHDQVAVIILMSPALGIEPLKGFVILIELKS 120
Db 61 DNCTTYLNPVGHVADANITISQYACHDQVAVIILMSPALGIEPLKGFVILIELKS 120
Qy 121 EGRQCOQLIKDPKOLNSFKRTGMSOPFLMKFETDYFYKVVPPPSIKESNTHPFF 180
Db 121 EGRQCOQLIKDPKOLNSFKRTGMSOPFLMKFETDYFYKVVPPPSIKESNTHPFF 180
Qy 181 RTACDILLQPNLACKFPKPRNLTISOHGSDMVSPDHPHNGSPFTYHYLKHG 240
Db 181 RTACDILLQPNLACKFPKPRNLTISOHGSDMVSPDHPHNGSPFTYHYLKHG 240
Qy 241 PEKRTKQEOETTESCLQVNSPGDYIIELVDDTNTTRKVMYALPVHSPMAGPIRA 300
Db 241 PEKRTKQEOETTESCLQVNSPGDYIIELVDDTNTTRKVMYALPVHSPMAGPIRA 300
Qy 301 MAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTAALPRERLPPKVF 360
Db 301 MAITVPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTAALPRERLPPKVF 360
Qy 361 CYSSKDGQNHMNVVOCFAFYFLQFCGCEVALDLMBDFSLCREGQREWVIOKIHESQFIIV 420
Db 361 CYSSKDGQNHMNVVOCFAFYFLQFCGCEVALDLMBDFSLCREGQREWVIOKIHESQFIIV 420
Qy 421 VCSKGMKTFVDKKNYKHKGGRSGSGKGLFLVAVSAIAEKLROAKOSSSALSKFIAYVF 480
Db 421 VCSKGMKTFVDKKNYKHKGGRSGSGKGLFLVAVSAIAEKLROAKOSSSALSKFIAYVF 480
Qy 481 DVSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540
Db 481 DVSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQEPQHTROGSRNNYFRSKSGR 540

```

QY 541 SLTVAI CNMHQFI DEBDFEKOFPFHPPLRYRBPVLEKPSGLVNDVWCKPESD 600
 DB 541 SLTVAI CNMHQFI DEBDFEKOFPFHPPLRYRBPVLEKPSGLVNDVWCKPESD 600
 QY 601 FCIAKEAPVLTGATGPADSGHESQHGLDQDGARPALDGSALQPLHTVKAQSPDMR 660
 DB 601 FCIAKEAPVLTGATGPADSGHESQHGLDQDGARPALDGSALQPLHTVKAQSPDMR 660
 QY 661 DSGIYDSVPSSELSPLMEGLSTDTETSSLTESVSSSGLGEEPPALPSKLSSGSC 720
 DB 661 DSGIYDSVPSSELSPLMEGLSTDTETSSLTESVSSSGLGEEPPALPSKLSSGSC 720
 QY 721 KADIGCRSTDELRHAYAP 738
 DB 721 KADIGCRSTDELRHAYAP 738

RESULT 7
 AAU09956
 ID AAU09956 standard; protein; 738 AA.
 AC AAU09956;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (hli-17) receptor like protein substitution #6.
 XX
 KW Interleukin 17, hli-17 receptor like protein; immunomodulatory;
 KW anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KW heptic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KW anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KW vascular; cytotoxic; anti-leukemic; anti-fertility; ophthalmological;
 KW hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KW bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KW mutin.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 515
 FT /label= Asp, Glu
 FT
 XX WO200168859-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001WO-US008678.
 XX
 PR 16-MAR-2000; 2000US-0189816P.
 PR 28-NOV-2000; 2000US-00724460.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Jing S;
 PI
 DR WPI; 2001-611392/70.
 XX
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 XX
 PS Claim 23; Page: 158pp; English.
 XX
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytotoxic, anti-leukemic, anti-fertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with

CC inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
 CC include, for example, immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis, cancer (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also be used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rlp may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17rlp antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to
 CC information given in claim 23
 CC
 XX
 SQ Sequence 738 AA;
 Query Match 99.8%; Score 3941; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MAPWLOLCVFFTVNACLNGSQLAAVAGSGGAMGVDTGMRGVGPASRNSGLYNTFYK 60
 DB 1 MAPWLOLCVFFTVNACLNGSQLAAVAGSGGAMGVDTGMRGVGPASRNSGLYNTFYK 60
 QY 61 DNCTTYLNPVGHVADADQNTTISQYACHDQYAVITLSPALGIEFLKGFVYILBELKS 120
 DB 61 DNCTTYLNPVGHVADADQNTTISQYACHDQYAVITLSPALGIEFLKGFVYILBELKS 120
 QY 121 EGRGCOQLIKDPKOLNSFKRTGMSOPFLMKETDVFVVPVPPSKNSNYPFPF 180
 DB 121 EGRGCOQLIKDPKOLNSFKRTGMSOPFLMKETDVFVVPVPPSKNSNYPFPF 180
 QY 181 RTRACDILLQPDNLACKPFWKPRNLNISQHSQDMQVSPHAPHNGFRFFYLHYLKXHG 240
 DB 181 RTRACDILLQPDNLACKPFWKPRNLNISQHSQDMQVSPHAPHNGFRFFYLHYLKXHG 240
 QY 241 PKRRTCKQEQTEFTTSCILQNVSPQDYIILVDYDNTTRKVMYALKVHSPWAPIPRA 300
 DB 241 PKRRTCKQEQTEFTTSCILQNVSPQDYIILVDYDNTTRKVMYALKVHSPWAPIPRA 300
 QY 301 MAITVPLVVISAPATLFTWCKRKKQOENYSHLDESSSSTYTALPRERLRPRPKVFL 360
 DB 301 MAITVPLVVISAPATLFTWCKRKKQOENYSHLDESSSSTYTALPRERLRPRPKVFL 360
 QY 361 CYSSKDGQNHMMVWOCFAFYLDPCGCEVALDLMEDFSLCRGOREBMYOKIHESQFIIV 420
 DB 361 CYSSKDGQNHMMVWOCFAFYLDPCGCEVALDLMEDFSLCRGOREBMYOKIHESQFIIV 420
 QY 421 VCSKGMKCYFVDKKNYKHKGGGSGKGLFLVAVASAIKRLQAKOSSAALSKEFLAYVF 480
 DB 421 VCSKGMKCYFVDKKNYKHKGGGSGKGLFLVAVASAIKRLQAKOSSAALSKEFLAYVF 480
 QY 481 DYSCEGDVPGIIDLSTKTRLMNLPOLCSHLSRHDGLOEPQHTROGSRMYFPFSKSR 540
 DB 481 DYSCEGDVPGIIDLSTKTRLMNLPOLCSHLSRHDGLOEPQHTROGSRMYFPFSKSR 540
 QY 541 SLTVAI CNMHQFI DEBDFEKOFPFHPPLRYRBPVLEKPSGLVNDVWCKPESD 600
 DB 541 SLTVAI CNMHQFI DEBDFEKOFPFHPPLRYRBPVLEKPSGLVNDVWCKPESD 600
 QY 601 FCIAKEAPVLTGATGPADSGHESQHGLDQDGARPALDGSALQPLHTVKAQSPDMR 660
 DB 601 FCIAKEAPVLTGATGPADSGHESQHGLDQDGARPALDGSALQPLHTVKAQSPDMR 660
 QY 661 DSGIYDSVPSSELSPLMEGLSTDTETSSLTESVSSSGLGEEPPALPSKLSSGSC 720

[illegible]

	CC	miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
	CC	DNA and its complements may also used as diagnostic probes to detect and
	CC	quantitate the presence of similar nucleic acids in samples and identify
	CC	patients needing restorative therapy. The IL17IP may also be used as
	CC	antigens in the production of antibodies against the proteins and in
	CC	assays to identify modulators of expression and activity. The anti-
	CC	IL17IP antibodies and antagonists may also be used to down regulate
	CC	expression and activity. Note: This sequence is not given in the
	CC	specification but is based on the human Interleukin 17 (IL-17) receptor
	CC	like protein sequence (AAU09904) and has been created according to
	CC	information given in claim 24
	xx	
SQ	Sequence 738 AA:	
	Query Match	99.7%; Score 3937; DB 4; Length 738;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 737; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1	MAMPILQLCSVPFTTNACLNGSQLVAAGSGSRAMGVDTCCRGIGCPASRNGLTNITPKY 60
DB	1	MAMPILQLCSVPFTTNACLNGSQLVAAGSGSRAMGVDTCCRGIGCPASRNGLTNITPKY 60
OY	61	DNCTTYANPVGKAVIADAKONTTISQVACHDPAVTILMSPGALIEFLKGRVILEELKS 120
DB	61	DNCTTYANPVGKAVIADAKONTTISQVACHDPAVTILMSPGALIEFLKGRVILEELKS 120
OY	121	EGRQCQOOLIKDPKQLNSSFKRTMESOPFLNMKEFDYFVKVPPPSIKNESNYHPFF 180
DB	121	EGRQCQOOLIKDPKQLNSSFKRTMESOPFLNMKEFDYFVKVPPPSIKNESNYHPFF 180
OY	181	RTRACDLILPDNLACRPFKPRRLINATSHGSMDQVSFDAHPHNGRRPFLIHYTKLKHG 240
DB	181	RTRACDLILPDNLACRPFKPRRLINATSHGSMDQVSFDAHPHNGRRPFLIHYTKLKHG 240
OY	241	PFRKRTCKOBOTTEETSTCLONVSPGYIIEVDPTTTRKVMHYALKPVSPMAGPIRA 300
DB	241	PFRKRTCKOBOTTEETSTCLONVSPGYIIEVDPTTTRKVMHYALKPVSPMAGPIRA 300
OY	301	MAITVPLVVISAFATLFTVMCRKKQOEINTYSHLDESSSESTYTALPREBLRPKVYL 360
DB	301	MAITVPLVVISAFATLFTVMCRKKQOEINTYSHLDESSSESTYTALPREBLRPKVYL 360
OY	361	CYSSECDGNHNNTVQCRAVFIQDFCGCEVALDMEDPSLCREGRENVYIQKHESQPIIV 420
DB	361	CYSSECDGNHNNTVQCRAVFIQDFCGCEVALDMEDPSLCREGRENVYIQKHESQPIIV 420
OY	421	VCSNGMKRYFVDKNKYKKKGGRGGSKGEFLVVASAIAEKLROKXOSSAALSFEIAYF 480
DB	421	VCSNGMKRYFVDKNKYKKKGGRGGSKGEFLVVASAIAEKLROKXOSSAALSFEIAYF 480
OY	481	DYSCGEGVPGLIDSTKYRLMDNI.POLCSHLASHRDHGLEBQGHTROGSRANTYFRSXSGR 540
DB	481	DYSCGEGVPGLIDSTKYRLMDNI.POLCSHLASHRDHGLEBQGHTROGSRANTYFRSXSGR 540
OY	541	SLYYAICNMHQFIDEBDPWFEKQFPHPHPLRYRBPLYLEKFGDGLVINDVMCKRGPESD 600
DB	541	SLYYAICNMHQFIDEBDPWFEKQFPHPHPLRYRBPLYLEKFGDGLVINDVMCKRGPESD 600
OY	601	FCLVVEAPVYGATBPASQHSQHSGCIGLDQCEARPALDGSAALOPLIHTVYAGSPSDMR 660
DB	601	FCLVVEAPVYGATBPASQHSQHSGCIGLDQCEARPALDGSAALOPLIHTVYAGSPSDMR 660
OY	661	DSGIYDSSVSESSELPLMEGLSTDQTETSILTRESVSSSGLGEEBEPALPSKLSSGSC 720
DB	661	DSGIYDSSVSESSELPLMEGLSTDQTETSILTRESVSSSGLGEEBEPALPSKLSSGSC 720
OY	721	KADIGCSRSYTDELHAHAVP 738
DB	721	KADIGCSRSYTDELHAHAVP 738

ID AAU09955 standard; protein; 738 AA.
 AC AAU09955;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Human Interleukin 17 (IL-17) receptor like protein subcltution #5.
 XX
 KM Interleukin 17, IL-17 receptor like protein; immunomodulatory;
 KM anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;
 KM heparic; anabolic; anorectic; anti-alzheimer's; anti-parkinsonian;
 KM anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;
 KM vascular; cytostatic; anti-leukemic; anti-infertility; ophthalmological;
 KM hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;
 KM bone disease; vascular disorder; eye disorder; cancer; human; mutant;
 KM
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 385
 FT /label= Cys, Ser, Ala
 XX
 PN MO200168859-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 15-MAR-2001; 2001MO-US008678.
 PF
 PR 16-MAR-2000; 2000US-0189816P.
 PR 28-NOV-2000; 2000US-00724460.
 XX
 PA (AMGE-) AMGEN INC.
 PI
 PI Jing S;
 DR WPI; 2001-611392/70.
 DR
 PT Nucleic acids encoding interleukin 17 receptor like polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. leukemia, asthma, diabetes,
 PT psoriasis and glaucoma.
 PT
 XX
 PS Claim 22; Page; 158pp; English.
 PS
 CC The invention describes novel nucleic acids encoding interleukin (IL) 17
 CC receptor like polypeptides useful as vaccines and in gene therapy. These
 CC have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
 CC immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
 CC anti-parkinsonian, anti-convulsant, anti-asthmatic, dermatological,
 CC osteopathic, vascular, cytostatic, anti-leukemic, anti-infertility and
 CC ophthalmological activities. The IL-17 receptor like nucleic acids and
 CC proteins may be used to prevent and treat diseases associated with
 CC inappropriate IL-17 receptor like polypeptide (IL17rp) expression. These
 CC include, for example immune disorders (e.g. inflammation, diabetes and
 CC transplant rejection), infections (e.g. hepatitis and septicemia),
 CC weight disorders (e.g. anorexia, cachexia and obesity), neuronal
 CC dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
 CC lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
 CC (e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
 CC bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
 CC (e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
 CC breast cancer), reproductive disorders (e.g. infertility and
 CC miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
 CC DNA and its complements may also used as diagnostic probes to detect and
 CC quantitate the presence of similar nucleic acids in samples and identify
 CC patients needing restorative therapy. The IL17rp may also be used as
 CC antigens in the production of antibodies against the proteins and in
 CC assays to identify modulators of expression and activity. The anti-
 CC IL17rp antibodies and antagonists may also be used to down regulate
 CC expression and activity. Note: This sequence is not given in the
 CC specification but is based on the human interleukin 17 (IL-17) receptor
 CC like protein sequence (AAU09904) and has been created according to

CC Information given in claim 22
 XX
 SQ Sequence 738 AA;
 XX
 Query Match 99.7%; Score 3937; DB 4; Length 738;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 737; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX
 QY 1 MAPWLOLCVFFPVVNAALNGSOLAAGGGGAAAGVDTGCMGVGASRNSGLXNTFFK 60
 DB 1 MAPWLOLCVFFPVVNAALNGSOLAAGGGGAAAGVDTGCMGVGASRNSGLXNTFFK 60
 QY 61 DNGTTLVNPGKRVADDAONITTSOYACHDOYAVTILMSPGALGIFLGFRTLEBLKS 120
 DB 61 DNGTTLVNPGKRVADDAONITTSOYACHDOYAVTILMSPGALGIFLGFRTLEBLKS 120
 QY 121 EGRQCOOLILKPKOLNSPKRTGMSQPLNMKEPETDYFVKVPPSIKNSNYPFPF 180
 DB 121 EGRQCOOLILKPKOLNSPKRTGMSQPLNMKEPETDYFVKVPPSIKNSNYPFPF 180
 QY 181 RTACDILLQPDNLACKPFWKPRNLTISQSGDMQVSPHAPNFGFRFFYLTKLKHG 240
 DB 181 RTACDILLQPDNLACKPFWKPRNLTISQSGDMQVSPHAPNFGFRFFYLTKLKHG 240
 QY 241 PPRKTKCKOQTETTSCLQNVSPGDYIIBLVDTNTTRKVMYALKVHSPMAGPIRA 300
 DB 241 PPRKTKCKOQTETTSCLQNVSPGDYIIBLVDTNTTRKVMYALKVHSPMAGPIRA 300
 QY 301 MATVPLVVISAFATLFTVCRKQOENIYSHLDESSSSTYTAALPRERLRPKVL 360
 DB 301 MATVPLVVISAFATLFTVCRKQOENIYSHLDESSSSTYTAALPRERLRPKVL 360
 QY 361 CISSKQGNHNVVOCFAVFLDFCGCEVALDMEDFSICRSGQREWVIOKTHESQITV 420
 DB 361 CISSKQGNHNVVOCFAVFLDFCGCEVALDMEDFSICRSGQREWVIOKTHESQITV 420
 QY 421 VCSKGMKVFVDKKNYHKGSGSGKGLFLVAVSAIAKLQAOKSSSALSKFLAVF 480
 DB 421 VCSKGMKVFVDKKNYHKGSGSGKGLFLVAVSAIAKLQAOKSSSALSKFLAVF 480
 QY 481 DYSCEGDVGIIDLSTKYKLMNLPQLCSHLHSRDHGLQEPQHTQGRSRRNFRSKSG 540
 DB 481 DYSCEGDVGIIDLSTKYKLMNLPQLCSHLHSRDHGLQEPQHTQGRSRRNFRSKSG 540
 QY 541 SLVVALCNHQTIDEEPDPFEKQVFPFPRRYRPRVLEKEDSGVLVNDVCKPESD 600
 DB 541 SLVVALCNHQTIDEEPDPFEKQVFPFPRRYRPRVLEKEDSGVLVNDVCKPESD 600
 QY 601 FCILKVAAPVLTGATGAPADSGHESQHGGLDDGEARPLDSSALQPLHTVKAQSPBDMR 660
 DB 601 FCILKVAAPVLTGATGAPADSGHESQHGGLDDGEARPLDSSALQPLHTVKAQSPBDMR 660
 QY 661 DSGIYSSVPSSELPLMEGLSTDDTETSSLTESVSSSGGCEBPPLPSTLSSGSC 720
 DB 661 DSGIYSSVPSSELPLMEGLSTDDTETSSLTESVSSSGGCEBPPLPSTLSSGSC 720
 QY 721 KADLCGRSYTDELAHAVP 738
 DB 721 KADLCGRSYTDELAHAVP 738
 XX
 RESULT 10
 ABB07628
 ID ABB07628 standard; protein; 739 AA.
 XX
 AC ABB07628;
 XX
 DT 20-MAY-2002 (first entry)
 XX
 DE Human cytokine receptor, Zcytor18 splice variant.
 XX
 KM Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
 KM pulmonary alveolar proteinosis; familial periodic fever; antitumour;

KM erythroleukemia; chromosome 3p14.3; gene therapy; splice variant.
 XX Homo sapiens.
 OS
 XX MO200208259-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001MO-US023253.
 XX
 PR 26-JUL-2000; 2000US-0220747P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Presnell SR, Kuestner RE, Gao Z;
 XX
 DR WPI; 2002-217048/27.
 XX
 DR N-PSDB; ABA95035, ABA95036.
 XX
 PT New cytokine receptor polypeptide designated zcytor18, useful for
 PT inhibiting cell proliferation associated with psoriasis or tumor growth,
 PT and modulating immune system by binding to endogenous zcytor18 ligand.
 XX
 PS Claim 1; Page 102-106; 119pp; English.
 XX
 CC The invention relates to an isolated cytokine receptor polypeptide
 CC designated zcytor18. The zcytor18 polypeptides can be expressed by
 CC standard recombinant methodology. The polypeptides can be used to inhibit
 CC cell proliferation associated with psoriasis or tumor growth. The
 CC encoding nucleic acids are useful for providing zcytor18 in vivo by gene
 CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
 CC vivo diagnosis, and the zcytor18 probes and primers can be used to detect
 CC and localize zcytor18 gene expression in tissue samples. The probes are
 CC also useful for detecting gross aberrations in chromosome 3 in which
 CC zcytor18 gene resides. The zcytor18 polynucleotides can also be used in
 CC linkage-based testing of pulmonary alveolar proteinosis, familial
 CC periodic fever and erythroleukemia, and erythroleukemia associated with
 CC polymorphisms of cytokine receptors. The present sequence represents a
 CC human zcytor18 splice variant
 XX
 XX Sequence 739 AA;
 SQ
 Query Match 99.2%; Score 3918; DB 5; Length 739;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 734; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 421 VCSKGMKYPVDKKNYGHKGGSGSGKGLFLVAVASIAEKLRLQAKSSSALSKPIAYVF 480
 DB 421 VCSKGMKYPVDKKNYGHKGGSGSGKGLFLVAVASIAEKLRLQAKSSSALSKPIAYVF 480
 QY 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLEPQOHTROGSRNYPFRSKGR 540
 DB 481 DYSCEGDVPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLEPQOHTROGSRNYPFRSKGR 540
 QY 541 SLVVAICNMHOFIDDEPDWFEKQFVFPFPPRPRRYEPVLEKPDGSLVNDVWCKGSPESD 600
 DB 541 SLVVAICNMHOFIDDEPDWFEKQFVFPFPPRPRRYEPVLEKPDGSLVNDVWCKGSPESD 600
 QY 601 FCLKTEAPVLTGATGPADSOHESQHGLDQDGEARPALDGSALOPILHTVKAGSPSDMPR 660
 DB 601 FCLKTEAPVLTGATGPADSOHESQHGLDQDGEARPALDGSALOPILHTVKAGSPSDMPR 660
 QY 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGIGBEPALPKLSSGSC 720
 DB 661 DSGIYDSSVPSSELSPLMEGLSTDTQETSSLTESVSSSGIGBEPALPKLSSGSC 720
 QY 721 KADLCGRSTTDELHAYAP 738
 DB 721 KADLCGRSTTDELHAYAP 738
 RESULT 11
 ADU69242
 ID ADU69242 standard; protein, 739 AA.
 XX
 AC ADU69242;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE Human SEF amino acid SEQ ID NO.2.
 XX
 XX fibroblast growth factor; SEF; similar expression of FGF genes;
 KM cytostatic; cardiovascular-gen.; antiarteriosclerotic; cardiant;
 KM vasotrophic; hypertensive; nephrotropic; gene therapy; diagnosis;
 KM prognosis; proliferative disorders; cardiovascular disorders;
 KM renal disease; glomerular disease.
 XX
 OS Homo sapiens.
 XX
 OS US2004235104-A1.
 XX
 PD 25-NOV-2004.
 XX
 PF 07-MAY-2004; 2004US-00842006.
 XX
 PR 08-MAY-2003; 2003US-0469522P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Yang R;
 XX
 DR WPI; 2004-821320/81.
 DR N-PSDB; ADU69241.
 XX
 PT New isolated SEF nucleic acid and polypeptide, useful for monitoring,
 PT treating, or diagnosing proliferative and/or differentiative disorders,
 PT e.g. ovarian cancer, breast cancer, or cardiovascular disorder including
 PT arteriosclerosis.
 XX
 PS Claim 1; SEQ ID NO 2; 46bp; English.
 XX
 CC The invention relates to a novel isolated SEF (similar expression of FGF
 CC genes) nucleic acid molecule (I). An SEF of the invention has cytostatic,
 CC cardiovascular-gen., antiarteriosclerotic, cardiant, vasotrophic,
 CC hypotensive, and nephrotropic activity, and may have a use in gene
 CC therapy. The SEF nucleic acids and polypeptides can be used for
 CC diagnostic assays, prognostic assays, and monitoring clinical trials.
 CC They can also be used for treating a subject at risk of or susceptible to

Db 301 VAITFLVVISAFATLFTVWCRKQOENIYSHLDESSSESTYTALPRRLPRKVF 360
Qy 361 CYSSKGGNNMNVQCFAYFLQDFCGCEVALDLMEBPSLCREGQREWVIOKIHESQPIY 420
Db 361 CYSSKGGNNMNVQCFAYFLQDFCGCEVALDLMEBPSLCREGQREWVIOKIHESQPIY 420
Qy 421 VCSKGMKTFYDKKQYKHKGGGSGKGLFLVVASIAELROAKOSSSAAISKFTAVYF 480
Db 421 VCSKGMKTFYDKKQYKHKGGGSGKGLFLVVASIAELROAKOSSSAAISKFTAVYF 480
Qy 481 DVSCEGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPQHTQGSRRNYFRSKSGR 540
Db 481 DVSCEGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPQHTQGSRRNYFRSKSGR 540
Qy 541 SLTYVALICNMHQFIDEBPDWFEKQFVPPHPLRYREPVLEKFSGLVNDVMCKPGEPSD 600
Db 541 SLTYVALICNMHQFIDEBPDWFEKQFVPPHPLRYREPVLEKFSGLVNDVMCKPGEPSD 600
Qy 601 FCLEKAPVLTGATGPADSOHESQHGGLDQDEARPALDGSAALOPLHTYKAGSPSDMP 660
Db 601 FCLEKAPVLTGATGPADSOHESQHGGLDQDEARPALDGSAALOPLHTYKAGSPSDMP 660
Qy 661 DSGIYDSSVPSSELSPLMEGLSTDQETSTSLTESVSSSGLGEBEPALPSKLSSGSC 720
Db 661 DSGIYDSSVPSSELSPLMEGLSTDQETSTSLTESVSSSGLGEBEPALPSKLSSGSC 720
Qy 721 KADLCGRSTYDELAHAVAP 738
Db 721 KADLCGRSTYDELAHAVAP 738

RESULT 13

ID ABB07626 standard; protein; 753 AA.
AC ABB07626;
XX 20-MAY-2002 (first entry)
XX Human cytokine receptor, Zcytor18 amino acid sequence.
XX Cytokine receptor; Zcytor18; cell proliferation; antipsoriatic; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumor;
XX erythroleukemia; chromosome 3p14.3; gene therapy.
OS Homo sapiens.
XX WO200208259-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-05023253.
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO) ZYMOGENETICS INC.
XX Preenell SR, Kuestner RE, Gao Z;
XX MPI; 2002-217048/27.
XX DR N-PSDB; ABA95031, ABA95032.
XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
XX Claim 1; Page 2; 11pp; English.
XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumor growth. The

CC encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
CC therapy techniques. Zcytor18 oligonucleotide probes are useful for in
CC vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
CC and localize Zcytor18 gene expression in tissue samples. The probes are
CC also useful for detecting gross aberrations in chromosome 3 in which
CC Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
CC linkage-based testing of pulmonary alveolar proteinosis, familial
CC periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
CC human Zcytor18 amino acid sequence
XX

SQ Sequence 753 AA;

Query Match 98.8%; Score 3901; DB 5; Length 753;

Best Local Similarity 97.6%; Pred. No. 0;

Matches 734; Conservative 1; Mismatches 3; Indels 14; Gaps 1;

Qy 1 MAPWTLQCSVFPTVACNGSQLAVAAGSGRAGVDTGMR-----GVGP 46
Db 1 MAPWTLQCSVFPTVACNGSQLAVAAGSGRAGVDTGMRKAAARPRLCVANEVGP 60
Qy 47 AARNSGLVNITTKYKNDCTTYLNPVGVKHYADQNTTIOYACHDQVATYILMSRGLTE 106
Db 47 AARNSGLVNITTKYKNDCTTYLNPVGVKHYADQNTTIOYACHDQVATYILMSRGLTE 106
Qy 61 AARNSGLVNITTKYKNDCTTYLNPVGVKHYADQNTTIOYACHDQVATYILMSRGLTE 120
Db 61 AARNSGLVNITTKYKNDCTTYLNPVGVKHYADQNTTIOYACHDQVATYILMSRGLTE 120
Qy 107 PLKGRVILIELKESGRQCOQLLDPKQNLNSFRRTGMSOPFLNMKEETDYPKVVVF 166
Db 107 PLKGRVILIELKESGRQCOQLLDPKQNLNSFRRTGMSOPFLNMKEETDYPKVVVF 180
Qy 121 PLKGRVILIELKESGRQCOQLLDPKQNLNSFRRTGMSOPFLNMKEETDYPKVVVF 180
Db 121 PLKGRVILIELKESGRQCOQLLDPKQNLNSFRRTGMSOPFLNMKEETDYPKVVVF 180
Qy 167 PSIKNESNHPFFRTTRACDILLQPDNLACKFWKPRNLINISQHSQDQVSDHAPHNFG 226
Db 167 PSIKNESNHPFFRTTRACDILLQPDNLACKFWKPRNLINISQHSQDQVSDHAPHNFG 240
Qy 181 PSIKNESNHPFFRTTRACDILLQPDNLACKFWKPRNLINISQHSQDQVSDHAPHNFG 240
Db 181 PSIKNESNHPFFRTTRACDILLQPDNLACKFWKPRNLINISQHSQDQVSDHAPHNFG 240
Qy 227 FRFFLYHKLKHEGSPKRTCKQEBQETSTGLQNVSPGDIITILYDNTTRKVMYTA 286
Db 227 FRFFLYHKLKHEGSPKRTCKQEBQETSTGLQNVSPGDIITILYDNTTRKVMYTA 300
Qy 241 FRFFLYHKLKHEGSPKRTCKQEBQETSTGLQNVSPGDIITILYDNTTRKVMYTA 300
Db 241 FRFFLYHKLKHEGSPKRTCKQEBQETSTGLQNVSPGDIITILYDNTTRKVMYTA 300
Qy 287 LKPVHSPMAGPIRAAATVPLVVISAFATLFTVWCRKQOENIYSHLDESSSESTYTAA 346
Db 287 LKPVHSPMAGPIRAAATVPLVVISAFATLFTVWCRKQOENIYSHLDESSSESTYTAA 360
Qy 301 LKPVHSPMAGPIRAAATVPLVVISAFATLFTVWCRKQOENIYSHLDESSSESTYTAA 360
Db 301 LKPVHSPMAGPIRAAATVPLVVISAFATLFTVWCRKQOENIYSHLDESSSESTYTAA 360
Qy 347 LPRERLPRPKVFLCYSSKDGNNMNVQCFAYFLQDFCGCEVALDLMEBPSLCREGQRE 406
Db 347 LPRERLPRPKVFLCYSSKDGNNMNVQCFAYFLQDFCGCEVALDLMEBPSLCREGQRE 420
Qy 361 LPRERLPRPKVFLCYSSKDGNNMNVQCFAYFLQDFCGCEVALDLMEBPSLCREGQRE 420
Db 361 LPRERLPRPKVFLCYSSKDGNNMNVQCFAYFLQDFCGCEVALDLMEBPSLCREGQRE 420
Qy 407 WYIOKIHESQPIIYVCSKGMKTFYDKKQYKHKGGGSGKGLFLVVASIAELROAKO 466
Db 407 WYIOKIHESQPIIYVCSKGMKTFYDKKQYKHKGGGSGKGLFLVVASIAELROAKO 480
Qy 421 WYIOKIHESQPIIYVCSKGMKTFYDKKQYKHKGGGSGKGLFLVVASIAELROAKO 480
Db 421 WYIOKIHESQPIIYVCSKGMKTFYDKKQYKHKGGGSGKGLFLVVASIAELROAKO 480
Qy 467 SSSAALSKFTIAYFPDYSCEGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPQHTR 526
Db 467 SSSAALSKFTIAYFPDYSCEGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPQHTR 540
Qy 481 SSSAALSKFTIAYFPDYSCEGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPQHTR 540
Db 481 SSSAALSKFTIAYFPDYSCEGDVPGILDSTKRYLMDNLPOLCSHLHSRDHGLQEPQHTR 540
Qy 527 QGSRRNYFRSKSGRSLYVAICNMHQFIDEBPDWFEKQFVPPHPLRYREPVLEKFSGL 586
Db 527 QGSRRNYFRSKSGRSLYVAICNMHQFIDEBPDWFEKQFVPPHPLRYREPVLEKFSGL 600
Qy 541 QGSRRNYFRSKSGRSLYVAICNMHQFIDEBPDWFEKQFVPPHPLRYREPVLEKFSGL 600
Db 541 QGSRRNYFRSKSGRSLYVAICNMHQFIDEBPDWFEKQFVPPHPLRYREPVLEKFSGL 600
Qy 587 VLNDVMCKPGEPSDCLKVEAAVLTGATGPADSOHESQHGGLDQDEARPALDGSAALOPL 646
Db 587 VLNDVMCKPGEPSDCLKVEAAVLTGATGPADSOHESQHGGLDQDEARPALDGSAALOPL 660
Qy 601 VLNDVMCKPGEPSDCLKVEAAVLTGATGPADSOHESQHGGLDQDEARPALDGSAALOPL 660
Db 601 VLNDVMCKPGEPSDCLKVEAAVLTGATGPADSOHESQHGGLDQDEARPALDGSAALOPL 660
Qy 647 LHTVAGSPDMRPRSGIYDSSVPSSELSPLMEGLSTDQETSTSLTESVSSSGLGEBE 706
Db 647 LHTVAGSPDMRPRSGIYDSSVPSSELSPLMEGLSTDQETSTSLTESVSSSGLGEBE 720
Qy 661 LHTVAGSPDMRPRSGIYDSSVPSSELSPLMEGLSTDQETSTSLTESVSSSGLGEBE 720
Db 661 LHTVAGSPDMRPRSGIYDSSVPSSELSPLMEGLSTDQETSTSLTESVSSSGLGEBE 720
Qy 707 PPALPSKLSSGSCRADLGCRSTYDELAHAVAP 738
Db 707 PPALPSKLSSGSCRADLGCRSTYDELAHAVAP 752

RESULT 14
ABB07627
ID ABB07627 standard; protein; 753 AA.


```

XX AC ABB07627;
XX 20-MAY-2002 (first entry)
XX Human cytokine receptor, Zcytor18 variant sequence.
XX Cytokine receptor; Zcytor18; cell proliferation; antiproliferative; human;
XX pulmonary alveolar proteinosis; familial periodic fever; antitumour;
XX erythroleukemia; chromosome 3p14.3; gene therapy; variant.
XX Homo sapiens.
XX Key Location/Qualifiers
XX FH Misc-difference 269 /label= T269M
XX FT /note= "wild-type Thr is replaced with Met"
XX FT Misc-difference 750 /label= V750A
XX FT /note= "wild-type Val is replaced with Ala"
XX PN WO200208259-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001MO-US023253.
XX 26-JUL-2000; 2000US-0220747P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Presnell SR., Kuestner RE, Gao Z;
XX MPI; 2002-217048/27.
XX DR N-PSDB; ABA95033, ABA95034.
XX New cytokine receptor polypeptide designated zcytor18, useful for
XX inhibiting cell proliferation associated with psoriasis or tumor growth,
XX and modulating immune system by binding to endogenous zcytor18 ligand.
XX Disclosure; Page 94-98; 119pp; English.
XX The invention relates to an isolated cytokine receptor polypeptide
XX designated Zcytor18. The Zcytor18 polypeptides can be expressed by
XX standard recombinant methodology. The polypeptides can be used to inhibit
XX cell proliferation associated with psoriasis or tumor growth. The
XX encoding nucleic acids are useful for providing Zcytor18 in vivo by gene
XX therapy techniques. Zcytor18 oligonucleotide probes are useful for in
XX vivo diagnosis, and the Zcytor18 probes and primers can be used to detect
XX and localize Zcytor18 gene expression in tissue samples. The probes are
XX also useful for detecting gross aberrations in chromosome 3 in which
XX Zcytor18 gene resides. The Zcytor18 polynucleotides can also be used in
XX linkage-based testing of pulmonary alveolar proteinosis, familial
XX periodic fever and erythroleukemia, and erythroleukemia associated with
XX polymorphisms of cytokine receptors. The present sequence represents a
XX human Zcytor18 variant amino acid sequence
XX SQ Sequence 753 AA;
XX Query Match 98.6%; Score 3891; DB 5; Length 753;
XX Best Local Similarity 97.3%; Pred. No. 0;
XX Matches 732; Conservative 1; Mismatches 5; Indels 14; Gaps 1;
XX 1 MAPMTQLCSVFTFNACLNGSQLAAAGSGRAMGVDTGSMR-----GVGP 46
XX 1 MAPMTQLCSVFTFNACLNGSQLAAAGSGRAMGVDTGSMRKAARAPRLCVANGVGP 60
XX 47 ASRNSGLVNTFFKYNCTTYLNPVGKRVADANITISQYACHDQVAVITLMSGALGIE 106
XX 61 ASRNSGLVNTFFKYNCTTYLNPVGKRVADANITISQYACHDQVAVITLMSGALGIE 120
XX 107 FLKGFVITLBEKSEGRQCOQLIKDPKQUNSSFKRTGMESQFLMMKFEITDYFVAVVPP 166

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Db 121 FLKGFVITLBEKSEGRQCOQLIKDPKQUNSSFKRTGMESQFLMMKFEITDYFVAVVPP 180
Qy 167 PSIKNESNTHPPFFRTACDILLQPDNLACKFPKPRNINISQHSQSDMOVSFPAHANG 226
Db 181 PSIKNESNTHPPFFRTACDILLQPDNLACKFPKPRNINISQHSQSDMOVSFPAHANG 240
Qy 227 FRFFVLYHLKKGHPKRTCKQOEFTETSCILQNVSGDYITELVDDTNTTRKMHYA 286
Db 241 FRFFVLYHLKKGHPKRTCKQOEFTETSCILQNVSGDYITELVDDTNTTRKMHYA 300
Qy 287 LKRVHSPMAGPIRAMAITYPLVVISAFATLFTVMCRKQOENIYSHLDESSSSSTYTA 346
Db 301 LKRVHSPMAGPIRAMAITYPLVVISAFATLFTVMCRKQOENIYSHLDESSSSSTYTA 360
Qy 347 LPERLRPPRPKVFYLCYSSFDGQNNMNVVCCFAYFLQDFCGCEVALDLMEDFSICREGORE 406
Db 361 LPERLRPPRPKVFYLCYSSFDGQNNMNVVCCFAYFLQDFCGCEVALDLMEDFSICREGORE 420
Qy 407 WYIQKHESQFTIIVCSKGMKTVDDKQYKHKGGGSGKGLFLVAVASALAEKLRQARQ 466
Db 421 WYIQKHESQFTIIVCSKGMKTVDDKQYKHKGGGSGKGLFLVAVASALAEKLRQARQ 480
Qy 467 SSSAALSKFTIAYVFDYSCGDPVGLDLSTKRYLMDNLPLQCSHLSPDHGLQEPQHTR 526
Db 481 SSSAALSKFTIAYVFDYSCGDPVGLDLSTKRYLMDNLPLQCSHLSPDHGLQEPQHTR 540
Qy 527 QGSRNRYFRSKGSLIYVAINCMHQFIDEPPMFEKQVFPFHPPLRYEPVLEKEDSL 586
Db 541 QGSRNRYFRSKGSLIYVAINCMHQFIDEPPMFEKQVFPFHPPLRYEPVLEKEDSL 600
Qy 587 VANDWCKRPSPDPLKRYAPVLCATGPADQHSQHGLQDQDGPALDGSALQPL 646
Db 601 VANDWCKRPSPDPLKRYAPVLCATGPADQHSQHGLQDQDGPALDGSALQPL 660
Qy 647 LHTVKAQSPDMPRDSGIVDSVPSSELSLPLMEGLSTQETSTLTSVSSSGLGEEB 706
Db 661 LHTVKAQSPDMPRDSGIVDSVPSSELSLPLMEGLSTQETSTLTSVSSSGLGEEB 720
Qy 707 PPALPSKLLSSGCKRADLCGRSYTDELAAVAP 738
Db 721 PPALPSKLLSSGCKRADLCGRSYTDELAAVAP 752
XX RESULT 15
XX AEB55654
XX ID AEB55654 standard; protein; 738 AA.
XX AC AEB55654;
XX 22-SEP-2005 (first entry)
XX Human DCSR8 polypeptide.
XX Protein engineering; cytokine receptor; DNA cytokine receptor subunit;
XX DCSR8; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
XX interstitial lung disorder; asthma; allergy; atherosclerosis;
XX gastrointestinal-gen.; antiinflammatory; antiaesthetic; anti-allergic;
XX antiproliferative; antitumor; antileukemic; respiratory-gen.; immunosuppressive;
XX antitumor; DCSR9 agonist; DCSR9 antagonist; IL-17C antagonist;
XX IL-17C agonist; human; DCSR8; receptor; antisense therapy; RNAi therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX FH Misc-difference 34 /label= Gln, Arg, Pro or Leu
XX FT /note= "encoded by CNG"
XX FT Misc-difference 42 /label= Lys, Arg, Thr or Met
XX FT /note= "encoded by ANG"
XX FT Misc-difference 125 /label= Ser, Gly, Arg or Cys
XX FT /note= "encoded by NGC"

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FT Misc-difference 136
FT /label= Ile, Val, Leu or Phe
FT /note= "encoded by NTC"
FT Misc-difference 150
FT /label= Leu or Phe
FT /note= "encoded by TTN"
XX MO2005065711-A2.
XX
XX 21-JUL-2005.
XX
XX 22-DEC-2004; 2004MO-US042935.
XX
XX 29-DEC-2003; 2003US-00749144.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Gorman DM;
XX
XX WPI; 2005-506792/51.
XX
XX N-PSDB; AEB55653.
XX
XX Modulating activity of cell, involves contacting cell with an agonist or
XX antagonist of DNA cytokine receptor subunit.
XX
XX Example 5; SEQ ID NO 10; 130pp; English.
XX
XX The invention relates to modulating (M1) activity of cell, by contacting
XX cell with an agonist or antagonist of DNA cytokine receptor subunit
XX (DCRS9) or of Interleukin (IL)-17C where the cell modulates psoriasis,
XX inflammatory bowel disorder (IBD), interstitial lung disorder, asthma or
XX allergy, or atherosclerosis. Also provided are methods for treating (M2)
XX the disorders which involves administration of the modulator and
XX diagnosing (M3) a disorder as mentioned above that involves contacting a
XX sample from a test subject with a binding composition that specifically
XX binds to a polypeptide or nucleic acid of DCRS9 or IL-17C. (M1) is useful
XX for modulating an activity of a cell. (M2) is useful for treating a
XX subject suffering from a disorder such as psoriasis, IBD, interstitial
XX lung disorder, asthma or allergy, or atherosclerosis, where the
XX interstitial lung disorder is idiopathic pulmonary fibrosis, eosinophilic
XX granuloma, or hypersensitivity pneumonitis. The IBD is Crohn's disease or
XX ulcerative colitis. The present sequence represents a human DCRS8
XX polypeptide.
XX
XX Sequence 738 AA:
XX
Query Match 97.2%; Score 3835.5; DB 9; Length 738;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 722; Conservative 3; Mismatches 12; Indels 1; Gaps 1;
QY 1 MAPWLOLCVFFFTVNAQINISQYACHDOVAVTILMSPGALGIEFLKGFVYLEELKS 60
DB 1 MAPWLOLCVFFFTVNAQINISQYACHDOVAVTILMSPGALGIEFLKGFVYLEELKS 60
QY 61 DNCTTYLNPVGRKIVADQNITISQYACHDOVAVTILMSPGALGIEFLKGFVYLEELKS 120
DB 61 DNCTTYLNPVGRKIVADQNITISQYACHDOVAVTILMSPGALGIEFLKGFVYLEELKS 120
QY 121 EGRQCOQLIKDKPQXNSFKRTGMSQPLNKKFETDYFVKVPPPSIKNESNYHPPFF 180
DB 121 EGRQCOQLIKDKPQXNSFKRTGMSQPLNKKFETDYFVKVPPPSIKNESNYHPPFF 180
QY 121 EGRQXOOLIKDKPQXNSFKRTGMSQPLNKKFETDYFVKVPPPSIKNESNYHPPFF 179
DB 121 EGRQXOOLIKDKPQXNSFKRTGMSQPLNKKFETDYFVKVPPPSIKNESNYHPPFF 179
QY 181 RFPACDLLQPDNLACKPFPKPRNLINISQHGSDMOVSFDHAPNNGFRFFYLHYKLKHG 240
DB 181 RFPACDLLQPDNLACKPFPKPRNLINISQHGSDMOVSFDHAPNNGFRFFYLHYKLKHG 240
QY 241 PFRKRTCKOQOTETTSCLQONVSPGDIYIELVDNTTRKVMHVALKPVHSPMAGPIRA 300
DB 241 PFRKRTCKOQOTETTSCLQONVSPGDIYIELVDNTTRKVMHVALKPVHSPMAGPIRA 299
QY 301 MAITVPLVVISAFATLFTVWCRKQOENIYSHLDESSSESTYTAALPRERLAPRPKVEL 360
DB 301 MAITVPLVVISAFATLFTVWCRKQOENIYSHLDESSSESTYTAALPRERLAPRPKVEL 359

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QY 361 CYSSKDGQNHMMVWOCFAFYLODFGCEVALDLMEDFSLCRBGOHEWVIOKTHESQPIIV 420
DB 360 CYSSKDGQNHMMVWOCFAFYLODFGCEVALDLMEDFSLCRBGOHEWVIOKTHESQPIIV 419
QY 421 VCSKMKTFVDDKNTKXKGGGSGKGEFLVAVSALAEKLRQAKOSSAALSKFLAYVF 480
DB 420 VCSKMKTFVDDKNTKXKGGGSGKGEFLVAVSALAEKLRQAKOSSAALSKFLAYVF 479
QY 481 DYSCEGDVPGIIDLSTKXRLMDNLPOLCSHLHSRPHGLQEPQHTROGSRNRYPPRSKGR 540
DB 480 DYSCEGDVPGIIDLSTKXRLMDNLPOLCSHLHSRPHGLQEPQHTROGSRNRYPPRSKGR 539
QY 541 SLTYVAICNNHQFIDEEDPWFEXQFVFPFPPRYREBPVLEKESGLVINDVWCKRGPSBD 600
DB 540 SLTYVAICNNHQFIDEEDPWFEXQFVFPFPPRYREBPVLEKESGLVINDVWCKRGPSBD 599
QY 601 FCLKYBAPVLAGATGPADSGHESQHGGLDQDGEARPALDGSALQPLHTVKAQSPSDMPR 660
DB 600 FCLKYBAPVLAGATGPADSGHESQHGGLDQDGEARPALDGSALQPLHTVKAQSPSDMPR 659
QY 661 DSGIYDSSVPSSELSLPLMEGLSTDOTETSSLTESVSSSGIGREPPALPSKLLSSGSC 720
DB 660 DSGIYDSSVPSSELSLPLMEGLSTDOTETSSLTESVSSSGIGREPPALPSKLLSSGSC 719
QY 721 KADLCGRSYTDELHNAVAP 738
DB 720 KADLCGRSYTDELHNAVAP 737

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Search completed: March 1, 2006, 10:26:10
Job time : 94 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:26:21 ; Search time 44 Seconds
(without alignments)
1613.818 Million cell updates/sec

Title: US-10-616-788-2

Perfect score: 3948

Sequence: 1 MAPMTQLGCVFPTVNAACNG.....SCKADLCGRSYDELAAVAP 738

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 80:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2993	75.8	564	2	T42695
2	169.5	4.3	846	2	T27282
3	124	3.1	718	2	T30113
4	115.5	2.9	901	2	F83781
5	114	2.9	757	2	T09081
6	114	2.9	2946	2	T00867
7	112.5	2.8	663	2	A39897
8	110	2.8	3788	2	T13960
9	110	2.8	917	2	T04661
10	109.5	2.8	3942	2	T42730
11	109	2.8	3788	2	T30851
12	108	2.7	535	2	T17212
13	108	2.7	532	2	I49239
14	106.5	2.7	638	2	D86477
15	105.5	2.7	970	2	S63059
16	105.5	2.7	1007	2	T24643
17	104	2.6	536	2	T16124
18	103.5	2.6	998	2	S37627
19	103	2.6	641	2	T05497
20	103	2.6	1462	1	B36182
21	103	2.6	1571	2	T14155
22	102.5	2.6	1571	2	T14155
23	102.5	2.6	1639	2	T50119
24	102	2.6	664	2	T51247
25	101.5	2.6	806	1	JN0612
26	101.5	2.6	807	1	I51153
27	101	2.6	786	2	T39585
28	101	2.6	813	2	B47485
29	101	2.6	859	2	A49307

30	101	2.6	930	2	A84668	Argonaute (AGO1)-1
31	101	2.6	1275	2	A38985	nucleotide exchange
32	100.5	2.5	822	2	A47485	ABR protein 1 - hu
33	100.5	2.5	963	2	AD2381	type I site-specif
34	100	2.5	901	2	JC6093	dead ringer nuclea
35	100	2.5	2437	2	S53611	MIBP1 protein - ra
36	99.5	2.5	794	2	S59069	213 protein - mous
37	99.5	2.5	938	2	T05533	hypothetical prote
38	99.5	2.5	2251	2	T24490	hypothetical prote
39	99	2.5	820	2	S33794	hypothetical prote
40	98.5	2.5	353	2	T33782	hypothetical prote
41	98.5	2.5	1121	2	T25715	hypothetical prote
42	98	2.5	787	2	T27632	hypothetical prote
43	98	2.5	794	2	T27633	hypothetical prote
44	98	2.5	828	2	A88860	protein ZC518.3 [i
45	98	2.5	984	2	A39753	protein-tyrosine k

ALIGNMENTS

RESULT 1

T42695
hypothetical protein DKFZp434N1928.1 - human (fragment)

C/Spectes: Homo sapiens (man)

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #ext_change 09-Jul-2004

C/Accession: T42695

R/Bioecker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A/Reference number: Z22230

A/Accession: T42695

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-564 <AAA>

A/Cross-references: UNIPROT:Q9UFA0; UNIPARC:UPI00006EF02; EMBL:AL133097

C/Experimental source: adult testis; clone DKFZp434N1928

A/Note: DKFZp434N1928.1

Query Match 75.8%; Score 2993; DB 2; Length 564;
Best Local Similarity 99.5%; Pred. No. 4.3e-231;
Matches 560; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	176	HPFFRTTRACDLILQDNLACRPFMRRLNLSQHSQSDVQSPDAPHPNPFPTLHYK	235
DB	1	HPFFRTTRACDLILQDNLACRPFMRRLNLSQHSQSDVQSPDAPHPNPFPTLHYK	60
QY	236	LKHGPPKRTCKQOBTETTSCLQNVSPGDIIELVDTNTRKVMHYALKPVS PMA	295
DB	61	LKHGPPKRTCKQOBTETTSCLQNVSPGDIIELVDTNTRKVMHYALKPVS PMA	120
QY	296	GPTRAMATVPLVVISAPATLFTVMCRKQOENIYSHLDESSSSTYALPRERLPR	355
DB	121	GPTRAMATVPLVVISAPATLFTVMCRKQOENIYSHLDESSSSTYALPRERLPR	180
QY	356	PKYFLCYSSKDGNNHNVVQCPAYFLQDRCGEVALDLMEDSLCEGQRENTYQKIHSS	415
DB	181	PKYFLCYSSKDGNNHNVVQCPAYFLQDRCGEVALDLMEDSLCEGQRENTYQKIHSS	240
QY	416	QPIIVVCSGKMKFVQKKNYKHKGGSGSGKELFLVAASATAEKLROAKOSSSALSKF	475
DB	241	QPIIVVCSGKMKFVQKKNYKHKGGSGSGKELFLVAASATAEKLROAKOSSSALSKF	300
QY	476	IANYFDYSCGDVPGILDLSTKRYLMDNLPOLCSHLASRDHGLQEPGQHTROGSRNRYR	535
DB	301	IANYFDYSCGDVPGILDLSTKRYLMDNLPOLCSHLASRDHGLQEPGQHTROGSRNRYR	360
QY	536	SKSGRSLVYALICMHOPIDEBPDWFEKQVPPHPPPLRREPYLEKFGDGLVINDVCKP	595
DB	361	SKSGRSLVYALICMHOPIDEBPDWFEKQVPPHPPPLRREPYLEKFGDGLVINDVCKP	420
QY	596	GPSDFCLVEAPVVGATGAPDSQHSQSGGLDQGEAPALDGSAAALPLHTTVAGASP	655

Db 421 GPESDFLKAEAVNIGATGPGADSGHESQHGLDQGEARPALDGSALQPLHTVKAASP 480
Qy 656 SDMPROSGIYDSSVPSSELPLMEGLSTPOTETSSLTESVSSSGGEEEPALPESKL 715
Db 481 SDMPROSGIYDSSVPSSELPLMEGLSTPOTETSSLTESVSSSGGEEEPALPESKL 540
Qy 716 SSGSKADLCRSYTDLHAHAVP 738
Db 541 SSGSKADLCRSYTDLHAHAVP 563
RESULT 2
T27282
hypothetical protein Y64G10A.e - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T27282
R/Alnough, R.
submitted to the EMBL Data Library, September 1999
A/Reference number: Z20336
A/Accession: T27282
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-846 <WTL>
A/References: UNIPROT:Q9NAA64; UNIPARC:UPI000007CBB7; EMBL:AL110498; PIDN:CAM54470.
A/Experimental source: clone Y64G10A
C/Genetic:
A/Gene: CESP:Y64G10A.e
A/Intons: 106/1; 196/3; 261/1; 301/3; 386/1; 416/2; 475/1; 510/3; 580/2; 815/3
C/Superfamily: Caenorhabditis elegans hypothetical protein Y64G10A.e
Query Match 4.3%; Score 169.5; DB 2; Length 846;
Best Local Similarity 21.4%; Pred. No. 4.7e-05;
Matches 141; Conservative 82; Mismatches 225; Indels 211; Gaps 37;
Qy 85 QVACHDQVATILWSPALGIEFLKGFVILELKSERQCOQLIKDPKQLNSSFRTG 144
Db 294 QY-CFEYEYERLDDSS---GIVMLQSAITKDELRTG-----ITNGRPVQFGRF----- 338
Qy 145 MESOPFLANKFETDYFVKVVPFSPISKESYHPPFFRTACDLILQPDNLAC-KPFKPR 203
Db 339 ---NFTDILDTDLPSVIPISAHN-----GRC-LCVTNGSCSLAADKPV 382
Qy 204 NLNISQSGSMQVSDFAHNFGRFYLHYKLGEGFPKRTCKOKOTETSSCLQNV 263
Db 383 KLT-----RIEKPRATSN-----QTESDGAKEKDKEDTWT----- 415
Qy 264 SPQDYILEVDVDTTRKVNH-YALKEVHSPWAGPIRAMAIVPLVVISAFATL--FTVM 320
Db 416 -----WHYVA-----ITGSAIIMLILFISVCAGLKCYKXF 445
Qy 321 CRKKQENIYSHLDESSBSTYTAALPRELRPRPVFLCYSKGQGMNNTVQCAYF 380
Db 446 NKKKASNI--HLINENPAFS-HSGSIPL-ILKOSISVLIVY-SHDSAOHEAAVLAEAL 500
Qy 381 LDPEGCEVALDLMEDSLCREGREVVIQKIHSGRIIVYCSGKMYCFYDKNKKYKGG 440
Db 501 LRDVFNINVLHDVDEDDI--EENAEYINSIVANKYIINISG-AVF--RTVFROR- 555
Qy 441 GRGSGKGLFLVNSAIAEKLRQAKQSSAALSKFIIVFYDSCGDV--FGILDLSTKY 498
Db 556 -----EPAIERITTRND-----VIDMOGELALQHPVISCFSY 591
Qy 499 -----RLMD-NLPOLCSHLHRDGLQSPGHTROGSHRNFRSKSGSLYVAI 546
Db 592 TNPKYVPFPIRRLQYSIP--NSIMTMTALTQPARPQLAGFNQVFAF-----LQAAI 644
Qy 547 CMNHQFIDBERDWEK-----QVPPHPPPIARR----- 575
Db 645 SRKLNTYESDPWENTHRRVATRRVSELAHNTVPL-PSLEKVKVDEDAFGQMETLPI 703
Qy 576 EPVLEK-----DSGLVLDVNMCKPQPSDFCLKVAVPATGATGPADSGHES 622

Db 704 DELKEFPAARKDLEVEVLSEVDKLELDYKCAFP-----IHVEPTEPVLEBAEPME 758
Qy 623 QHGLDQDEARPALDGSAA---LQPL-HYTKAGSPDMRDSGITYSS-VPSSELS 675
Db 759 AEED-REDEDVDVSVEGQTRIEELQRLIVH-----KDMHDSGNLDSATVSGSDFS 809
RESULT 3
T30113
hypothetical protein F56D1.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R/Chisoe, S.; Wilson, R.
submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid F56D1.
A/Reference number: Z20737
A/Accession: T30113
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-718 <CHI>
A/Cross-references: UNIPROT:Q10128; UNIPARC:UPI000013C0C4; EMBL:U39997; PIDN:AAA81100.1;
C/Genetic:
A/Gene: CESP:F56D1.2
A/Intons: 93/1; 121/2; 163/3; 459/1; 517/3; 555/1; 615/3; 667/3
C/Superfamily: Caenorhabditis elegans hypothetical protein F56D1.2
Query Match 3.1%; Score 124; DB 2; Length 718;
Best Local Similarity 21.1%; Pred. No. 0.16;
Matches 82; Conservative 63; Mismatches 150; Indels 94; Gaps 19;
Qy 349 RERLRPRP-----KVFPCYSKDGQGMNNTVQCAYFLQDFCGEVALDLMEDS 398
Db 398 RDRVRSREVRNIALTFVKMIVYAD-DNDLITDCYKGLVENLRKASCDDPVFDLKLT 456
Qy 399 LCREGREVITOKIHESOPFIIVCSKMYFYDKNKKYKGGSGKGLFLVAVSAIA 458
Db 457 AEGIVSRMLVQDISLKKFIIIVSDCAKILDTSETHQVQAPPADLFGPAMEMI- 515
Qy 459 EKLKQAKOSSAALSKFIIVFYSCGDV--GILDLSTKRLMDNLQOLCSHLHRD 515
Db 516 --TRDTNHPPEARKKYAAVRFNY--PHVPMLALINPT-FILPEQAQLTAFLHNV 570
Qy 516 HGLQSGQHTROGSRNRYFRSKSGSLY--VAICMHQFIDBERPWFKEQVY----- 566
Db 571 H-----TERANVTQNISBAQIHENMLCASMMSEFPVAPNFWLTKRKPDELA 619
Qy 567 FHPPLRRYRBPVLEKEDSGLVLDVNMCKPESDFCLKVAEPVATGATGPADSGHESQHG 626
Db 620 LH--LKQSPVIVPIQT-----EED--RIAAISIKYLVPPQALVDS-- 657
Qy 627 LDODGEARPALDGSALQPLHTVKAQSPDM--PDSGITYSSVSSSELPLMGLST 664
Db 658 -DED-----DVLLQF--HSHQNOPILILPPOCG-----PDS-----SD 690
Qy 685 DQETSLTESVSSSGGLEEPPALPSK 713
Db 691 SESDSSSESSESNDNG---EDPKTIVK 716
RESULT 4
F83781
transposase (08) / ABC transporter (ATP-binding protein) BH1054 [imported] - Bacillus ha
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: F83781
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and c
A/Reference number: AB36501; M0ID:20512582; PMID:11058132
A/Accession: F83781
A/Status: preliminary
A/Molecule type: DNA

A:Residues: 1-901 <STO>
A:Cross-references: UNIPROT:Q9K04; UNIPARC:UPI00000CA39B; GB:AP001510; GB:BA000004; NID:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1054

Query Match 2.9%; Score 115.5; DB 2; Length 901;
Best Local Similarity 19.8%; Pred. No. 1.1;
Matches 113; Conservative 76; Mismatches 168; Indels 215; Gaps 28;

QY 47 ASRNSGLYNTFKYDCTTYLNPVKVIAADQNIITISQY-ACHDQVAVTILMSPGALGI 105
DB 333 ALKESGL-PLPKTLIADAGYSSSNVYAMADELFETLIPS----- 371
QY 106 EPLKGFVILIELKSGR-----OCCOL--ILKPKQLANSFKTKGMSOPLANKF 155
DB 372 ---HTFR-OBQKSFAPKGRPHNRCDETDYVWCNCRKVSFKYTKRTDY---GY 423
QY 156 ETDYFV-----KVVP-PSI-----KNESNHPFPFTRACDILLQPDNLACPFMKPR 203
DB 424 ARPKVYECSCCECPKPECTKARGRQVHTNPFY-----EELKAKOQOLK 471
QY 204 NLNISQHG-----SDMVSPDAPHNFGFFPYLYLKHGEPKRTCKOBTET 255
DB 472 ---SEGRITLYQKRTDVSFVGHVKNIGFRLLHKG----- 507
QY 256 TSCILQVSPQDIYIELVDNTTRKVMYALKPFHSPWAGPIRAMAITYPLVIS-AFA 314
DB 508 -----ESVH-----IELGLVALANLR 524
QY 315 TLFTVMCRKKOENIYSHLDESESESTYTAALPRRLRPKYFLCYSSKDGNNHNV 374
DB 525 KRATVDRSKPEPNTNKHREN-----RIKRF-----SRPYVL 558
QY 375 QCF---AYFLQDFGCEVALDLMEDFSLCREGQREWY---IQKHESOPFIYVCSKGM 427
DB 559 RCFMDSFPFKSKQKQVAFALPD-KLRREGEMMLEVDLSTYNNQVY---KGIN 612
QY 428 YFVDDKNNYKHKGGSGKSELFLVAVSAI-----AEKLRQAKOSSAALSK 474
DB 613 MPEKEMVGLIPNGAGKSTTISMSLQPTSGDVLKSGSIHKSKAIRSILGVVPQ 672
QY 475 FLVVPDYSCB-----GDVPGILDLSKYRLMDNLPOLCSHLHSRHHGLOEPQHTROG 528
DB 673 ELVAVHDLTKRELAFAGKYGLKGBELKRR-WESTQLV-----GLBE-----RQN 718
QY 529 SRNRYFSKSGSLYVACMHQ---FIDEP 557
DB 719 DRVHTSGCMKRLNIAVALHBEELIMDEP 750

RESULT 5

T09081
telomere-associated reco-like helicase - smut fungus (Ustilago maydis) (fragment)
C:Species: Ustilago maydis (corn smut)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T09081
R:Sanchez-Alonso, P.; Guzman, P.
Genetics 148, 1043-1054, 1998
A>Title: Organization of chromosome ends in Ustilago maydis: reco-like helicase motifs
A/Reference number: Z16557; MUID:98198830; PMID:9539423
A/Accession: T09081
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-757 <SNM>
A:Cross-references: UNIPROT:O13399; UNIPARC:UPI000006BCA3; EMBL:AF030885; NID:g2642221;
A:Experimental source: strain FB2
C:Genetics:
A:Gene: UPASreco
C:Keywords: DNA binding

Query Match 2.9%; Score 114; DB 2; Length 757;
Best Local Similarity 20.2%; Pred. No. 1.1;

Matches 110; Conservative 56; Mismatches 188; Indels 190; Gaps 27;

QY 254 ETTSCILQVNSPDYIELVDNTTRKVMYALKPFHSPWAGPI---RAMAITYPL- 307
DB 77 ETTILIPYALNMAKIDVNN---IRYHWQF-GSKKAAPIYVSTEAATTLAFKE 131
QY 308 -----VVISAFATLFTVMCRKKOENIYSHLDESESESTYTAALP----- 348
DB 132 YANRLDQQLRDIIVIDECHLTITANSYRSMMQLANHVDVETQYTWLTATLPPIEDA 191
QY 349 -BERLRPRKVF-----LCYSSKDGNNHNVQCF-AYFLQDFGCEVALDLMEDF 397
DB 192 FISHNLTKFLYIRESTNRNLCYVTAHRSNMTCYAVAVYD-ECRARDIY--- 246
QY 398 SLCREGQREWVIOKHESOPFIYVCSKGMKYFYDK-----KNYKHKGGSGS- 444
DB 247 ---NGQRD-----RIIYCTIS--KELVARILEMGLCAVSSSESEADKAAITQ 290
QY 445 ---GKGEFLVAVSAIABLRQAKOSSAALSKFLAVVPDYSCGDPVPIIL--DISTKY 498
DB 291 DWICGKSPVIVATSA-----LGVGFDPHVRVFIHLGLPDLITDF 331
QY 499 -----RLMDNLPOLCSHLHSRHHGLOBPQHTRQGSRRNFRS 536
DB 332 SQSSGRAGRDGMARESTILAGPQDDBAP-ASGKASAEKGVAPG---ADKEMQLYRS 387
QY 537 KSGRSLYVALCNMHQPIDEEPMFEKQFVPHPPLRYRBPVLEKFDGLVNDWCKPG 596
DB 388 RK---YCLRGLVSLQDLQSDW-----RMWCEGPDQLCSVC 419
QY 597 PEEDFLKVAAPVLAGTPADSOH---ESQHGGLDODGEARPALDGAALQPLHTYKAG 653
DB 420 GGHNF-----QARGPDQPHFTAPAGAPSTQGSRRHPMGSS--HPSNR----- 463
QY 654 SPDMRDSGITVDSVPSSE-TSLPLMEGLSTQETSTSLTESVSSS---SGLGESEPPA 709
DB 464 -----GSHRPSHSGSHPSIHSGSHHSIHSS--HPSIHSGHGGGRKQKQPD 510
QY 710 LPSK 713
DB 511 PPSB 514

RESULT 6

T00867
hypothetical protein At2g45540 [imported] - Arabidopsis thaliana
N/Alternate names: hypothetical protein F17K2.7
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: T00867; G84891
R:Roundley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.
submitted to the EMBL Data Library, March 1998
A:Description: Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence.
A/Reference number: Z14207
A/Accession: T00867
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2946 <ROU>
A:Cross-references: UNIPARC:O64634; UNIPARC:UPI00000AA3F8; EMBL:AC003680; NID:g2979540; I
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: G84891
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2946 <STO>
A:Cross-references: UNIPARC:UPI00000AA3F8; GB:AE002093; NID:g2979554; PIDN:AA06163.1; G8
C:Genetics:
A:Gene: F17K2.7; At2g45540

A:Map position: 2
 A:Introns: 652/1; 913/3; 1165/3; 1210/3; 1245/3; 1283/3; 1309/2; 1336/3; 1438/3; 1638/2;
 ; 2449/2; 2481/3; 2643/1; 2890/3; 2931/3

Query Match 2.8%; Score 114; DB 2; Length 2946;
 Best Local Similarity 18.8%; Pred. No. 8.3;
 Matches 162; Conservative 105; Mismatches 315; Indels 282; Gaps 40;

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QY 2 APMLQCSVFETYNACLSQSLVAAGG-SGRAMGVDTCCMGVGRSRRSGLYNTIFKY 60
DB 393 ATATYIESPDTLTAATAAATAAATAAKSGK-----TSMASAAAAAALAG----- 439
QY 61 DNGCTTYLNPVKGKVIADQNTITISQVACHDOAVATILMSGALIEPLKGFVILELKS 120
DB 440 -EGTAHMRPLFSPLSADNNGIEAVFHA-----QPL-----VVEGSG 475
QY 121 EGR-----QC-----QOLIKDPKQLNSSFRKTMESQPLMKFET 157
DB 476 KGRKSSLHFTHAFKPCQMYEIGLEHSGCKGLGKAESELRLYIDGSLYESRPF----- 528
QY 158 DYFVKVVPFSPKSNESYHPPF-----RTRACDILLQ--PDNLACKP 139
DB 529 -----DPRISK-----PLSFCCIGTNPPTMAGLQRRRRQCPLEMGFPYIIEKPI 576
QY 200 MKPRNLNLSQHGSDMOVSPDAPHPNFGRFFYLHYKLHKGEPKRTCKOQOTTETTS-- 257
DB 577 GPRMARLARGGDVLPFCNGA---GLPHLATNDYVRN-----YAEESILDADI 624
QY 258 -----CLLONVSPGDYIIELVDTNTRK-----VMHYA--LKFVHSPWA--- 295
DB 625 GGYTHLLYHPCLLSGRCPD--ASLSGAGTLRRPAVLQGVHVAATMKKEVESFMALAYG 682
QY 296 GPIRAMAITY-----PLVVISAFALFTVM-----CRKQ 335
DB 683 GPMISLPLTVSVHKSLEPCLGNLPLSLSTVTLAAVFRIMSYAIOHPANNEELCTQG 742
QY 326 QE---NIYSHLDESSSESTYTAALPRELRPRPKVLCYSSKDGQNNHNVOCFAVFLQ 382
DB 743 PELIARLSTYLHSLASLDKRDGVGEEL--VAIVSLCQSQK--INHVLKVLFRLL 799
QY 383 DFCGCEVALDLMEDFSLCREGQREVIQKIHESQFIIVCSKGMK-----YF 429
DB 800 D-----LKIM---SLCNYGLQKQLSLQDMVFTATAMRDEALIQLLDGCRCYMM 849
QY 430 VDKK---YKHGGCGSGSGKGLFLVAVAIAEAKLQAKQSSAA--LSKFLAVYDYS 483
DB 850 ISEKDSSTTPDLGNTRQMGELNALIDELLVITELMGASPSLAADLERLLGFIIDSP 909
QY 484 CEGDVPGLDLSSTKYRLMDNL--POLCSHLHRDHLQOE---PGQHTROGSRNRYFSK 537
DB 910 QPNQVAVRLHMLRLVVOQPAARAQMAFAVFTISGIEITLLVLQREAKTGEDNVLAMGR 969
QY 538 SGRSLYVAICNMHOFIDEEPDMWEKQVPPHPPRLRYREPLVEKFDGSLVANDV-MCKPG 596
DB 970 SGRK-----SSTDPSKES--PYN-----ESGSYKQLDNPNDNEIGFDLP 1008
QY 597 PESDFCLKVEAPVLGANG--PADSQHESQHGGLDQDGAARALDGSALQLQLHTVKAQSP 655
DB 1009 PDGN---SVEDDNGSLNVPESVQKEKHG-----STP 1038
QY 656 SDMPRDSGIVDSVPSSELSLPLMEGLSTQDETSTSLTESVSSSGGLGE---EEPPA-- 709
DB 1039 VVCDSDSVSISNNTIRLS-----AEIGGISLISADSAANNVYNDNSDAV 1087
QY 710 -----LPSKLLSSGSCADLGCAS 728
DB 1088 VGIIRLIGALISSGHLTFDPDARS 1111

```

RESULT 7
 A39897
 GTPase-activating protein RAP1GAP short form - human
 C:Species: Homo sapiens (man)

C>Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 05-Oct-2004
 C:Accession: A39897
 R:Rabinfeld, B.; Munemitsu, S.; Clark, R.; Conroy, L.; Watt, K.; Crozier, W.J.; McCormick
 Cell 65, 1033-1042, 1991
 A:Title: Molecular cloning of a GTPase activating protein specific for the Krev-1 protein
 A:Reference number: A39897; PMID:1904317
 A:Accession: A39897
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1663 <RUB>
 A:Cross-references: UNIPROT:P47736; UNIPARC:UPI000013381A; GB:M64788; NID:G190855; PDB:
 C:Superfamily: Rapi GTPase-activating protein

Query Match 2.8%; Score 112.5; DB 2; Length 663;
 Best Local Similarity 19.7%; Pred. No. 1.2;
 Matches 144; Conservative 80; Mismatches 261; Indels 247; Gaps 33;

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QY 153 MKFETDYPVKVVPFSPKSNESYHPPFRTACDILLQPD----- 192
DB 21 LKTEBDY-----IPYSEV-----HEVLGRGEPPLILPQFGGYWIGTNNHITSIPETE 70
QY 193 -----NLACKP-----FKPRNLNLSQHGSDMOVSPDAPHPNFGRFFYLHYK 235
DB 71 PLQSPPTTKYKLECNPTARIYRKHFLGKEHFN-----YSLDTA--LGHVLFSLKXD 119
QY 236 L-----KHGEPFKRTCKOQOTTETTSCLLONVSPGDYIIELVDTNTRKRMHYALKPVH 291
DB 120 VIDQSHLLKLLRTKRTYTHDYLPISLTEPRVNVQMACLVCEADVADR-----FYPL 173
QY 292 SPWAGPIRAMAITYPLVVIS--APATLFTVMCKRKKQDNIYSHLDESSSESTYTAALP 348
DB 174 YPKAS---RLIYTPDEHVISNNKFGVITYQKQGTSEB---LFTSEBSAPAFVFLIE 225
QY 349 RERLRPRPKVPLCYSSKDGQNNHNVOCFAVFLQDPGCEVALDLMB---DFSICR-- 401
DB 226 -----FLGQKYK-----LQDPKGRGGILDVTHGQTGESVYCNRR 260
QY 402 -----EGREBNVLOKIHESQFIIVCSKGMKFFVNDK-----KMYK 436
DB 261 NKEIMFHVSTKLPYTGDAQOLQKRNHIGNDIVAN-----VFQDENTPVPDMTASNL 314
QY 437 H-----KGGRGSGKGLFLVAVASAIAE-----KLQAKQSSSALSKFLTA 477
DB 315 HAVVVVQABGGG---PDGFLPKVSVTARDDVPPFGPRLPDPAVFRKGPFOEFLTKLIN 371
QY 478 VYFDYSC-EGDVPGLDLSSTKYRLMDNLPOLCSHLHSRD-HGLQEPGQHTROGSRNRYF- 534
DB 372 A--EVACYAERKAKLEERTRALLETLYEEL-HIHSQEMGIGDGEDKENGSGGGGFF 428
QY 535 -----RSKSGREL-----YVAICNMHOFIDEEPDMWE---KQVFPHPPLR 573
DB 429 ESFKRIVIRRSQGMADMGSLNKKENTVSTSHSGSPAPNNPDLAKAAGILYIPGSKPTPK 488
QY 574 YREPVLEKPDGSLVANDVCKPESDFCLKVEAPVLGATGPADSHESQHGGLDQDGA 633
DB 489 KSGPFGSRRSSAIGIENI-----QEVQEKESPPAGKTP--DSGHVQEPKSE----- 535
QY 634 RPAIDGSALQLPLHTVYKAGSPDMPRDSGIVDSVPSSELS-----LPLMEGLSTQDE 688
DB 536 ---NSTOSPEMPPTTKRAETAAQRAALXDFSSSSSSASFSASVETETEDVDEBDG 591
QY 689 TSS-----LTSVSSSSG-----LGEBPPLPSKL 714
DB 592 LBSVSSSGTPPHKRDSTIYSTWLEDSVITSSGSSPPSPSPHPHDAGKLDPAPEIKIQ 651
QY 715 LSSGSCADLGC 726
DB 652 EASGCHMPQLGC 663

```

RESULT 8
 T13960
 beige protein homolog - rat

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Sep-1999 #sequence_rev: 20-Sep-1999 #text_change: 09-Jul-2004
 C/Accession: T13960
 R/Mori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.
 submitted to the EMBL Data Library, November 1998
 A:Description: Deletion in the beige gene of the beige rat due to recombination between
 A:Reference number: Z17637
 A/Accession: T13960
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-3788 <MOR>
 A:Cross-references: UNIPROT:Q922X9; UNIPARC:UPI000005B7B; EMBL:AB020019; NID:d1241953;
 A:Experimental source: strain DA; spleen
 C/Genetics:
 A:Gene: beige

Query Match 2.8%; Score 112.5; DB 2; Length 3788;
 Best Local Similarity 19.9%; Pred. No. 16;
 Matches 146; Conservative 98; Mismatches 260; Indels 231; Gaps 40;

QY 20 GSOLAVAGSGRAMGVDTGCMR--GVGPASRNSGLYNTFKDNCCTTYLNPVGKAVIAD 77
 DB 651 GERTLOGTLCAGSGSCGLPSPSYRFOGILP---SSGSDFLMKDLEAYONFIQOE--DR 705
 QY 78 AONITISQVACH--DOVAVTILMSRGLGIEFLKGFVILBELKSEG---RQCQOLILK 131
 DB 706 LHNTQJASHICNLIQKGNVIVQW-----KLNYITNPVQKQVGVHHCQQLSI- 754
 QY 132 DPKOLNSPFRGTGMEQPFANMKRET-DYFVKVVP-----PPSILN-----ESN 174
 DB 755 -----TSAQTHMSQGLKQYLPEVGLQIYIKLPIILKSRVIRDLFLSCNGVNHIELN 807
 QY 175 Y-----HPR-FRTTRACDILLQPDNLACRPFMKPRNLNISQHSQDMQVSPDHAHNFGE 227
 DB 808 YLDGISHSHAKAETLIVSLGEQOKRAAVPGV--DELIDIQEILSSISV----- 853
 QY 228 RPFYLYKLGHEPFRKTKCKQEGTETTSCLQNSPQDYIIELVDTNTTKRMVYAL 267
 DB 854 -----SPSLHK-----QOASTDPSCLSK-----FYASLRITDPKRTVHQ-- 890
 QY 288 KPVHSPWAGPIRAMAIVPLVVISAPATLFTVMCRKKQENITYSHLDESSSESTY--TA 345
 DB 891 -----DHNTINIFLCVAF-----LCVSGEADSDRESAN--ESEDTSIGYSTA 932
 QY 346 ALPERELRPPKVPFLCYSSKQGNHNNV---QCFAYFLQDFCGCEVALDLWEDFSLCR 401
 DB 933 SEPLSHMLPRLSL-----ENVVLPSPSCLHH-----AADIW---SMCR 967
 QY 402 EGGRBNV--IQKHESQFI---IVGSKGKTPVQKQYKHKGGSGKGLF----- 450
 DB 968 -----MYMLNSVFOKQFHLRGFOVCH-LIFMILOKFRSHTEDEGRGQEGSVNKKQ 1021
 QY 451 -LVAVSAIAEKLRQAKOSSAALSKPIAVYFDYSCEDVPGILD-----LSTK----- 497
 DB 1022 GLKRISOPEMILKEDVSSSTAPEPGFLKASADRYSELESQMLPTSAQOLATISITGEA 1081
 QY 498 -----YRLMDNLPOLCSH---LHSRDHGLQEPGQHTROGSRNRYFRSKGR 540
 DB 1082 KTFPMQESFETCQSIRLLESLALICLHSABASQOKMELPSQ-----SL 1126
 QY 541 SLVVAICMNHQPIDEEP-----DMFEKQFVFPHPPLRYRPPVLEKEDSGVLN 589
 DB 1127 SLNNTICELADHLSQSKVAETELAKPLFDALLRVALGNHSAIDLPGDVTYEKSHPS--E 1183
 QY 590 DWACKQFESDFCLKVE-----APVLGATG--PADSOHSSOHGGLDQDEAPALDGS-S 640
 DB 1184 RYLSQSG--DFSEBAEDSQCCSLKLGEEBEGYEADESINPDQGETDDGVEPLBAEGFS 1240
 QY 641 AALQP--LHHTVXAG 653
 DB 1241 GSIVPNNLLESLTHG 1255

RESULT 9

T04661
 hypothetical protein F8D20.70 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_rev: 23-Apr-1999 #text_change: 09-Jul-2004
 C/Accession: T04661
 R/Bevan, M.; Rose, M.; Hempel, S.; Entlian, K.D.; Jesse, T.; Hejnen, L.; Vos, P.; Mewes,
 submitted to the Protein Sequence Database, July 1998
 A/Reference number: Z15381
 A/Accession: T04661
 A/Molecule type: DNA
 A/Residues: 1-917 <BEV>
 A:Cross-references: UNIPROT:O81789; UNIPARC:UPI00000A12E3; EMBL:AL031135
 A:Experimental source: cultivar Columbia; BAC clone F8D20
 C/Genetics:

Query Match 2.8%; Score 110; DB 2; Length 917;
 Best Local Similarity 17.9%; Pred. No. 3;
 Matches 162; Conservative 129; Mismatches 294; Indels 322; Gaps 40;

QY 19 NSQOLAVA--AGSGRAMGVDTG-----W--RGVGPAS 48
 DB 92 NSGRVSVGYSNGDILWISIPSKGEGSPSSAMICKNLGYKSKRIPASLKMYABGKAS 151
 QY 49 R-----NSGLYITFKYDNCCTTYLNPVGKAV--TADQNI--TISQVACHQDVAVTIL 97
 DB 152 RYVVISSSSSLQVVLNDEGTETRMKLGHVSEPCADMEMIADVNEGSKHQDPLFVL 211
 QY 98 WSPGALGI--EFLKGFVILBELKSGRQCQQLIKDPQOLNSPFRGTGMEQPF--FLNM 153
 DB 212 GKSGRYAVDYDVIIEKYLLOSQSKSSPSLPKETVVLKLPFSDSSTITWGKFLTPSHLNL 271
 QY 154 KEPTDY-----FVKVVPSPSINSESN---YHFEF-----FRTTRACDILLQPDNLACK- 197
 DB 272 SDE-DYLAQAKDVAVPLPHTVPEKSSRSNHPGFGRVKNVYITGHCDDGTISVWDMTCSP 330
 QY 198 -----PMKPR-NLINSQHG-----SDMQVSPDHAHNFGRPFYLYKLGK-- 238
 DB 331 PIVLFLKQIDQDDVSRGKALATLALHYDSNGLLYSGDNGVRLRYRPFYLTENSF 390
 QY 239 ---EGPFKR-----KTCQEQETETTSCLQNVSP-----GDYIIELVDTNTT 279
 DB 391 IPRQSLKKGNNHI VQSVKIKLTSITTCIQKQNSKHLAIGSDGHSLEVID----- 445
 QY 280 RKMVHALKPYHSPMAGPIRAMAIVPLVVISAPATLFT----- 318
 DB 446 -----ALTPVY-----LOVSLVIEBANVLYKHLASDICPGIISLQFESCIY 488
 QY 319 -----VMCKKQENITYSHLDESSSESTYTAALPRELRPPKVPFLCYSSKQGNHNN 372
 DB 489 QGEEKVLLVAVWEDSSVFA-LDSDTGNMIGTMIRK-----KPKVLYVQIILDK- 558
 QY 373 VVOCFAYFLQDFCGCEVALDLWEDFSLCREGQREWYIQKHESQFIIVCS----- 423
 DB 539 -----QDTSG-----NGFPTSRES-----IYEISIRQPSVLVCSBRAIYISL 577
 QY 424 ---KGMKTPVQKQYKHKG-----GGRGSGKELPLVAVSALAE-----KLAQAKQ 466
 DB 578 AHVVOGVKVKLAKKKKSSSPICSAFTYGTSGVG--LTLVFTDGTVEIRSLPELSQLAQ 634
 QY 467 S-----SSAALSKPIAVYFDYSCED-----VPGILDSTKRLMDNLPOLC 508
 DB 635 TSIRGFTYSSPKNSLPETITISAMGDLLVMVNGDELLVSSVLPQKETPRVLVESH----- 680
 QY 509 SHLSRDHGLQEPGQHTROGSR--NFRYSKSGSLVVAICMNHQPIDEEPPWFEK 562
 DB 691 NRYKKDQNSVCHGIIITSSSPREKSKMFGSVFRTKSKRTTDPBSSKTEBELSKIFST 750
 QY 563 QFVPF-----HPPPLRYRPPVLEKFDPSGL----- 586

Db 751 ANPMMNNVNSREINTITRVEDEBELDIDIDIDHHPNQOQOEKKEGIIISGSKK 810
 Qy 587 VLNDWMCKPPEBDFCLKVAEPAVLGATGPADSGHESQHGL-----DQDGEA 633
 Db 811 MARFSPFKCKLQOMAKNKKSVV---TYDEKREKNGATVDQIKKKYGTSSDEMGAA 866
 Qy 634 RPLDGSALQLPLHTVTKAGSPDMPRDSGIYDSSVSPSELSPLMEGSLTDQETSSLT 693
 Db 867 KMA-----QSKLQD-----NLKKGISLRTTEWEDTA 894
 Qy 694 ESYVSSS 700
 Db 895 KSFSSTA 901

RESULT 10 142730

Bassoon protein - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T42730
 R/Dieck, S.; Sammarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex, J. Cell Biol. 142, 499-509, 1998
 A/File: Bassoon, a novel zinc-finger CAG/glutamine-repeat protein selectively localized
 A/Reference number: Z2249; MUID:98345363; PMID:9679147
 A/Accession: T42730
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-3942 <DIR>
 A/Cross-references: UNIPROT:O88737; UNIPARC:UPI0000029B58; EMBL:Y17034; NID:G3413809; PI
 A/Experimental source: strain 129 SVJ
 C/Genetics:
 A:Map position: 9P1
 A:Intons: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
 A/Note: Bassoon
 C/Function:
 A:Description: may be involved in cytomatrix organization at the site of neurotransmitter
 A/Note: component of the presynaptic cytoskeleton
 C/Keywords: coiled coil; zinc finger

Query Match 2.8%; Score 109.5; DB 2; Length 3942;
 Best Local Similarity 19.0%; Pred. No. 29;
 Matches 56; Conservative 28; Mismatches 111; Indels 99; Gaps 9;
 Qy 502 DNLPOLCSHLSDHKGIOEGQHTROSSRNRYFRSKSGSLYVAIC-----NMHQFIDE 556
 Db 3535 DTCPQFCS-----SHMPDVQEHVKQGPRAHAYKREGVMLDSDHCVSDSEAYHLGOEB 3589
 Qy 557 PDMPFK-----QVPRFHPPLRYRBPVLEKPKDGLVL 588
 Db 3590 TDMFDKPRDARSDFRNHGHVTVSSQKGRPARHSTYDDEPP---EEGLMPHDEGPG 3645
 Qy 589 NDWMCK-----PGESDFCLKVEAPVL 610
 Db 3646 RHNSAKENRHSDHGRHSGHAGEPRRAAKPHARMGRHARPHQAS-----PAPAM 3700
 Qy 611 -----GATPADSQHESQ-----HGLDDGEARPLDGSALQLPLHTVTKAGSPSDMP 659
 Db 3701 QKKQGPYPSSADYSSQSSRAPSAVNHASBKSGRQHNTGSPALQPVADTQAPOMQGRQ 3760
 Qy 660 RBDGIYDSSVSPSELSPLMEGSLTDQETSSLTESVSSSSSGIEEPRPLPK 713
 Db 3761 AADPGQSGPPSSRQT---PSGTASRQPTQOQOQOQOQOQGLGQAPQAPSQ 3811

RESULT 11 T30851

lysosomal trafficking regulator, long splice form - mouse
 N:Alternate names: beige protein house
 C/Species: Mus musculus (house mouse)
 C>Date: 23-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T30851

R:Barbosa, M.D.F.S.; Tchernev, V.T.; Kingmore, S.F.
 submitted to the EMBL Data Library, September 1996
 A:Description: Two bg or not two bg? longest isoform of mouse Lysc (beige) gene.
 A/Reference number: Z20903
 A/Accession: T30851
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-3788 <BAR>
 A/Cross-references: UNIPROT:P97412; UNIPARC:UPI0000028F2F; EMBL:U70015; NID:G1813541; PI
 A/Experimental source: strain C57BL/6J
 C/Genetics:
 A:Gene: Lysc
 A:Map position: 1
 C/Keywords: alternative splicing

Query Match 2.8%; Score 109; DB 2; Length 3788;
 Best Local Similarity 19.8%; Pred. No. 30;
 Matches 157; Conservative 104; Mismatches 282; Indels 250; Gaps 45;

Qy 20 GSQIAVAAAGSGSGRAMGVDTGWR--GVGPASRNSGLNYTPKYDNTTYLNPVKHVIAD 77
 Db 651 GRTLGTLGCAPTSLPSPSTRFGILP---SSGSEDLMKDLEAVQSVFQGE--DR 705
 Qy 78 AQNTTISOYACH--DQAVTILMSPGALGIBLKGFRTVLEELKSEG---RQCOQLIK 131
 Db 706 LNHITQIANHCMLQKGNVYVQW-----KLYNYIFNPVLQGVLELVHHCQQLSIP 755
 Qy 132 DPKQNLNSFKRKGMEQPLNKKFET-DYFVAVVP-----FPGIKR-----EEN 174
 Db 756 S-----AQTHMCSQLKQVLPQEVLAQLYLTKLPALKRSVIRDLFSLSCNGVNHILELN 807
 Qy 175 Y-----HPF-FPRTACDLLOPDLNACKPFKPKRNLNISQHSMDQVFSFHAPNFGF 227
 Db 808 YLDGIRSHLKAETIIVLGEQKDAVLVD--DGLDIOQELBELSV-----853
 Qy 228 RFFYLHYKLHSGPFRKTKCKOQTETTSCLLQNVSPEDYIIELVDDNTTRKVMHYAL 287
 Db 854 -----GPSLHK-----QNASDPSCLRK-----FASLREPPPKRKTTH--- 889
 Qy 288 KPVNSWAPRITAMATTVLVVISAATLPTWCKRQKQOENIYSHDESSBSSTYTAAL 347
 Db 890 QDVA-----INTIMFLCVAF-----LCVSKEDS-----DRSNAESBDTSGY 928
 Qy 348 PRERLRPKPVFLCYSSKQGOHNNVY---OCFAFLDPCGEVALDLMEDPFLCREG 403
 Db 929 DSRPSRPLSHMLPCLSLD-----VLPSPCLNH-----ADIIW---SWCR--- 967
 Qy 404 QREWV--IQKHESQFI-----IVVCSKMKYFVDKKNYHKKGGSGKGEFL-----L 451
 Db 968 ---WYMLNSVFQKHRLGFGVQVCH-LIFMIIQKLFPSHTEQGRQSGEMSRNNOEL 1023
 Qy 452 VAVSAIAELKRAQKSSSAAALSKFIIVFYDSCGVPRIL--DLSTKRYMDN----- 503
 Db 1024 IRIS-----YPELTLKGVSSATAPDLGLFKKSDSVFGQS 1060
 Qy 504 ---LPQLCSHLNRDGLQEPQHTROGSRNRYFRSKSGSLYVAICNMHQFIDEPRWF 560
 Db 1061 QPVLTSAQIYATF---SVPRG-----KRAFMSQOSETSLQSTRLESILD----- 1104
 Qy 561 EKOFPVHPPLRYRBPVLEKPDGLVNDVMCK-----PGESDFCLKY 605
 Db 1105 ---ICLHARACQOQMELELPSQGLSVENICELEHLSQSKVAETELAKPLFDALLNV 1160
 Qy 606 EAPVLC---ATGPADS---QHESQHGLDDGEARPLDGSALQLPLHTVTKAGSPSD 657
 Db 1161 ---ALGNHSDADLCPGDAVTEKSHPSSEELISQPGDSEBARSDQCCSLKLGEBEYED 1217
 Qy 658 M---PRDSGIYDSSVSPSELSPLMEGSLTDQETSSLTESVSSSSGLGE---EPPPALP 711
 Db 1218 SSSNPDVDVTDQDGV---ELN-PEAEGFS-GSLVSNMLLENLTH---GEIIPYICMLG 1268
 Qy 712 SKLLSGSCKADL 724


```

Db      365 HQYHCKKCNVSHVCAGSLRDLDAHNR-----HTLLISPSGKCCSACGREST 416
Qy      253 TETTSCLLQNVSPGDYIIEIVDDTTTRKVMYALKPVSPMAGPIRAMAITYPLVVIS 312
Db      417 GFSYIC--SNKGCODFLDV-----RCISVLEVFIRHSH-----PIFIST 457
Qy      313 PAFLLFWCKKQKQENIYSHLDESSSE--SSTYTA--LPRE---RLRPRKVPFLCYSSKOG 367
Db      458 YNSKDELICVCKKRCIGALQCTLCFTWCYSCTAIIPDIHYKFPDKHPLTSCGSAD- 516
Qy      368 QNHMNVVQCFAYFLADPFCGCEVALDLMEDPSLCREGREWVIOKIHESQPIIVVCSKGMK 427
Db      517 -----NYTWCEV-----CEKOLDPKEMWPTCNK-----CCITIH-----LHCIFGSS 553
Qy      428 YFVDDKKNYKKGCGKSGKGEFLVAVSAIAEKLROAKOSSAALSKEFLAVVDPYSCGD 487
Db      554 VFM-----KPG-----SIIPDYGKVKQ 570
Qy      488 VPGIIDLSTKYRLMDNLPOLCSHLHSRDHGLQERQHTRGSRNR--YPRSKSGSLY-V 544
Db      571 V-----FRNNSYTRQLCYMCHNCTGL-----IFEGYRNMATYYNHSNRSTHRM 616
Qy      545 AICNM 549
Db      617 IFCSL 621

```

RESULT 15

863059

hypotheetical protein YNL118c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypotheetical protein N1917

C:Species: Saccharomyces cerevisiae

C:Date: 27-Apr-1996 #sequence, revision 03-May-1996 #text, change 05-Oct-2004

C:Accession: S63059; S59701; S67340

R:De Antoni, A.; D Angelo, M.; Dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, G.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63047

A:Accession: S63059

A:Molecule type: DNA

A:Residues: 1-970 <DEA>

A:Cross-references: UNIPROT:P53550; UNIPARC:UPI000000056F; EMBL:Z71394; NID:G1302044; PI

R:Experimental source: strain S288C

R:Tzagoloff, A.A.

submitted to the EMBL Data Library, June 1995

A:Description: Suppressor of a yeast pet mutant.

A:Reference number: S59701

A:Accession: S59701

A:Molecule type: DNA

A:Residues: 1,424,'U',426-970 <TZA>

A:Cross-references: UNIPARC:UPI0000168DB7; EMBL:LA3065; NID:G870733; PID:G870734

A:Experimental source: strain D273-10B

R: d'Antoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, G.

submitted to the EMBL Data Library, February 1996

A:Description: The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces ce

A:Reference number: S67327

A:Accession: S67340

A:Molecule type: DNA

A:Residues: 1-970 <DAN>

A:Cross-references: UNIPARC:UPI000000056F; EMBL:Z69382; NID:G1183941; PID:e221828; PID:G

C:Genetics:

A:Gene: SGD:PSU1

A:Cross-references: SGD:S0005062; MIPS:YNL118C

A:Map position: 14L

F:129-163/Domain: mult domain homology <MUT>

Query Match 2.7%; Score 105.5; DB 2; Length 970;

Best Local Similarity 19.7%; Pred. No. 7.6; Indels 213; Gaps 30;

Matches 112; Conservative 72; Mismatches 171; Indels 213; Gaps 30;

Qy 260 LQNVSPGDYIIE--LV-----DQNTTRKVMYALKPVSPW--AGPIRAMAITYP 306

Db 9 LENVTSVDRLELDLVRFIINCNEEDLSVERELFHE-----EASWFTYDFIKLMPPTLP 64

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Qy      307 LVVISAFAFLFWCKKQKQENIYSHLDESSSESTYTAAP-----RELR----- 353
Db      65 SLKISFAQLIITKLCPLWKMDI--RVDAALQOFSTKYSIPVRGAIAINENLSKLLVQ 122
Qy      354 -----PRPRVFLCYSSKQGNMNVQCFAYFLADPFCGCEVALDLMEDPSLCREGO 404
Db      123 GRESDSWSPGKLI-----SKD-----ENDIDCIREVKE-----EIGFDLTD----- 160
Qy      405 REMVIOKHESQPIIVVCSKGMKTFYDDKKNYKKGCGKSGKGEFLVAVSAIAEKLROAKOSSAALSKEFLAVVDPYSCGD 457
Db      161 -----YIDNDFI-----ERNIOGNK-----IFLISGVSEVFNFKPQ 194
Qy      458 -----AEKLR--QAKOSSAALSKEFLAVVDPYSCGD 487
Db      195 VNRNEIDKIEWPDPFKLSKTMYSNITKYILNSMMPRLSMWLHQROIKNEIDLKSTAEQ 254
Qy      488 VPGIIDLSTKYRLMDNLPOLCSHLHSR-----DHGLQEPGQHTR 526
Db      255 LKLLIGI-TKEGQIDPGRLELMLHTAVQANSNNNAVNSQGVPSQELQHLKEQSGEHNQ 313
Qy      527 QGSRNRYFYSKSGSLYVAICNNHQFIDEEPWFQVFPFHPPPLRYEPPVLEKEDSG- 585
Db      314 QKDQSSFSQOQPSIFPSL-----SEPPANNKNTI---PPTW-----PMANVFMSP 358
Qy      586 ---LVNDVCKKPGP-----ESDFCLKVAAPV-----LGATGPADSGHESQHGGLDQD 631
Db      359 QLPATMGPPAPFPFPMLEPLTNNNSANPIPTVPNPAPAPNPAPFVPMNHN----- 412
Qy      632 EARPALDGSAAALQPLHTVKAQSPSDMPDPSGIYDSSVPSBSLSPLMEGLSTDQETSS 691
Db      413 -----LSGPVAVQPF-----SLPPAPLPDSDG-YSSSSSGQLL-----D 445
Qy      692 LRESVSSSGLGEBEPALPSKLSGS 719
Db      446 IINSKKPDSNVQSSKKPKL-KILOKGT 471

```

Search completed: March 1, 2006, 10:30:58
 Job time : 49 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 10:24:46 ; Search time 232 Seconds
(without alignments)
2244.310 Million cell updates/sec

Title: US-10-616-788-2
Perfect score: 3948
Sequence: 1 MAPWLCVFFVFNACLNG.....SCRADLCGRSYTDELHVAAP 738

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3912	99.1	739	2	Q8NFS0_HUMAN
2	3908	99.0	739	2	Q8NFM7_HUMAN
3	3716	94.1	707	2	Q58E27_HUMAN
4	3706	93.9	707	2	Q6RVF4_HUMAN
5	3681.5	93.2	728	2	Q6UW15_HUMAN
6	3396.5	86.0	738	2	Q8JZL1_MOUSE
7	3158	80.0	595	2	Q8N113_HUMAN
8	2993	75.8	564	2	Q9UPA0_HUMAN
9	2893	73.3	741	2	Q7T2L7_CHICK
10	2828	71.6	697	2	Q8AV76_CHICK
11	2665.5	67.5	594	2	Q8K447_MOUSE
12	2606.5	66.0	582	2	Q8R5J8_MOUSE
13	1966	49.8	745	2	Q8QHQ9_BRARE
14	1957	49.6	745	2	Q8QHQ6_BRARE
15	1335	33.8	470	2	Q4RLH0_TETNG
16	1325.5	33.6	445	2	Q4VBV6_BRARE
17	543	13.8	109	2	Q8HXE8_MACFA
18	313	7.9	866	1	117RA_HUMAN
19	298	7.5	864	1	117RA_MOUSE
20	202	5.1	769	2	Q69HQ3_CICOTN
21	169.5	4.3	846	2	Q9NA64_CABEL
22	165	4.2	50	2	Q4T7L3_TETNG
23	153.5	3.9	831	2	Q6OXB5_CAEHR
24	134.5	3.4	502	1	117RB_HUMAN
25	127.5	3.2	210	2	Q5NUJ0_FUGRU
26	127.5	3.2	443	2	Q61GL7_CAEHR
27	124.5	3.2	990	2	Q7PWU5_ANOGA
28	124	3.1	718	1	YSO2_CABEL
29	121.5	3.1	1190	2	Q6H470_ORYSA
30	120.5	3.1	1081	2	Q5NRP3_SOLDE
31	120	3.0	1376	2	Q4N457_THERA

32	117.5	3.0	617	2	Q8K4C1_MOUSE	Q8K4C1_mus musculus
33	117.5	3.0	2317	2	Q4SH16_TETNG	Q4SH16_tetradodon n
34	115.5	2.9	637	2	Q6AZ51_RAT	Q6AZ51_rattus norv
35	115.5	2.9	901	2	Q9KE04_BACHD	Q9KE04_bacillus ha
36	115	2.9	726	2	Q6A063_MOUSE	Q6A063_mus musculus
37	115	2.9	859	1	MYRIE_HUMAN	Q6A063_mus musculus
38	115	2.9	859	1	MYRIE_HUMAN	Q6A063_mus musculus
39	115	2.9	1202	2	Q4QEP5_LEIMA	Q4QEP5_leishmania
40	114	2.9	539	2	Q4NSA6_THERA	Q4NSA6_thelateria p
41	114	2.9	757	2	Q13399_USTMA	Q13399_ustilago ma
42	114	2.9	2946	2	Q64634_ARATH	Q64634_arabidopsis
43	113.5	2.9	549	2	Q8KGB4_CHLOB	Q8KGB4_chlorobium
44	113	2.9	4736	2	Q7YT99_MYTGA	Q7YT99_mytilus gal
45	112.5	2.8	562	2	Q9J755_HUMAN	Q9J755_homo sapien

ALIGNMENTS

RESULT 1					
ID	Q8NFS0_HUMAN	PRELIMINARY;	PRT;	739 AA.	
AC	Q8NFS0;				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DE	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Gilbert J.M., Gorman D.M.;				
RL	Submitted (JBC-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AF458067; AAM77571.1; -; mRNA.				
DR	Ensembl: ENSG00000144730; Homo sapiens.				
DR	GO: GO:0016020; C:membrane; IEA.				
DR	GO: GO:0004888; F:transmembrane receptor activity; IEA.				
DR	GO: GO:0006954; P:inflammatory response; IEA.				
DR	InterPro: IPR000157; TIR.				
DR	SEQUENCE: 739 AA; 82440 MW; 1670803DDDCD0F17 CRC64;				
Query Match 99.1%; Score 3912; DB 2; Length 739;					
Best Local Similarity 99.3%; Pred. No. 2.7e-284;					
Matches 733; Conservative 1; Mismatches 4; Indels 0; Gaps 0;					
QY	1	MAPWLCVFFVFNACLNGSOLAVAGSGRAMGVDTGMRGVGPARSRNSGLNITFKY	60		
DB	1	MAPWLCVFFVFNACLNGSOLAVAGSGRAMGVDTGMRGVGPARSRNSGLNITFKY	60		
QY	61	DNCTTYLNPVQKIVYADQNIITISQVACHDOQVAVTILMSGALGIEFLKFRVILELKS	120		
DB	61	DNCTTYLNPVQKIVYADQNIITISQVACHDOQVAVTILMSGALGIEFLKFRVILELKS	120		
QY	121	EGROCOQQLIKDPKOLNSFFKRTGMSQPLNKFETDYVKKVPSPINSNTNHPFF	180		
DB	121	EGROCOQQLIKDPKOLNSFFKRTGMSQPLNKFETDYVKKVPSPINSNTNHPFF	180		
QY	181	RTAACDILLQPDNLACPKFPKPNLINSQHSQMOVSPDAPNFGRRFFYLHKLKHG	240		
DB	181	RTAACDILLQPDNLACPKFPKPNLINSQHSQMOVSPDAPNFGRRFFYLHKLKHG	240		
QY	241	PFKRTCKOQOTETTSCLQNVSPGDIIELVDDNTTRKVMHYALKPHSPWAGPIRA	300		
DB	241	PFKRTCKOQOTETTSCLQNVSPGDIIELVDDNTTRKVMHYALKPHSPWAGPIRA	300		
QY	301	MAITVPLVVISAPATLFTVNCRRKQOENIYSHLDESSSESTYTAALPRRLRPKPVFL	360		
DB	301	MAITVPLVVISAPATLFTVNCRRKQOENIYSHLDESSSESTYTAALPRRLRPKPVFL	360		
QY	361	CYSKQGNMNVVQCAVYLPDPCGCEVALDLMEDESLCREQRENVIKIHESQITIV	420		

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Db      361  CYSKQGNHNNVVOCAFVLQDFCGCEVALDLMEDFSLCRGGRBNVIOKIHESQFTIV 420
Qy      421  VCSKGMKYPVDKKNYKKGGRSGKGEFLVAVASIAEKLROAKQSSSALSKFTIAYVF 480
Db      421  VCSKGMKYPVDKKNYKKGGRSGKGEFLVAVASIAEKLROAKQSSSALSKFTIAYVF 480
Qy      481  DYCCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSSRRNFRSKGR 540
Db      481  DYCCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSSRRNFRSKGR 540
Qy      541  SLVVAICNNHOFIDEEPDWFEKQFVPPHPPRYRREPVLEKFPDGLVNDVCKPGEBSD 600
Db      541  SLVVAICNNHOFIDEEPDWFEKQFVPPHPPRYRREPVLEKFPDGLVNDVCKPGEBSD 600
Qy      601  FCLKVEAPVVGATGPADSGHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSPMPR 660
Db      601  FCLKVEAPVVGATGPADSGHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSPMPR 660
Qy      661  DSGIYDSVPSSELSPLMEGLSTDQETSSLTESVSSSGIGEEPPALPSKLLSGSC 720
Db      661  DSGIYDSVPSSELSPLMEGLSTDQETSSLTESVSSSGIGEEPPALPSKLLSGSC 720
Qy      721  KADLGCGRSYTDELHAAVAP 738
Db      721  KADLGCGRSYTDELHAAVAP 738

RESULT 2
Q8NFM7_HUMAN PRELIMINARY; PRT; 739 AA.
ID Q8NFM7
AC Q8NFM7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 17 receptor-like protein long form.
GN Name=IL17RD; Synonyms=IL17RLM;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Kong Z., Huang G., Huang Y., Chen P., Zhang S.,
RA Liu L., Chang Z.;
RT "hsel inhibits PC-12 cell differentiation by interfering with Ras-
RT mitogen-activated protein kinase MAPK signaling."
RL J. Biol. Chem. 278:50273-50282(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Xiong S.O., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X.Y.,
RA Chen Y., Liu L., Fu X.Y., Chang Z.J.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DE EMBL: AF94308; AAM74077.1; -; mRNA.
DE ENSEMBL: ENSG00000144730; Homo sapiens.
DR HGNC: HGNC:17616; IL17RD.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:004888; P:transmembrane receptor activity; IEA.
DR InterPro: IPR00157; TIR.
KW Receptor.
SQ SEQUENCE 739 AA; 82441 MW; BCD2A95261B0277 CRC64;

Query Match 99.0%; Score 3908; DB 2; Length 739;
Best Local Similarity 99.2%; Pred. No. 5,4e-284;
Matches 732; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Db      61  DNCTTYLNPVGKVIADANQITTSQVACHDOVAVNTILMSGALGIEFLKGFVILBELKS 120
Qy      121  EGRQCOQLILKDPKOLNSPKRTGMSOPFLMKNKFTDYFVKVVPSPISKESNTPPFF 180
Db      121  EGRQCOQLILKDPKOLNSPKRTGMSOPFLMKNKFTDYFVKVVPSPISKESNTPPFF 180
Qy      181  RTKACDILLQPDNLACKPFWKPRPNLNI SQHSGDMQSPHAPNPFRRFFLYLKJKEG 240
Db      181  RTKACDILLQPDNLACKPFWKPRPNLNI SQHSGDMQSPHAPNPFRRFFLYLKJKEG 240
Qy      241  PPKRKTCKOQETTESCLQNVSPGDYIIELVDDTNTTRKVMRYALKVHSPWAPPIRA 300
Db      241  PPKRKTCKOQETTESCLQNVSPGDYIIELVDDTNTTRKVMRYALKVHSPWAPPIRA 300
Qy      301  MATTVLVVISAPATLFTWCKRKOQENTYSHLDESSSSSTYTAALPREBLRPRKVL 360
Db      301  MATTVLVVISAPATLFTWCKRKOQENTYSHLDESSSSSTYTAALPREBLRPRKVL 360
Qy      361  CYSKQGNHNNVVOCAFVLQDFCGCEVALDLMEDFSLCRGGRBNVIOKIHESQFTIV 420
Db      361  CYSKQGNHNNVVOCAFVLQDFCGCEVALDLMEDFSLCRGGRBNVIOKIHESQFTIV 420
Qy      421  VCSKGMKYPVDKKNYKKGGRSGKGEFLVAVASIAEKLROAKQSSSALSKFTIAYVF 480
Db      421  VCSKGMKYPVDKKNYKKGGRSGKGEFLVAVASIAEKLROAKQSSSALSKFTIAYVF 480
Qy      481  DYCCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSSRRNFRSKGR 540
Db      481  DYCCEGDVPGILDLSTKYRLMDNLPOLCSHLHSRDHGLQEPGQHTTRGSSRRNFRSKGR 540
Qy      541  SLVVAICNNHOFIDEEPDWFEKQFVPPHPPRYRREPVLEKFPDGLVNDVCKPGEBSD 600
Db      541  SLVVAICNNHOFIDEEPDWFEKQFVPPHPPRYRREPVLEKFPDGLVNDVCKPGEBSD 600
Qy      601  FCLKVEAPVVGATGPADSGHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSPMPR 660
Db      601  FCLKVEAPVVGATGPADSGHESQHGLDQGEARPALDGSALQPLLHTYKAGSPSPMPR 660
Qy      661  DSGIYDSVPSSELSPLMEGLSTDQETSSLTESVSSSGIGEEPPALPSKLLSGSC 720
Db      661  DSGIYDSVPSSELSPLMEGLSTDQETSSLTESVSSSGIGEEPPALPSKLLSGSC 720
Qy      721  KADLGCGRSYTDELHAAVAP 738
Db      721  KADLGCGRSYTDELHAAVAP 738

RESULT 3
Q58E27_HUMAN PRELIMINARY; PRT; 707 AA.
ID Q58E27
AC Q58E27
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE IL17RD protein.
GN Name=IL17RD;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Testis;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Helen F.,
RA Diatchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.T., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

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QY 641 AALQPLHTYKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQETSTLTFESVSSS 700
 DB 609 AALQPLHTYKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQETSTLTFESVSSS 668
 QY 701 GLGEEPPALPSKLLSSGSCADIGCRSYTDELHAHAV 738
 DB 669 GLGEEPPALPSKLLSSGSCADIGCRSYTDELHAHAV 706
 RESULT 5
 Q6UW15_HUMAN PRELIMINARY; PRT; 728 AA.
 ID Q6UW15_HUMAN PRELIMINARY; PRT; 728 AA.
 AC Q6UW15;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE I117Rhom.
 GN ORFNames=UNQ6115;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brubak J.,
 Chen Y., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 Eaton D., Foster J.S., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 Lewis L., Liao D., Mark M.R., Robble E., Sanchez C., Schoenfeld J.,
 Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vages A.,
 Vanden R.L., Watanabe C., Wleand D., Wood K., Xie M.-H.,
 Yansua D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 Wood W.I., Godowski P.J., Gray A.M.;
 RA "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RL bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL; AY358774; AA089134.1; -; mRNA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0006954; P:inflammatory response; IEA.
 DR InterPro; IPR000157; TIR.
 SQ SEQUENCE 728 AA; 81310 MW; 4AD93F8B1C78C6 CRC64;
 Query Match 93.2%; Score 3681.5; DB 2; Length 728;
 Best Local Similarity 97.5%; Pred. No. 5.1e-267;
 Matches 694; Conservative 2; Mismatches 3; Indels 13; Gaps 1;
 QY 40 GMRGVGPASNSGLNITFTKYNCTTYLANVGVKAVINDAONITISQYACHDOVAVTILMS 99
 DB 16 GEGGVGPASNSGLNITFTKYNCTTYLANVGVKAVINDAONITISQYACHDOVAVTILMS 75
 QY 100 PGALGIEFLKGFVYLIELSESGRQCOQLIKPKOLNSFKRTGMSQSFILMKKEFTDY 159
 DB 76 PGALGIEFLKGFVYLIELSESGRQCOQLIKPKOLNSFKRTGMSQSFILMKKEFTDY 135
 QY 160 FVKVVPSPISIKNSNYPFFRTACDLILQPDNLACKPFMKPRLNLSQ----- 209
 DB 136 FVKVVPSPISIKNSNYPFFRTACDLILQPDNLACKPFMKPRLNLSQHGSDMQVSPD 195
 QY 210 ---HGSDMQVSPDHPAPNFGRRFFLYHKLKHSGPFRTCKOQOTETTSCILQNVSPG 266
 DB 196 HADHGSMDQVSPDHPAPNFGRRFFLYHKLKHSGPFRTCKOQOTETTSCILQNVSPG 255
 QY 267 DYIIELVDDTNTTRKVMHVALKPVHSPAGPIRAMATTVLVNYSATLFTVMCRKQKQ 326
 DB 256 DYIIELVDDTNTTRKVMHVALKPVHSPAGPIRAMATTVLVNYSATLFTVMCRKQKQ 315
 QY 327 ENIYSHLDESSSSSTYTAALPRERLPRPKVFLCYSSKDGONHNMVVOCPAYFLQDFCG 386

DB 316 ENIYSHLDESSSSSTYTAALPRERLPRPKVFLCYSSKDGONHNMVVOCPAYFLQDFCG 375
 QY 387 CEVALDLMEDFSICRGOREWYOKTHESOFITIVGSKMKYFVDDKNTKHKGGSGSK 446
 DB 376 CEVALDLMEDFSICRGOREWYOKTHESOFITIVGSKMKYFVDDKNTKHKGGSGSK 435
 QY 447 GELFLVAVALAEKRLQAKQSSSALSKFLAVFDYSCGDDVGLDLSKRYLMDNLQ 506
 DB 436 GELFLVAVALAEKRLQAKQSSSALSKFLAVFDYSCGDDVGLDLSKRYLMDNLQ 495
 QY 507 LCSHLHSDHGLQEPQHTROGSRNNYFRSKGSLIYVAICMWHQFIDEEDPFERQFVP 566
 DB 496 LCSHLHSDHGLQEPQHTROGSRNNYFRSKGSLIYVAICMWHQFIDEEDPFERQFVP 555
 QY 567 FHPPEPRYREPYLEKSDGLVINDVWCKGPPSDFLKXTEAPVLTGATGADSGHESQHG 626
 DB 556 FHPPEPRYREPYLEKSDGLVINDVWCKGPPSDFLKXTEAPVLTGATGADSGHESQHG 615
 QY 627 LPDQGEARPALDGSALQPLHTYKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQ 686
 DB 616 LPDQGEARPALDGSALQPLHTYKAGSPDMPRDSGIYDSSVPSSELSLPLMEGLSTDQ 675
 QY 687 TETSSLTFESVSSSGLGEEPPALPSKLLSSGSCADIGCRSYTDELHAHAV 738
 DB 676 TETSSLTFESVSSSGLGEEPPALPSKLLSSGSCADIGCRSYTDELHAHAV 727
 RESULT 6
 Q8JZL1_MOUSE PRELIMINARY; PRT; 738 AA.
 ID Q8JZL1_MOUSE PRELIMINARY; PRT; 738 AA.
 AC Q8JZL1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Transmembrane protein (Interleukin 17 receptor-like protein long
 DE form).
 GN Name=I117rd; Synonym=I117rlm, Sef;
 OS Mus musculus (Mouse).
 OC Bakayota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21959295; PubMed=11960706; DOI=10.1016/S0925-4773(02)00018-7;
 RA Lin W., Furchauer M., Thise B., Thise C., Jing N., Ang S.-L.;
 RT "Cloning of the mouse Sef gene and comparative analysis of its
 RT expression with Pgf8 and Spfy2 during embryogenesis.";
 RL Mech. Dev. 113:163-168(2002).
 RN [2]
 RT "Sef inhibits PC-12 cell differentiation by interfering with Ras-
 RT mitogen-activated protein kinase MAPK signaling.";
 RL J. Biol. Chem. 278:50273-50282(2003).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=BALB/c;
 RA Xiong S.Q., Huang G.R., Zhao Q.H., Chen P.L., Rong Z.L., Ye X.Y.,
 Chen Y., Liu L., Fu X.Y., Chang Z.J.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF459444; AAM28441.1; -; mRNA.
 DR EMBL; AF494210; AAM74079.1; -; mRNA.
 DR Ensembl; ENSMUSG0000040717; Mus musculus.
 DR MGI; MGI:2159727; I117rd.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003676; P:nucleic acid binding; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR GO:0008270; F:zinc ion binding; IEA.
 DR InterPro: IPR000157; TIR.
 DR InterPro: IPR007087; ZnF_C2H2.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_1.
 DR Receptor: Transmembrane.
 DR SEQUENCE 738 AA; 82347 MW; D8C66230E3E8226 CRC64;

Query Match 86.0%; Score 3396.5; DB 2; Length 738;
 Best Local Similarity 86.6%; Pred. No. 1.2e-245;
 Matches 642; Conservative 38; Mismatches 34; Indels 7; Gaps 4;

QY 1 MAPWLCSEVFTYVNAAGSQAQVAAAGSGRAGVDTTCGRVGPASRNGLYNTYKY 60
 DB 1 MAPWLCSEVFTYVNAAGSQAQVAAAGSGRAGVDTTCGRVGPASRNGLYNTYKY 60
 QY 61 DNTCTYVNPVKGKVIADQNTTISQVACHDQVAVTILMSPALGIEFLKGRVILEIKS 120
 DB 61 DNTCTYVNPVKGKVIADQNTTISQVACHDQVAVTILMSPALGIEFLKGRVILEIKS 120
 QY 121 EGRQCOOLILKDPKQNLSPKRTGMSOPFLMKFETDYFVKVYPPPSIKNESYHPPF 180
 DB 121 EGRQCOOLILKDPKQNLSPKRTGMSOPFLMKFETDYFVKVYPPPSIKNESYHPPF 180
 QY 181 RTACADLLQPDNLACKPFWKPRMANTISQHSQDVQSFDAHPNFGRFFLYLKLKHEG 240
 DB 181 RTACADLLQPDNLACKPFWKPRMANTISQHSQDVQSFDAHPNFGRFFLYLKLKHEG 240
 QY 241 PPRKRTKQRTTETTSCLLQNVSPGYIIEVDNTTRKVMYALKPVHSPWAGPRA 300
 DB 241 PPRKRTKQRTTETTSCLLQNVSPGYIIEVDNTTRKVMYALKPVHSPWAGPRA 300
 QY 301 MATVPLVISAFTLFTWCRKQENIYSHLDESSSESTYTAALPRELRPRVFL 360
 DB 301 MATVPLVISAFTLFTWCRKQENIYSHLDESSSESTYTAALPRELRPRVFL 360
 QY 361 CYSKQDQNMNVQCFAYFLQDFCGCEVALDLMEDSLCREGQREWIQKIHESQPIY 420
 DB 361 CYSKQDQNMNVQCFAYFLQDFCGCEVALDLMEDSLCREGQREWIQKIHESQPIY 420
 QY 421 VCSKGMKYFYDKKFKKGGSGRGAQGEFPLVAVSAIAEKLRAKQSSAALSKFIAYVF 480
 DB 421 VCSKGMKYFYDKKFKKGGSGRGAQGEFPLVAVSAIAEKLRAKQSSAALSKFIAYVF 480
 QY 481 DYCCEGVPGILDSTYRLMDNLPOCSHLHSDHGLQEP-GQHTQSGRRNYFRKSG 539
 DB 481 DYCCEGVPGILDSTYRLMDNLPOCSHLHSDHGLQEP-GQHTQSGRRNYFRKSG 539
 QY 539 RSLVYVAINCNAHQFIDEEPWFQKQFVFPHPPLRYREPVLEKPSGLVLDVMSKPPES 597
 DB 539 RSLVYVAINCNAHQFIDEEPWFQKQFVFPHPPLRYREPVLEKPSGLVLDVMSKPPES 597
 QY 600 DFLKVAEPAVLGATGAPADSOH--ESQHGGLDQDEARPALDGSAALOPLLTAVAGSPSD 657
 DB 600 DFLKVAEPAVLGATGAPADSOH--ESQHGGLDQDEARPALDGSAALOPLLTAVAGSPSD 657
 QY 658 MPDQSGIYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSS 717
 DB 658 MPDQSGIYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSGLGEEPPALPSKLLSS 717
 QY 718 GSCKADLCRSYDELTAHAVP 738
 DB 718 GSCKADLCRSYDELTAHAVP 738

RESULT 7
 ID 08N113_HUMAN PRELIMINARY; PRT; 595 AA.
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Interleukin 17 receptor-like protein short form (Hypothetical protein DKFZp634L0320).

GN Name=IL17RLM; Synonyms=DKFZp634L0320;
 OS Homo sapiens (Human).
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 CC Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Tissue=Testis;
 RG The German cDNA Consortium;
 RA Ottensmeyer F., Obermaier B., Deutschenbauer S., Schapp A.,
 RA Mewes H.W., Weil B., Amid C., Oanger A., Fob G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF494211; AAM74080.1; -; mRNA.
 DR EMBL; AL833913; CAD38769.1; -; mRNA.
 DR Ensembl; ENSG00000144730; Homo sapiens.
 DR GO:0016020; C:membrane; IEA.
 DR GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro: IPR000157; TIR.
 DR Hypothetical protein; Receptor.
 DR SEQUENCE 595 AA; 66846 MW; 7E6BB64F73B2112 CRC64;

Query Match 80.0%; Score 3158; DB 2; Length 595;
 Best Local Similarity 99.5%; Pred. No. 6.9e-228;
 Matches 591; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 145 MESQPLMKFETDYFVKVPPPSIKNESYHPPFRTACDILLQPDNLACKPFWKPRN 204
 DB 1 MESQPLMKFETDYFVKVPPPSIKNESYHPPFRTACDILLQPDNLACKPFWKPRN 204
 QY 205 LNTSQHSQDVQSFDAHPNFGRFFLYLKLKHEGPKKTKQKQRTTETTSCLLQNV 264
 DB 205 LNTSQHSQDVQSFDAHPNFGRFFLYLKLKHEGPKKTKQKQRTTETTSCLLQNV 264
 QY 265 PGDYIIEVDNTTRKVMYALKPVHSPWAGPRAVAIVPLVISAFTLFTWCRK 324
 DB 265 PGDYIIEVDNTTRKVMYALKPVHSPWAGPRAVAIVPLVISAFTLFTWCRK 324
 QY 325 QQENIYSHLDESSSESTYTAALPRELRPRVFLCYSSKQDQNMNVQCFAYFLQDF 384
 DB 325 QQENIYSHLDESSSESTYTAALPRELRPRVFLCYSSKQDQNMNVQCFAYFLQDF 384
 QY 385 CGCEVALDLMEDSLCREGQREWIQKIHESQPIIIVCSKGMKYFYDKKFKKGGSGS 444
 DB 385 CGCEVALDLMEDSLCREGQREWIQKIHESQPIIIVCSKGMKYFYDKKFKKGGSGS 444
 QY 445 GKGELFLVAVSAIAEKLRAKQSSAALSKFIAYVDYSCGVPGLDSTYRLMDNL 504
 DB 445 GKGELFLVAVSAIAEKLRAKQSSAALSKFIAYVDYSCGVPGLDSTYRLMDNL 504
 QY 505 POLCSHLHSDHGLQEPGQHTQSGRRNYFRSNGSLVYVAINCNAHQFIDEEPWFQKQF 564
 DB 505 POLCSHLHSDHGLQEPGQHTQSGRRNYFRSNGSLVYVAINCNAHQFIDEEPWFQKQF 564
 QY 565 VPHAPPPLRYREPVLEKPSGLVLDVMSKPPESDFCLKVAEPAVLGATGAPADSOHSD 624
 DB 565 VPHAPPPLRYREPVLEKPSGLVLDVMSKPPESDFCLKVAEPAVLGATGAPADSOHSD 624
 QY 625 GGLDQGEARPALDGSAALOPLLTAVAGSPSPMPDQSGIYDSSVPSSESLPLMEGLST 684
 DB 625 GGLDQGEARPALDGSAALOPLLTAVAGSPSPMPDQSGIYDSSVPSSESLPLMEGLST 684
 QY 685 DQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLCRSYDELTAHAVP 738
 DB 685 DQETSSLTSSVSSSGLGEEPPALPSKLLSSGCKADLCRSYDELTAHAVP 738

RESULT 8

Q9UFA0 HUMAN PRELIMINARY; PRT; 564 AA.
 ID Q9UFA0;
 AC Q9UFA0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein DKFZp434N1928 (Fragment).
 GN Name=DKFZp434N1928;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RA Bloecher H., Bloecher M., Brandt P., Mewes H.W., Gassenhuber J.,
 RA Wleemann S.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL133097; CAB61408.1; -; mRNA.
 DR PIR; T42695; T42695.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR000157; TIR.
 KM Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 564 AA; 63134 MW; 6B3AA5BD4523E86C CRC64;

Query Match 75.8%; Score 2993; DB 2; Length 564;
 Best Local Similarity 99.5%; Pred. No. 1.5e-215;

Matches 56; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

176 HPPFRTACDILLQPNLACKPFWKPRNINISQHGSDMQVSPDHADPHNGFRFPYLHYK 235
 1 HPPFRTACDILLQPNLACKPFWKPRNINISQHGSDMQVSPDHADPHNGFRFPYLHYK 60
 236 LKHEGPRKRTCKQEQOTTETTSCLQNVSPGDIYIELVDNTTRKVMHAKLPVHSPMA 235
 61 LKHEGPRKRTCKQEQOTTETTSCLQNVSPGDIYIELVDNTTRKVMHAKLPVHSPMA 120
 296 GPIRAMAITYPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPR 355
 121 GPIRAVAITYPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPR 180
 356 PKVFLCYSSKQGNHMMVVOCAFAYLQDFGCEVALDLMEDFSLCREGQEWYIOKIHES 415
 181 PKVFLCYSSKQGNHMMVVOCAFAYLQDFGCEVALDLMEDFSLCREGQEWYIOKIHES 240
 416 QPITIVVCSKMKYFVDKQYKHKGGSGKGEFLVAVASIAIEKLRQAKOSSAALSKP 475
 241 QPITIVVCSKMKYFVDKQYKHKGGSGKGEFLVAVASIAIEKLRQAKOSSAALSKP 300
 476 IAYYFDVSCGSDVPGIIDLSTKRYLMONLPGLCGSHLSRBDHGOEPGQHTROGSRNRYFR 535
 301 IAYYFDVSCGSDVPGIIDLSTKRYLMONLPGLCGSHLSRBDHGOEPGQHTROGSRNRYFR 360
 536 SKGSRSLYYAICNMHQPIDEBPWFEPKQVPPFHPPLRYREPVLYKEPDSGLVINDVCKP 595
 361 SKGSRSLYYAICNMHQPIDEBPWFEPKQVPPFHPPLRYREPVLYKEPDSGLVINDVCKP 420
 596 GPSDFCLKATPYLGAATGPAADSGHSGGLDGDGAPALDGSALQPLTLTVKAGSP 655
 421 GPSDFCLKATPYLGAATGPAADSGHSGGLDGDGAPALDGSALQPLTLTVKAGSP 480
 656 SDMPRDSGIVDSVPSSESLPLMEGSLTDQETSSLTESVSSSGAGEEPALPESKL 715
 481 SDMPRDSGIVDSVPSSESLPLMEGSLTDQETSSLTESVSSSGAGEEPALPESKL 540
 716 SSGSKADLCGRSYTDELAAVAP 738
 |||

DB 541 SSGSKADLCGRSYTDELAAVAP 563

RESULT 9

Q772L7 CHICK PRELIMINARY; PRT; 741 AA.
 ID Q772L7;
 AC Q772L7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FGF signaling antagonist SRF.
 GN Gallus gallus (Chicken).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RX NCBI_TaxID=9031;
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22660508; PubMed=12766772; DOI=10.1038/nb989;
 RA Kawakami Y., Rodriguez-Leon J., Koch C.M., Buscher D., Itoh T.,
 RA Rava A., Ng J.K., Rodriguez Esteban C., Takahashi S., Henrique D.,
 RA Schwarz M.F., Asahara H., Izpisua Belmonte J.C.;
 RT "Wk3 mediates the cellular response to FGF8 signalling in the
 vertebrate limb."
 RL Nat. Cell Biol. 5:513-519(2003).
 DR EMBL; AY278204; AAP70001.1; -; mRNA.
 DR Ensembl; ENSGALG0000005499; Gallus gallus.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR GO; GO:0006954; P:inflammatory response; IEA.
 DR InterPro; IPR000157; TIR.
 SQ SEQUENCE 741 AA; 83553 MW; 64B8E88241AC60CF CRC64;

Query Match 73.3%; Score 2893; DB 2; Length 741;
 Best Local Similarity 73.5%; Pred. No. 7.1e-208;

Matches 545; Conservative 79; Mismatches 112; Indels 6; Gaps 5;

1 MAPWILQCVFFTVNACLNGSOLAFAVAGSG--RAMGVDTCCMRGVSPARNSGLNITF 58
 1 MAPWILQCVFFTVNACLNGSOLAFAVAGSG--RAMGVDTCCMRGVSPARNSGLNITF 60
 59 KYDNCITTYLNPVGVKVIADQNTTISQVACHQDAVTILMSFGALGIEFLKSPVILBEL 118
 61 KYDNCITTYLNPVGVKVIADQNTTISQVACHQDAVTILMSFGALGIEFLKSPVILBEL 120
 119 KESGRCCQQLIKDPQLNSSFRTGMSQPLNKKFEFDYVKKVPFISINSESYHFF 178
 121 KESGRCCQQLIKDPQLNSSFRTGMSQPLNKKFEFDYVKKVPFISINSESYHFF 180
 179 PFRTACDILLQPNLACKPFWKPRNINISQHGSDMQVSPDHADPHNGFRFPYLHYK 238
 181 PFRTACDILLQPNLACKPFWKPRNINISQHGSDMQVSPDHADPHNGFRFPYLHYK 240
 239 EGPFRKRTCKQEQOTTETTSCLQNVSPGDIYIELVDNTTRKVMHAKLPVHSPMA 298
 241 EGPFRKRTCKQEQOTTETTSCLQNVSPGDIYIELVDNTTRKVMHAKLPVHSPMA 300
 299 RAMAITYPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPRPV 358
 301 RAMAITYPLVVISAFATLFTVMCRKQOENIYSHLDESSSESTYTAALPRELRPRPV 360
 359 PLCYSSKQGNHMMVVOCAFAYLQDFGCEVALDLMEDFSLCREGQEWYIOKIHESQFI 418
 361 PLCYSSKQGNHMMVVOCAFAYLQDFGCEVALDLMEDFSLCREGQEWYIOKIHESQFI 420
 419 IVCSSKMKYFVDKQYKHKGGSGKGEFLVAVASIAIEKLRQAKOSSAALSKP 478
 421 IVCSSKMKYFVDKQYKHKGGSGKGEFLVAVASIAIEKLRQAKOSSAALSKP 479
 479 YPDYSCGSDVPGIIDLSTKRYLMONLPGLCGSHLSRBDHGOEPGQHTROGSRNRYFR 538
 480 YPDYSCGSDVPGIIDLSTKRYLMONLPGLCGSHLSRBDHGOEPGQHTROGSRNRYFR 539
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QY 539 GRSLYVAICNMHOFIDEEPDMFEKQFVPFHPPLRYREPVLEKEPDSGLVINDVCKEPE 598
DB 540 GRSLYVAICNMHOFIDEEPDMFEKQFIPPLPHPLHYSEPMWEKDSGLVINDVCKEPE 599
QY 599 SDPCLKVAEPVLGATGADPSOHESQHGGLDQDGEARP-ALDGSANLOPLHTTVKAGSPSD 657
DB 600 DDFYLTQDVNIIISA-GSSDSHCIIQHLNLGDEVETQDIQSGSSSVLPPLHVAASNLKD 658
QY 658 MPBDSGYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSGSLGEEPPVITSTFKL 716
DB 659 MPBDSGYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSGSLGEEPPVITSTFKL 718
QY 717 SGSCKADLCGRSYDELAHAVP 738
DB 719 PGICKALHGHITDELQALAP 740

RESULT 10
ID 08AV76_CHICK PRELIMINARY; PRT; 697 AA.
AC 08AV76;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Self protein (Fragment).
Name=SEF;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Facial mesenchyme;
MEDLINE=22651784; PubMed=12765832; DOI=10.1016/S0968-0004(03)00067-7;
RA Novatchkova M., Leibbrandt A., Werzowa J., Neubueser A.,
Bischoff P.;
RT "The STR-domain superfamily in signal transduction, development and
immunity.";
RL Trends Biochem. Sci. 28:226-229(2003).
DR EMBL; AJ508679; CAD48485.1; -; mRNA.
DR Ensembl; ENSGALG00000005499; Gallus gallus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR000157; TIR.
FT NON TER
SQ SEQUENCE 697 AA; 79259 MW; D288939E1727F2C3 CRC64;

Query Match 71.6%; Score 2828; DB 2; Length 697;
Best Local Similarity 75.5%; Pred. No. 4.9e-203;
Matches 527; Conservative 75; Mismatches 92; Indels 4; Gaps 4;

QY 43 GVGPARNSGLVITFYKDYNTTYLNPVGKVIADAOITISQYACHDOVAATILMSGA 102
DB 1 GLSSVTKNSGLNITFYKDYNTTYLNPVGKVIADAOITISQYACHDOVAATILMSGA 60
QY 103 LGIEPLKGFVILBELKSEGRQCOQILKDPKQLNSSFYKATGMSOPFLMKETDYFVK 162
DB 61 IGIEYLRGFEVILBELKSEGRQCOQVLRDPKQLSPFKATGMSNPFALKEFDYFVK 120
QY 163 VVFPFSIKNSNHPFFRTRACDLLOPNLACKPFMKRNINISQSGSDMOVSPHAP 222
DB 121 VVFPFSIKNSNHPFFRTRACDLLOPNLACKPFMKRNINISQSGSDMOVSPHAP 180
QY 223 HNGGFPPYLYKLGKGFPRKTKQEQETETTSCLQNVNSPDYIIEIYVDTNTRKY 282
DB 181 HNGGFPPYLYKLGKGFPRKTKQEQETETTSCLQNVNTDITNTRKY 240
QY 283 MHYALKRVSPMAQPIRAMAIVPLVVISAFATLFTVMCKRKOQENTYSHLDESSSST 342
DB 241 MHYALKRVSPMAQPIRAMAIVPLVVISAFATLFTVMCKRKOQENTYSHLDESSSST 300
QY 343 YTAALFRERLRPRPKVFLCTSSKDGNNHNVOCFAIFLDPGCEVALDMEDPSLCRE 402

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DB 301 YGALPVERLRPRPKVFLCTSSKDGNNHNVOCFAIFLDPGCEVALDMEDPSLCRE 360
QY 403 GOREWYIQTIESQFIIVVCSKEMKTFVDKXNKHKGSGSGKGLFLVAASAIKLR 462
DB 361 SOKEMWIKKINESQFIIVVCSKEMKTFVEKXNKHKGSGKGLFLFAVFAKLR 420
QY 463 QAKOSSAALSKRTIAYPDVSCGDPVGLIDLSITKRLMNLPOLCHHSRPHGOERG 522
DB 421 QAKONSN-DICKRTIAYPDVSCGDPVGLIDLSITKRLMNLPOLCHHSRPHGOERG 479
QY 523 QHTROGSRNYPFRSKGRSLYVAICNMHOFIDEEPDMFEKQFVPFHPPLRYREPVLEKEF 582
DB 480 VFPVNNYSKRTYFRSKGRSLYVAICNMHOFIDEEPDMFEKQFIPPLPHPLHYSEPMWEK 539
QY 583 DSGLVINDVCKEPEPSDFCLKVAEPVLGATGADPSOHESQHGGLDQDGEARPALD-GSA 641
DB 540 DSGLVINDVCKEPEPSDFCLKVAEPVLGATGADPSOHESQHGGLDQDGEARPALD-GSA 598
QY 642 ALQPLHTTVKAGSPDMPRDSGYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSG 701
DB 599 VLPPLHVAASNLKMPRDSGYDSSVPSSESLPLMEGLSTDQETSSLTSSVSSSG 658
QY 702 LGEEPPVITSTFKLPGICKALHGHITDELQALAP 738
DB 659 LGEEPPVITSTFKLPGICKALHGHITDELQALAP 696

RESULT 11
ID 08K447_MOUSE PRELIMINARY; PRT; 594 AA.
AC 08K447;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin 17 receptor-like protein short form.
Name=IL17rd; Synonyms=IL17rlm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
PubMed=12958313; DOI=10.1074/jbc.M306936200;
RA Xiong S., Zhao Q., Rong Z., Huang G., Huang Y., Chen P., Zhang S.,
Liu L., Chang Z.;
RT "Self inhibits PC-12 cell differentiation by interfering with Ras-
mitogen-activated protein kinase MAPK signaling.";
RL J. Biol. Chem. 278:50273-50282(2003).
DR EMBL; AF494209; AAM74078.1; -; mRNA.
DR MG1; MG1:2159727; IL17rd.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR000157; TIR.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
KW Receptor.
SQ SEQUENCE 594 AA; 66780 MW; EABE6B55DF4EC3 CRC64;

Query Match 67.5%; Score 2665.5; DB 2; Length 594;
Best Local Similarity 84.6%; Pred. No. 5.9e-191;
Matches 505; Conservative 35; Mismatches 50; Indels 7; Gaps 4;

QY 145 MESQPLNKKFETDYFVKVVPFSIKNSNHPFFRTRACDLLOPNLACKPFMKPNV 204
DB 1 MESQPLNKKFETDYFVKVVPFSIKNSNHPFFRTRACDLLOPNLACKPFMKPNV 60
QY 205 LNISQSGSDMOVSPHAPHNGGFPPYLYKLGKGFPRKTKQEQETETTSCLQNVNS 264

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Db 61 LNTSGSDMHWFDHAPQNFGRGFHVLTKLKHGEFRRRTCRQDQNTETTSCLQNVS 120
Qy 265 PGQYIIELVDDTTRKVMYIALKPNVSPWAGPIRAMAIVPLVISAFTLFTVWCRKK 324
Db 121 PGYIIELVDDSTTRKAAQYVKSVPWAGPIRAVAITVPLVISAFTLFTVWCRKK 180
Qy 325 QQENITSHLDESSSESTYTAALPRERLRPKPYFLCYSSKDGONHNVVQCFAYFLDPF 384
Db 181 QQENITSHLDESBESSTYTAALPRERLRPKPYFLCYSSKDGONHNVVQCFAYFLDPF 240
Qy 385 CGCEVALDLMEDFSCLCEGGEQEWIYQKHESQPIIVVCSKGMKYFVDKKNYKHKGGGRGS 444
Db 241 CGCEVALDLMEDFSCLCEGGEQEWIYQKHESQPIIVVCSKGMKYFVDKKNYKHKGGGRGS 300
Qy 445 GKRELPLVAVSAIAEKLRQAKQSSSALSKFIAYFPYSCGDPVPGILDLSTKRLMDN 504
Db 301 AQGEFPLVAVAAIAEKLRQAKQSSSALSKFIAYFPYSCGDPVPGILDLSTKRLMDN 360
Qy 505 POLCSHLHSRDHGLQEP-GQHTQGSRRNTFRSKSGSLVYALCNMHQPIDEBDMFEKQ 563
Db 361 PELCAHLHS---GQEVYLGQHPGHSRRNTFRSKSGSLVYALCNMHQPIDEBDMFEKQ 417
Qy 418 FIFQHPHPVAYQEPVLEKFPDGLVANDVISKPGESDFCRKVEACVLAGAPADSYSL 477
Db 622 SQHGGLDQDGEAPALDGSAAQPLLHTVYKAGSPSDMRDPSGIDSSVPSSELSPLMEG 681
Qy 478 SQHVGLDQDDEAPSCSAPALQPLLAHVKAGSPSEMPRDSGIYDSSVPSSELSPLMEG 537
Db 682 LSTPDQETSSLTSSVSSSGIGEEEPALPSKLLSSGSKADLCGRSYTELHVAAP 738
Qy 538 LSPDQETSSLTSSVSSSGIGEEEPALPSKLLSSGSKADLCGRSYTELHVAAP 593

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RESULT 12

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08RSJ8 MOUSE PRELIMINARY; PRT; 582 AA.
ID 08RSJ8_MOUSE PRELIMINARY; PRT; 582 AA.
AC 08RSJ8_MOUSE PRELIMINARY; PRT; 582 AA.
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Similar expression to FGF protein (Fragment).
GN Name=117rd; Synonyms=Self;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxId=10090;
OX RN [1]_TaxId=10090;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21824237; PubMed=11802165; DOI=10.1038/nb750;
RA Furlanher M., Lin W., Ang S.L., Thibse B., Thibse C.;
RT "Self is a feedback-induced antagonist of Ras/MAPK-mediated FGF
RT signaling";
RL Nat. Cell Biol. 4:170-174(2002).
DR EMBL; AF424604; ALU79530.1; -; mRNA.
DR MGI; MGI:2159727; I117rd.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR001087; Znf_C2H2.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
FT NON TER 1 1
SQ SEQUENCE 582 AA; 65263 MW; 5666B2981C4266E CRC64;

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Query Match 66.0%; Score 2606.5; DB 2; Length 582;
 Best Local Similarity 84.4%; Pred. No. 1.5e-186;
 Matches 494; Conservative 35; Mismatches 49; Indels 7; Gaps 4;

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Qy 157 TDYFVAVPEPSTIKNESNYHPEFRTACDLLLQPDNLACEFWKPRNINI SQHSGDMQV 216
Db 1 TDYFVAVPEPSTIKNESNYHPEFRTACDLLLQPDNLACEFWKPRNINI SQHSGDMQV 60
Qy 217 SFDHAPNFGPREFYLYLKLKHGEPKRTCKQEQTEFTTSCILQNVSPQDYIIELVDT 276
Db 61 SFDHAPNFGPREFYLYLKLKHGEPKRTCKQEQTEFTTSCILQNVSPQDYIIELVDS 120
Qy 277 NTRKRMVYALRPVSPWAGPIRAMAIVPLVISAFTLFTVWCRKKQENITSHLDE 336
Db 121 NTRKRAQYVAVSPWAGPIRAMAIVPLVISAFTLFTVWCRKKQENITSHLDE 180
Qy 337 SSESSTYTAALPRERLRPKPYFLCYSSKDGONHNVVQCFAYFLDPFCGCEVALDLMED 396
Db 181 SPESSTYTAALPRERLRPKPYFLCYSSKDGONHNVVQCFAYFLDPFCGCEVALDLMED 240
Qy 397 FSLCREGQEWIYQKHESQPIIVVCSKGMKYFVDKKNYKHKGGGRSGKGLFLVAVSA 456
Db 241 FSLCREGQEWIYQKHESQPIIVVCSKGMKYFVDKKNYKHKGGGRSGKGLFLVAVSA 300
Qy 457 IAEKLRQAKQSSSALSKFIAYFPYSCGDPVPGILDLSTKRLMDNLPOLCSHLHSRDH 516
Db 301 IAEKLRQAKQSSSALSKFIAYFPYSCGDPVPGILDLSTKRLMDNLPOLCSHLHSRDH 357
Qy 517 GLQEP-GQHTQGSRRNTFRSKSGSLVYALCNMHQPIDEBDMFEKQFVPHPPPLRYR 575
Db 358 GQEVYLGQHPGHSRRNTFRSKSGSLVYALCNMHQPIDEBDMFEKQFVPHPPVRYR 417
Qy 418 FIFQHPHPVAYQEPVLEKFPDGLVANDVISKPGESDFCRKVEACVLAGAPADSYSL 477
Db 576 EPLTEKPDGLVANDVYKPGESDFCRKVEACVLAGAPADSYSL 633
Qy 478 EPLTEKPDGLVANDVYKPGESDFCRKVEACVLAGAPADSYSL 417
Db 634 RPLDGSAAQPLLHTVYKAGSPSDMRDPSGIDSSVPSSELSPLMEG:STQETSSLT 693
Qy 478 QPSCSAPALQPLLAHVKAGSPSEMPRDSGIYDSSVPSSELSPLMEG:LSPDQETSSLT 537
Db 694 ESYVSSSGIGEEEPALPSKLLSSGSKADLCGRSYTELHVAAP 738
Qy 538 ESYVSSSGIGEEEPALPSKLLSSGSKADLCGRSYTELHVAAP 581

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RESULT 13

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08QHJ9 BRAR PRELIMINARY; PRT; 745 AA.
ID 08QHJ9_BRAR PRELIMINARY; PRT; 745 AA.
AC 08QHJ9_BRAR PRELIMINARY; PRT; 745 AA.
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Self.
GN Name=117rd; Synonyms=Self;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxId=7955;
OX RN [1]_TaxId=7955;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21824236; PubMed=11802164; DOI=10.1038/nb749;
RA Tsang M., Friesel R., Kudoh T., David I.;
RT "Identification of Self, a novel modulator of FGF signaling";
RL Nat. Cell Biol. 4:165-169(2002).
DR EMBL; AF364103; AAU76112.1; -; mRNA.
DR EMBL; ENSDARG0000005754; Danio rerio.
DR ZFIN; ZDB-GENE-020320-5; I117rd.
SQ SEQUENCE 745 AA; 83431 MW; 56FE1F0B9D98D84 CRC64;

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Query Match 49.8%; Score 1966; DB 2; Length 745;
 Best Local Similarity 52.4%; Pred. No. 2.3e-138;
 Matches 391; Conservative 111; Mismatches 198; Indels 46; Gaps 10;

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Db      7 LAHFPMASCLFLCTYASVNG-----GKRGNSDKCSYKQGTQTSMSDEGARKLGV 56
Qy      58 FKXDNCTTYINPVGKHVIAADONITISQVACHDOVATILMSPALGIBPLKGRVILIE 117
Db      57 FRDNCGVNMPKGAHIEVNNTTFSHLSCDSQAAYVMMASPLGIEHVKGFRVYLED 116
Qy      118 LKESGRCCOOLILKDPKOLNSFKRTGMSQPLANKFEFDYFVKVVPFSPISKESNYHP 177
Db      117 KNEBKQCOHLIKDPKOLNFSYKTIKMSQPSLSLAFETDYMVRIYVFPFLNDSFPP 176
Qy      178 FPFRTACDILLDPNLACKPFPKPRNLTISQHSQDQVSDHAPHNFGFRPFYLYK 237
Db      177 SFLRTNSCEVLADPDLVCKPFPKMLNVSQLSGSLHVFDDHAPSTFGSITYLYKLR 236
Qy      238 HEGPFRKTKQKQETTTSCLLQNSPGDYIIELVDTTTRKVMYALKPVHSPAGP 297
Db      237 QEBPFLKRCPEQNGPKTTCVLDVTPGYALIELRDSNTRQOTYHNSQVHSPAGP 296
Qy      298 IRAMAITVPLVISAFAITLFTVMCRKQKQENIYSHLDESESSSTYALPRELRPRK 357
Db      297 IRAMAITVPLVISAFAITLFTVMCRKQKQENIYSHLDESESSSTYALPRELRPRK 356
Qy      358 VPLCYSSKQDQNMNVQCAVFLQDFCGCEVALDMEDESLCREGOREWVIOKIHESQF 417
Db      357 IFLCYSSRDQAKHLAVIQSFAFLQDFCGCEVALDMEHELEICEKGQMSLSRRIDEAHF 416
Qy      418 IIVVCSGKMYFVDKKNYKHKGGK-----GSGKEFLVAVSAIAETLROAKQ 466
Db      417 IIVVCSGKLGKHFVKRHRKATSKENRREPSADSSSSSRDLFIYVSAIISELKEVHQ 476
Qy      467 SSSAALSKFLAVYFDYSCBGDVPGLDSTKYRLMDLPLQCSLHSHRDHGLQEPQHT 526
Db      477 KSS-DLSRFMSVYFDYSHETDVPSTLSLAPFKLMDLPQLFARLSRQLSTLDREPOPP 535
Qy      527 QGSRNRYFRKSGSLVYALCNMHOPIDEBDFEKOFPVFPPLRYRREPVLEKPSGL 586
Db      536 NVSKRNYFCSGKSRSLVYALYNNHQHTQEPDMEKELM---PPPLNKKTIPEKVDL 592
Qy      587 VLANDVCKPESDPCLKVEAPVL-----GATGPADSGHESQGLDODGEARPALDG 639
Db      593 VINEVKLKHGSESE-CPVRSNVLLIPQTPQGVSLSLRSDLEGGSSOD----- 642
Qy      640 SAALQPLHTVKGSPSDMRDGIYDSSVPSSELPLMEGLSTQDTETSSLTESVSS 699
Db      643 AGSCRPLHTDGSASPEMPRDSGIYDSSVPSSELPLMDGLSPHDNSSLADSVSS 702
Qy      700 SGLGEERPALPSKLSGSS-CKADL 724
Db      703 SGLGEERPAVSSLHCTAHTICRADL 728

RESULT 14
ID QGQJ6 BRARE PRELIMINARY; PRT; 745 AA.
AC QGQJ6;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE FGF signaling antagonist Sef.
GN Name=117rd; Synonym=ssef;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21824237; PubMed=11802165; DOI=10.1038/nbt750;
RA Furthauer M., Lin W., Ang S.L., Thise B., Thise C.;
RT "Sef is a feedback-induced antagonist of Ras/MAPK-mediated FGF
  signaling".
RL Nat. Cell Biol. 4:170-174(2002).
RN [2]

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RP NUCLEOTIDE SEQUENCE.
RA Furthauer M., Lin W., Siew-Ian A., Thise B., Thise C.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF401232; AAL78817.1; -; mRNA.
DR Ensembl; ENSDARG0000005754; Danio rerio.
DR ZFIN; ZDB-GENE-020320-5; 1117rd.
SQ SEQUENCE 745 AA; 83437 MW; 75B9BEDCC08A4652 CRC64;

Query Match 49.6%; Score 1957; DB 2; Length 745;
Best Local Similarity 52.1%; Pred. No. 1,1e-137;
Matches 389; Conservative 113; Mismatches 198; Indels 46; Gaps 10;

Qy      1 MAPMLQCSVFETVNAACNSQLAVAGSGRAGVDTGCMR-GVGPASRNSGL--YNIT 57
Db      7 LAHFPMASCLFLCTYASVNG-----GKRGNSDKCSYKQGTQTSMSDEGARKLGV 56
Qy      58 FKXDNCTTYINPVGKHVIAADONITISQVACHDOVATILMSPALGIBPLKGRVILIE 117
Db      57 FRDNCGVNMPKGAHIEVNNTTFSHLSCDSQAAYVMMASPLGIEHVKGFRVYLED 116
Qy      118 LKESGRCCOOLILKDPKOLNSFKRTGMSQPLANKFEFDYFVKVVPFSPISKESNYHP 177
Db      117 KNEBKQCOHLIKDPKOLNFSYKTIKMSQPSLSLAFETDYMVRIYVFPFLNDSFPP 176
Qy      178 FPFRTACDILLDPNLACKPFPKPRNLTISQHSQDQVSDHAPHNFGFRPFYLYK 237
Db      177 SFLRTNSCEVLADPDLVCKPFPKMLNVSQLSGSLHVFDDHAPSTFGSITYLYKLR 236
Qy      238 HEGPFRKTKQKQETTTSCLLQNSPGDYIIELVDTTTRKVMYALKPVHSPAGP 297
Db      237 QEBPFLKRCPEQNGPKTTCVLDVTPGYALIELRDSNTRQOTYHNSQVHSPAGP 296
Qy      298 IRAMAITVPLVISAFAITLFTVMCRKQKQENIYSHLDESESSSTYALPRELRPRK 357
Db      297 IRAMAITVPLVISAFAITLFTVMCRKQKQENIYSHLDESESSSTYALPRELRPRK 356
Qy      358 VPLCYSSKQDQNMNVQCAVFLQDFCGCEVALDMEDESLCREGOREWVIOKIHESQF 417
Db      357 IFLCYSSRDQAKHLAVIQSFAFLQDFCGCEVALDMEHELEICEKGQMSLSRRIDEAHF 416
Qy      418 IIVVCSGKMYFVDKKNYKHKGGK-----GSGKEFLVAVSAIAETLROAKQ 466
Db      417 IIVVCSGKLGKHFVKRHRKATSKENRREPSADSSSSSRDLFIYVSAIISELKEVHQ 476
Qy      467 SSSAALSKFLAVYFDYSCBGDVPGLDSTKYRLMDLPLQCSLHSHRDHGLQEPQHT 526
Db      477 KSS-DLSRFMSVYFDYSHETDVPSTLSLAPFKLMDLPQLFARLSRQLSTLDREPOPP 535
Qy      527 QGSRNRYFRKSGSLVYALCNMHOPIDEBDFEKOFPVFPPLRYRREPVLEKPSGL 586
Db      536 NVSKRNYFCSGKSRSLVYALYNNHQHTQEPDMEKELM---PPPLNKKTIPEKVDL 592
Qy      587 VLANDVCKPESDPCLKVEAPVL-----GATGPADSGHESQGLDODGEARPALDG 639
Db      593 VINEVKLKHGSESE-CPVRSNVLLIPQTPQGVSLSLRSDLEGGSSOD----- 642
Qy      640 SAALQPLHTVKGSPSDMRDGIYDSSVPSSELPLMEGLSTQDTETSSLTESVSS 699
Db      643 AGSCRPLHTDGSASPEMPRDSGIYDSSVPSSELPLMDGLSPHDNSSLADSVSS 702
Qy      700 SGLGEERPALPSKLSGSS-CKADL 724
Db      703 SGLGEERPAVSSLHCTAHTICRADL 728

RESULT 15
ID Q4RLH0 TESTNG PRELIMINARY; PRT; 470 AA.
AC Q4RLH0;
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAFI5020, whole genome shotgun sequence.

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(fragment).
ORFNames=GSTENG0032492001;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetradon.
NCBI_TaxID=99883;
[1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Maucell E., Bouneau L., Fischer C., Ozouf-Costraz C., Bernot A.,
RA Niclaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Desliya C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellio V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Castolico L., Poulat J., De Berardinis V.,
RA Cnaud C., Duprat S., Brottier P., Couanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schacherer V., Querier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
RT Genome duplication in the teleost fish Tetradodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
[2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope, Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB0105020; CAG10762.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 470 470
SQ SEQUENCE 470 AA; 53660 MW; 0FB99F24436E5124 CRC64;
Query Match 33.8%; Score 1335; DB 2; Length 470;
Best Local Similarity 54.8%; Pred. No. 2.6e-91;
Matches 259; Conservative 67; Mismatches 133; Indels 14; Gaps 4;
QY 105 IEFKGFVILIEBKSGROCOQILKDPKQLNSSFRTGMSQPLNKKETDYFVKV 164
DB 1 IEHVKGFRVYLEDKNPEGKRQCHILKDPQLNFSHKNTKLNQPFAGLTFDTDMVRVY 60
QY 165 PFPSSIKKESYHPPFPFTRACDILLQPDNLACRFKPRKRLNLSQHSQVSDHAPHN 224
DB 61 PFPSSLNMFSPFPSPFLTNCEVLLGSDSLVCKPFMKPTMNVSQLGSLNLAHVFEQAPSS 120
QY 225 FGRFPFLYHKLHNEGPFKKTCKQEQETFTTSCILQNVSPGDIIELVDTVTTRKVM 284
DB 121 FGFALYLYLYKLRQDGFKQRCRKPVPAYWLRALTKCPTTSSNVLSFLDMLITTLQLSR 180
QY 285 YALKPVHSPWAGPIRAMAIVTLPVLSAFATL-FTVWCRKKQENIYSHLDESSSESTY 343
DB 181 YKFPY- -PWAGPIRAMAIVTLPVLSAFATL-FTVWCRKKQENIYSHLDESSSESTY 237
QY 344 TALLPRERLAPRRVFLCYSSKQGNMNVVQCPAYFLQPCGCEVALDMEDEPSLCREG 403
DB 238 SAALNPERPMPBRKVPFLCYSNRQDPKHSNVISQFAYFLQPCCEVALDMEDEPSLCREG 297
QY 404 QREMVIOKHESQPIIIVGSKGMKYPVDKKNYKHGGGSGSK-----GELFLVAUSA 456
DB 298 QMWLSRQLDEADPIITVCGRLRYEYKSRKGSPIVRSQSGSLPPAASMGDLFPVSVSV 357
QY 457 IAEKLRQAKS---SSAALSKFLAVVPDYSCEGDVPGILDLSTYRLMDNLPOLCSHLHS 513
DB 358 IAEKLRQAKSGGAGVGLRSLYLVYFDYSSESDIPMTLTLASRFLMDQLPOLPSRLHS 417
QY 514 RDHGLQEPGQHTQSGRRNTFRSKSGSLVVAICNMQFTIDEBDFWFEKQFVP 566
DB 418 SQGSLAESSESLPVNVSRNRYFRSKSGSLVYSICNMHQHISQNPDMFDKQLAP 470

Search completed: March 1, 2006, 10:30:09
Job time : 237 secs

Db	241	GTGATGTCGAGCGCCAGAAATATCAACATACAGCCAGTATGCTTGGCATAGACCAAGATGGCA	300
Qy	301	GTCAACATCTCTTGGTCCCGACAGGGCCCTCGGCATTCGATTCGTAAGAATTTGGGGTA	360
Db	301	GTCAACATCTCTTGGTCCCGAGGGCCCTCGGCATTCGATTCGTAAGAATTTGGGGTA	360
Qy	361	ATACTGGAGAGCTGAAGTCCGAGGGGAAGAAGTCCCAACATCTGATTTCTAAGATCCG	420
Db	361	ATACTGGAGAGCTGAAGTCCGAGGGGAAGACAGTCCCAACATCTGATTTCTAAGATCCG	420
Qy	421	AAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGSAATCTCACTTTCTGTAATATG	480
Db	421	AAGCAGCTCAACAGTAGCTTCAAAAGAACTGGAATGSAATCTCAACCTTTCTGTAATATG	480
Qy	481	AAATTTGAAAGSAGTATATTTGTAAGGTTGGCCCTTTTCCTTCATTTAAAAAGAAAGC	540
Db	481	AAATTTGAAAGSAGNTATTTGTAAGGTTGGCTTTTCCTTCATTTAAAAAGAAAGC	540
Qy	541	AATTACACCCCTTCTCTTTAGAAACCGAGCTGTGAACCTGTGTTAAGACCCGGACAAT	600
Db	541	AATTACACCCCTTCTCTTTAGAAACCGAGCTGTGAACCTGTGTTAAGACCCGGACAAT	600
Qy	601	CTAGCTTGTAAACCTTTCTGGAAGGCTTGGAACTTGAAATACAGCCACATATGCTCCGAC	660
Db	601	CTAGCTTGTAAACCCCTTCTGGAAGGCTTGGAACTTGAAATACAGCCACATATGCTCCGAC	660
Qy	661	ATGCAGGTGTCCTTGCACACGACACGCAAACTTCGAGCTTCGATTTCTGATTTTCAAC	720
Db	661	ATGCAGGTGTCCTTGCACACGACACGCAAACTTCGAGCTTCGATTTCTGATTTTCAAC	720
Qy	721	TACAAGCTCAAGACGAAGAACCTTTCAAGCGAAAGACCTGTAAACAGAGCAAACTACA	780
Db	721	TACAAGCTCAAGACGAAGAACCTTTCAAGCGAAAGACCTGTAAACAGAGCAAACTACA	780
Qy	781	GAGACGACACAGCTGCTCCTTCAAAATGTTTCTCAAGGGGATTAATAATTTGAGTGGTG	840
Db	781	GAGACGACACAGCTGCTCCTTCAAAATGTTTCTCAAGGGGATTAATAATTTGAGTGGTG	840
Qy	841	GATGACACTTAACAACAAGAAAGATGATGCAATTATGCTTTAAAGCCAGTGCATCCCGC	900
Db	841	GATGACACTTAACAACAAGAAAGATGATGCAATTATGCTTTAAAGCCAGTGCATCCCGC	900
Qy	901	TGGGCGGGGCCCATATCAGAGCCATGCGCATCAAGTCCACTGTAATTCGACATTC	960
Db	901	TGGGCGGGGCCCATATCAGAGCCATGCGCATCAAGTCCACTGTAATTCGACATTC	960
Qy	961	GCGACGCTTCTCACTGTATGTGCGCGAAGACAAAGAAATATATATTTCACTTTA	1020
Db	961	GCGACGCTTCTCACTGTATGTGCGCGAAGACAAAGAAATATATATTTCACTTTA	1020
Qy	1021	GATGAAGAGAGCTCTGAGTCTTCCACATACCTGAGCACTCCCAAGAGAGGCTCCGG	1080
Db	1021	GATGAAGAGAGCTCTGAGTCTTCCACATACCTGAGCACTCCCAAGAGAGGCTCCGG	1080
Qy	1081	CCGGCGCCCGAAGGTCTTCTCTGCTATTTCAAGTAAGAATGGCCAGAAATCAATGAATGC	1140
Db	1081	CCGGCGCCCGAAGGTCTTCTCTGCTATTTCAAGTAAGAATGGCCAGAAATCAATGAATGC	1140
Qy	1141	GTCCAAGTCTTTCGCTACTTCTCCTCAAGACCTTCTGTGCTGTGAAGTGGCTCTGACCTG	1200
Db	1141	GTCCAAGTCTTTCGCTACTTCTCCTCAAGACCTTCTGTGCTGTGAAGTGGCTCTGACCTG	1200
Qy	1201	TGGGAAGACTTCAAGCTCTGTAGAGAAAGGCAAGAGATGGGTATCAAGAAATCCAC	1260
Db	1201	TGGGAAGACTTCAAGCTCTGTAGAGAAAGGCAAGAGATGGGTATCAAGAAATCCAC	1260
Qy	1261	GAGTCCCACTTCAATCATATGTTGTTGTTCCAAAGGTATGAAGTACTTTGTGACAAAGAG	1320
Db	1261	GAGTCCCACTTCAATCATATGTTGTTGTTCCAAAGGTATGAAGTACTTTGTGACAAAGAG	1320
Qy	1321	AACATCAAAACAAGAGAGTGGCCGAGGCTTCGGGAAAGAGAGCTTTCCTGTGGCG	1380

Db	1321	AACTAACAAACAAAGAGGTGGCCGAGGCTCGGGGAAAGAGACTTCTCTGGTGGC	1380
Qy	1381	GTGTCAAGCCATTGCGCGAAAAGCTTCGCGCAGGCCAGAGAGTTGTCGCGGGCCCTCAGC	1440
Db	1381	GTGTCAAGCCATTGCGCGAAAAGCTTCGCGCAGGCCAGAGAGTTGTCGCGGGCCCTCAGC	1440
Qy	1441	AAAGTTTATCGCGGTCTACTTGTATTATTTCTGCGAGGGAGACGTCCCCGGTATCTTAGAC	1500
Db	1441	AAAGTTTATCGCGGTCTACTTGTATTATTTCTGCGAGGGAGACGTCCCCGGTATCTTAGAC	1500
Qy	1501	CTGAGTACCAAGTACAGACTCATGAGCAATCTTCTCAGCTGTCCTTCCACCTGCACTCC	1560
Db	1501	CTGAGTACCAAGTACAGACTCATGAGCAATCTTCTCAGCTGTCCTTCCACCTGCACTCC	1560
Qy	1561	CGAGACCAAGGCTTCAGAGACCCGGGGCAGGACACGGGACAGGGCAGAGAGAACTAC	1620
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Qy	1681	GACGAGGAGCCGACGTGGTTGAAAACAGTGGTTCCTCCATCTCTCCACATGCGC	1740
Db	1681	GACGAGGAGCCGACGTGGTTGAAAACAGTGGTTCCTCCATCTCTCCACATGCGC	1740
Qy	1741	TACCGGAGGACGACTCTTGAGAAATTTGATTCGGGCTTGGTTTTAAATGATGTCATGTGC	1800
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Qy	1801	AAACCAAGGAGCTTGAAGTGAATTTGCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGGCAAC	1860
Db	1801	AAACCAAGGAGCTTGAAGTGAATTTGCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGGCAAC	1860
Qy	1861	GGACCAAGCCGACTCCGACACAGAGTCAGATGAGGGGGCTGGACCAAGACGGGGAGAGCC	1920
Db	1861	GGACCAAGCCGACTCCGACACAGAGTCAGATGAGGGGGCTGGACCAAGACGGGGAGAGCC	1920
Qy	1921	CGGCTCGCCCTTGAACGGTAGGCGCCGCTCGCAACCCCTGCTGCAACAGGTGMAAGCCGGC	1980
Db	1921	CGGCTCGCCCTTGAACGGTAGGCGCCGCTCGCAACCCCTGCTGCAACAGGTGMAAGCCGGC	1980
Qy	1981	AGCCCTTCGACATGCGCGGGGACTCAGGCACTATGACTGCTGTGCGCCCTCATCCGAG	2040
Db	1981	AGCCCTTCGACATGCGCGGGGACTCAGGCACTATGACTGCTGTGCGCCCTCATCCGAG	2040
Qy	2041	CTGTCTCTGCCACTGATGAGAAAGACTCTCGACGGACAGACAGAAAGTCTTCCCTAGAC	2100
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Qy	2101	GAGAGCGGTGCTCTCTTTCAGGCGCTGAGGAGAGAACTCTGCGCTTCTCTTCCAG	2160
Db	2101	GAGAGCGGTGCTCTCTTTCAGGCGCTGAGGAGAGAACTCTGCGCTTCTCTTCCAG	2160
Qy	2161	CTCTCTCTTCTGGGTCAATGCAAGACGATCTTGTCGGCAGCTACACTGATGAATCTC	2220
Db	2161	CTCTCTCTTCTGGGTCAATGCAAGACGATCTTGTCGGCAGCTACACTGATGAATCTC	2220
Qy	2221	CACCGGATCGCCCTTTGTGTAACAAAGAAAGAGTCTAACATTTGCCACTTTAGCTGCTG	2280
Db	2221	CACCGGATCGCCCTTTGTGTAACAAAGAAAGAGTCTAACATTTGCCACTTTAGCTGCTG	2280
Qy	2281	CCTCCCTCTGATTTCCCGAGCTCATCTCCCTGTTGACATGCCCCACTTGGAGCTGAGGCTC	2340
Db	2281	CCTCCCTCTGATTTCCCGAGCTCATCTCCCTGTTGACATGCCCCACTTGGAGCTGAGGCTC	2340
Qy	2341	CATAACAAGATATTGAGAGTAAATGCTGCGCAGTACTTGTCTCCCTTGGCCCCAACCT	2400
Db	2341	CATAACAAGATATTGAGAGTAAATGCTGCGCAGTACTTGTCTCCCTTGGCCCCAACCT	2400
Qy	2401	TTACCGGATATCTTGAACAACTCTCCAAATTTCTTAAATGATATGAGCTCTGAAAGGCA	2460
Db	2401	TTACCGGATATCTTGAACAACTCTCCAAATTTCTTAAATGATATGAGCTCTGAAAGGCA	2460

QY 2461 TGTCAATAAGCTCTGCAACAAGCTTGCCTCAATTGTGTAGTCTTGTGATGAGACCTGTT 2520
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QY 2521 GTGGAGAGTAGGAGAGAAATATGTAAAGAAAACAGGAAGATACCTGCACTATCATCTCA 2580
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Db 2641 TTTGTGAAAAAGGCACTTTTAACTATGCAAGCAAGAAATCAAGTCCACTATCTGC 2700
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Db 3061 CTACAGAGATTTAAAGCTCTAC 3083

RESULT 2
US-10-216-156-1
; Sequence 1, Application US/10216156
; Publication No. US2003009980A1
; GENERAL INFORMATION:
; APPLICANT: JUNG, Shuguan
; TITLE OF INVENTION: IL-17 Receptor Like Molecules and Uses Thereof
; FILE REFERENCE: 01017/36916A
; CURRENT APPLICATION NUMBER: US/10/216,156
; CURRENT FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: US/09/809,567
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/724,460
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/189,816
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3083
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22) .. (2235)
US-10-216-156-1

Query Match 100.0%; Score 3083; DB 5; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 3083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGCTGGGGGAGGCGACGCGCAATGAGCCCGTGGCTGCACTGCTCGCTCTTTTACG 60
Db 1 TGGCTGGGGGAGGCGACGCGCAATGAGCCCGTGGCTGCACTGCTCGCTCTTTTACG 60
QY 61 GTCAACGCTGCTCTCAAGCGCTGCGAGCTGCTGTGTCGCGCTGCGCGGCTCGCGCG 120
Db 61 GTCAACGCTGCTCTCAAGCGCTGCGAGCTGCTGTGTCGCGCTGCGCGGCTCGCGCG 120
QY 121 TGGGGGTGAGACCTGTGCTGAGGGGAGTGGGGGACGACGAGAAAGTGGGGCTG 180
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Db 181 TACACATGACCTTCAATATATGACATTTATACACCTTATGATTCAGTGGGGAAGAT 240
QY 241 GTGATTGCTGAGCGCCCAAGATATCACCATGACAGATATGCTTGCATGACCAAGTGGCA 300
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QY 301 GTCAACATCTTTGTGCTCCAGGGGCGCTGGGATGAAATTCCTGAAGAAATTTGGGGTA 360
Db 301 GTCAACATCTTTGTGCTCCAGGGGCGCTGGGATGAAATTCCTGAAGAAATTTGGGGTA 360
QY 361 ATATCGAGAGAGCTGAAGTCTGAGGGGAGACAGTGCACAACTGATTTCAAGAGATCCG 420
Db 361 ATATCGAGAGAGCTGAAGTCTGAGGGGAGACAGTGCACAACTGATTTCAAGAGATCCG 420
QY 421 AAGCAGCTCAAGATAGCTTCAAAAGAACTGGAATGAATTCACCTTTCTGAATATG 480
Db 421 AAGCAGCTCAAGATAGCTTCAAAAGAACTGGAATGAATTCACCTTTCTGAATATG 480
QY 481 AATTTGAAACGATTAATTTGCTAAAGGTTCCTTTCTCTCAATTAAGAAAGCAAG 540
Db 481 AATTTGAAACGATTAATTTGCTAAAGGTTCCTTTCTCTCAATTAAGAAAGCAAG 540
QY 541 AATTACCACTTTCTTTTGAACCCGAGCCTGAGCCTGTGTTAAGCCGCAAT 600
Db 541 AATTACCACTTTCTTTTGAACCCGAGCCTGAGCCTGTGTTAAGCCGCAAT 600
QY 601 CTAGCTTGTAAACCTTTCTGAAGCTGGAACCTGAACATGACGACGAGCTGCGAC 660
Db 601 CTAGCTTGTAAACCTTTCTGAAGCTGGAACCTGAACATGACGAGCTGCGAC 660
QY 661 ATGCAAGTCTCTTGAACGACGACGACCACTTGGGCTTCGCTTTCTTATCTTAC 720
Db 661 ATGCAAGTCTCTTGAACGACGACGACCACTTGGGCTTCGCTTTCTTATCTTAC 720
QY 721 TCAAGCTCAAGAGAGAGACCTTTCAAGCGAAGACCTGTAAAGAGAGAGCAATCA 780
Db 721 TCAAGCTCAAGAGAGAGACCTTTCAAGCGAAGACCTGTAAAGAGAGAGCAATCA 780
QY 781 GAGACGACGAGCTCTCTTCAAAATGTTTCTCAAGGGGATTAATAATGAGCTGTG 840
Db 781 GAGACGACGAGCTCTCTTCAAAATGTTTCTCAAGGGGATTAATAATGAGCTGTG 840
QY 841 GATGACATTAACCAAGAAAGATGATGATTAATGCTTAAAGCACTGCTCCCG 900
Db 841 GATGACATTAACCAAGAAAGATGATGATTAATGCTTAAAGCACTGCTCCCG 900
QY 901 TGGGGCGGGCCCATGACGAGCAATGAGCACTGAGTGCCTGATGATTCGCAATTC 960
Db 901 TGGGGCGGGCCCATGACGAGCAATGAGCACTGAGTGCCTGATGATTCGCAATTC 960
QY 961 GCGAGCTCTTCACTGTATGTGCGCAAGAGCAACAAAGAAATATATATTTCACTTTA 1020
Db 961 GCGAGCTCTTCACTGTATGTGCGCAAGAGCAACAAAGAAATATATATTTCACTTTA 1020
QY 1021 GATGAAGAGAGCTGTGAGCTTCTTCACTATCACTGACGACCTCCCAAGAGAGGCTCCGG 1080

Db	1021	GATBAGAGACTCTGAGCTTCCACATACCTGAGCACTCCAGAGAGAGGCTCCG	1089
Qy	1081	CCGCGGCGGAAGTCTTCTCTGCTATTCCAGTAAAGATGGCCAGATACATGATATGC	1140
Db	1081	CCGCGGCGGAAGTCTTCTCTGCTATTCCAGTAAAGATGGCCAGATACATGATATGC	1140
Qy	1141	GTCCAGTGTTCGCGCTACCTCCAGCACTTCGTGCTGTGAGGTGGCTCTGACCTG	1200
Db	1141	GTCCAGTGTTCGCGCTACCTCCAGCACTTCGTGCTGTGAGGTGGCTCTGACCTG	1200
Qy	1201	TGGGAAGACTTCAGGCTCTGTAGAGAGGGCAGAGAGATGGGTATCCAGAGATCCAC	1260
Db	1201	TGGGAAGACTTCAGGCTCTGTAGAGAGGGCAGAGAGATGGGTATCCAGAGATCCAC	1260
Qy	1261	GAGTCCCAAGTTCAATCATTTGTGGTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAAG	1320
Db	1261	GAGTCCCAAGTTCAATCATTTGTGGTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAAG	1320
Qy	1321	AACATCAAAACCAAAAGAGGTGGCCGAGAGCTTCGGGGAAAAGAGAGCTCTTCTGTGGCC	1380
Db	1321	AACATCAAAACCAAAAGAGGTGGCCGAGAGCTTCGGGGAAAAGAGAGCTCTTCTGTGGCC	1380
Qy	1381	GTGTCAAGCCATTCGCGAGAAAGCTCCGCGAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGC	1440
Db	1381	GTGTCAAGCCATTCGCGAGAAAGCTCCGCGAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGC	1440
Qy	1441	AAAGTTATTCGCGGCTCTACTTTGATTTATTCCTGCGAGGGAGACGTCCCGGATCCTAGAC	1500
Db	1441	AAAGTTATTCGCGGCTCTACTTTGATTTATTCCTGCGAGGGAGACGTCCCGGATCCTAGAC	1500
Qy	1501	CTGAGTACCAAGTACAGACTACAGGACAACTTCTCTCAGCTCTGTTCCTCCACTGCACTCC	1560
Db	1501	CTGAGTACCAAGTACAGACTACAGGACAACTTCTCTCAGCTCTGTTCCTCCACTGCACTCC	1560
Qy	1561	CGAGCAACCGGCTTCAGAGAGCCGGGAGCAGACGCGACAGGGCAGAGAGAACTAC	1620
Db	1561	CGAGCAACCGGCTTCAGAGAGCCGGGAGCAGACGCGACAGGGCAGAGAGAACTAC	1620
Qy	1621	TTCCGGAAGCAAGTCAGGCCGGTCCCTTACGTCCGCACTTTCACATGACACAGTTTAT	1680
Db	1621	TTCCGGAAGCAAGTCAGGCCGGTCCCTTACGTCCGCACTTTCACATGACACAGTTTAT	1680
Qy	1681	GACGAGAGAGCCCGACCTGCTGAAAAGCACTTCCTTCATCTCTCCACTGCGC	1740
Db	1681	GACGAGAGAGCCCGACCTGCTGAAAAGCACTTCCTTCATCTCTCCACTGCGC	1740
Qy	1741	TACGGGGAGCAAGCTTGGAGAAATTTGATTCGGGCTTGTTTAAATGATGATCATGTGC	1800
Db	1741	TACGGGGAGCAAGCTTGGAGAAATTTGATTCGGGCTTGTTTAAATGATGATCATGTGC	1800
Qy	1801	AAACCAAGGCTCTGAGAGTCACTTCGCTTAAAGTAGAGGCGCTGTTCTTGGGGCAAC	1860
Db	1801	AAACCAAGGCTCTGAGAGTCACTTCGCTTAAAGTAGAGGCGCTGTTCTTGGGGCAAC	1860
Qy	1861	GGACCAAGCTCGACTCCCAAGCAGAGAGTCAAGATGGGGGCTTGGACAAAGACGGGGAGCC	1920
Db	1861	GGACCAAGCTCGACTCCCAAGCAGAGAGTCAAGATGGGGGCTTGGACAAAGACGGGGAGCC	1920
Qy	1921	CGGCTGCGCTTGAAGGTAGAGCGCGCTCGCAACCTTCGTGACACAGTAAAGCCGGC	1980
Db	1921	CGGCTGCGCTTGAAGGTAGAGCGCGCTCGCAACCTTCGTGACACAGTAAAGCCGGC	1980
Qy	1981	AGCCCTTCGACATGCGCGGGAGCTCAAGCACTTATGACTGCTGTGCCCTCATCCGAG	2040
Db	1981	AGCCCTTCGACATGCGCGGGAGCTCAAGCACTTATGACTGCTGTGCCCTCATCCGAG	2040
Qy	2041	CTGTCTCTGCACTGATGAAAGAACTCTCGACGGAACAGACAGAAACGTCTTCCCTGACG	2100
Db	2041	CTGTCTCTGCACTGATGAAAGAACTCTCGACGGAACAGACAGAAACGTCTTCCCTGACG	2100
Qy	2101	GAGAGCGTGTCTCTCTTTCAGGCTGGGTAGAGAGAACTCTCGCCCTTCTTCCAG	2160
Db	2101	GAGAGCGTGTCTCTCTTTCAGGCTGGGTAGAGAGAACTCTCGCCCTTCTTCCAG	2160

Db	2101	GAGAGCGGTCCTCCTCTTCAGGCGCTGGGTAGAGGAACCTCTGCGCTTCTCTTCCAAG	2160
Qy	2161	CTCCTCTCTTCTGGGTCATGCAAGCAAGACTCTTGGTTCCGCAAGCTACATGAAGAACTC	2220
Db	2161	CTCTCTCTCTTGGGTCATGCAAGCAAGACTCTTGGTTCCGCAAGCTACATGAAGAACTC	2220
Qy	2221	CAGCGGTGCGCCCTTGTGTAACAAAAGAAAGACTTAAGCATTTGCCACTTTAGCTGCTG	2280
Db	2221	CAGCGGTGCGCCCTTGTGTAACAAAAGAAAGACTTAAGCATTTAGCTGCTG	2280
Qy	2281	CTTCCCTCTGAATCCCAAGCTCATCTCCCTGGTTGACATGCGCCACTTGAAGCTGAGGCTCT	2340
Db	2281	CCTCCCTCTGAATCCCAAGCTCATCTCCCTGGTTGACATGCGCCACTTGAAGCTGAGGCTCT	2340
Qy	2341	CATACCAAGATATTTTGAGATGAAATGCTGGCCAGTACTTGTCTCCCTTGCCCAACCTT	2400
Db	2341	CATACCAAGATATTTTGAGATGAAATGCTGGCCAGTACTTGTCTCCCTTGCCCAACCTT	2400
Qy	2401	TTACCCGATATCTTGAACAACTCCCAATTTTCTAAATGATATGAGCTCTGAAGGCA	2460
Db	2401	TTACCCGATATCTTGAACAACTCCCAATTTTCTAAATGATATGAGCTCTGAAGGCA	2460
Qy	2461	TGTCATTAAGTCTGACAAACAGCTTGCCAATTTTGTTAGTCTTGGATCAGACCTGT	2520
Db	2461	TGTCATTAAGTCTGACAAACAGCTTGCCAATTTTGTTAGTCTTGGATCAGACCTGT	2520
Qy	2521	GTCGAGAGTGGAGGAGAAATATGTAAAGAAAACAGAAATATCTGACATAATCATTTCA	2580
Db	2521	GTCGAGAGTGGAGGAGAAATATGTAAAGAAAACAGAAATATCTGACATAATCATTTCA	2580
Qy	2581	GACTTCATTGAGCTCTGCAAACTTGGCTGTGGCTATTGGCTATTTGGATTTGAAATGC	2640
Db	2581	GACTTCATTGAGCTCTGCAAACTTGGCTGTGGCTATTGGCTATTTGGATTTGAAATGC	2640
Qy	2641	TTTGTGAAAAAAGGCACTTTTACATCATATAGCCACAGAAATCAAGTCCAGTCTATCTGG	2700
Db	2641	TTTGTGAAAAAAGGCACTTTTACATCATATAGCCACAGAAATCAAGTCCAGTCTATCTGG	2700
Qy	2701	AAATCCATGTGTATATGGAGATAATGTTCTCATTTATTTTGAATPAAATTTAATATGGC	2760
Db	2701	AAATCCATGTGTATATGGAGATAATGTTCTCATTTATTTTGAATPAAATTTAATATGGC	2760
Qy	2761	ATGGGTGTTAAATTAAGCTTTGAGTCAAAAGTCAAGAAAGTGACTGAATATACAGTCACT	2820
Db	2761	ATGGGTGTTAAATTAAGCTTTGAGTCAAAAGTCAAGAAAGTGACTGAATATACAGTCACT	2820
Qy	2821	TTTATGAAATGAAAAAATT	2880
Db	2821	TTTATGAAATGAAAAAATT	2880
Qy	2881	CTGAGAGGGGCCCAAGCTTACGCGATACCCAGCTTCTGTCAAAATGATGTCCTTATATGA	2940
Db	2881	CTGAGAGGGGCCCAAGCTTACGCGATACCCAGCTTCTGTCAAAATGATGTCCTTATATGA	2940
Qy	2941	GTCGTATTTATTAAGCTTAGGCACTGGCCGTGTTTATCAACGTCTGATCTGGAAAACTGCT	3000
Db	2941	GTCGTATTTATTAAGCTTAGGCACTGGCCGTGTTTATCAACGTCTGATCTGGAAAACTGCT	3000
Qy	3001	AGCTTGGGATCTTTGTGAGAGGAACCTTACTTCTGTGTGTGACATAATTTGACAAACTAC	3060
Db	3001	AGCTTGGGATCTTTGTGAGAGGAACCTTACTTCTGTGTGTGACATAATTTGACAAACTAC	3060
Qy	3061	CTACAGAGATTTAAAGCTTAAG 3083	
Db	3061	CTACAGAGATTTAAAGCTTAAG 3083	

RESULT 3
US-10-616-788-1
; Sequence 1, Application US/10616788
; Publication No. US20040048338A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian

[illegible]

Accession	Sequence	Length
D8	CTCAGAGGGGCCAAGCTTACGCGTACCCAGTTTCTTGTCACAAAGTGTCCTTATGTGA	2940
D9	2941 GTCGATTATTATAGCTAGAGCATGCGCGGTCTGTTTACACGTCGTACTGCGGAAAACTGCT	3000
D10	2941 GTCGATTATTATAGCTAGAGCATGCGCGGTCTGTTTACACGTCGTACTGCGGAAAACTGCT	3000
D11	3001 AGCTTGGGATCTTTGTGAGGAACCTTACTTCTGTGTGTGACATTAATTGGACAAACTAC	3060
D12	3001 AGCTTGGGATCTTTGTGAGGAACCTTACTTCTGTGTGTGACATTAATTGGACAAACTAC	3060
D13	3061 CTACAGAGATTTAAGCTTTAAG 3083	
D14	3061 CTACAGAGATTTAAGCTTTAAG 3083	

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RESULT 4
US-10-842-006-3
  Sequence 3, Application US/10842006
  Publication No. US20040235104A1
  GENERAL INFORMATION:
  APPLICANT: Yang, Ruey-Bing
  TITLE OF INVENTION: A Novel Human SRE Mcl
  TITLE OF INVENTION: Therefor
  FILE REFERENCE: MP103-071P1M
  CURRENT APPLICATION NUMBER: US/10/842, 006
  CURRENT FILING DATE: 2004-05-07
  PRIOR APPLICATION NUMBER: 60/469522
  PRIOR FILING DATE: 2003-05-08
  NUMBER OF SEQ ID NOS: 12
  SOFTWARE: FASTSEQ for Windows Version 4.0.
  SEQ ID NO 3
  LENGTH: 3083
  TYPE: DNA
  ORGANISM: Homo Sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (22)...(2241)
US-10-842-006-3

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Query Match 100.0%; Score 3083; DB 8; Length 3083;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	TGGCTGGGGGAGGCGACCGGCATATGGCCCCGGTGGCTGGCAGCTCTCCGATCTCTTAAACG	60
Db	1	TGGCTGGGGGAGGCGACCGGCATATGGCCCCGGTGGCTGGCAGCTCTCCGATCTCTTAAACG	60
Oy	61	GTCAACGCTTCCTCAACGGCTCGCAGCTGGCTGTGGCCGCTGTGGCGGGATCCGCGCGCG	120
Db	61	GTCAACGCTTCCTCAACGGCTCGCAGCTGGCTGTGGCCGCTGTGGCGGGATCCGCGCGCG	120
Oy	121	TGGGGCGTGGACACTGTGGCTGGAGGGGAGTGGGGCGACGACAGAAAACATGGGGCTG	180
Db	121	TGGGGCGTGGACACTGTGGCTGGAGGGGAGTGGGGCGACGACAGAAAACATGGGGCTG	180
Oy	181	TAAACAATCACTTCAAAATATGACAAATTGTACACCTTCTGAATTCAGTGGGGAAAGCAT	240
Db	181	TAAACAATCACTTCAAAATATGACAAATTGTACACCTTCTGAATTCAGTGGGGAAAGCAT	240
Oy	241	GTGATTTGTGAAGCCCGAGATATATCAACATCAAGCAGATGTCTTGCATGACCAATGGGCA	300
Db	241	GTGATTTGTGAAGCCCGAGATATATCAACATCAAGCAGATGTCTTGCATGACCAATGGGCA	300
Oy	301	GTCAACATTTCTTTGGTCCCCCAGGGGCCCTCGGCATTCGAAATTCCTGAAGAATTTCCGGTA	360
Db	301	GTCAACATTTCTTTGGTCCCCCAGGGGCCCTCGGCATTCGAAATTCCTGAAGAATTTCCGGTA	360
Oy	361	ATACTGAGAGAGCTGAAGTCGAGGGGAGAGACAGTGCACAACTGATTTTAAAGGATCCG	420
Db	361	ATACTGAGAGAGCTGAAGTCGAGGGGAGAGACAGTGCACAACTGATTTTAAAGGATCCG	420
Oy	421	AAGCAGCTCAACATGACTTCAAAAGAACTGGAAATGGAATTCAACTTTCTGGAATATG	480
Db	421	AAGCAGCTCAACATGACTTCAAAAGAACTGGAAATGGAATTCAACTTTCTGGAATATG	480

Db 421 AAGACGCTCAACAGTAGCTTCAAAAGAACTGAAATGGAATCTCAACCTTTCTGAAATATG 480
QY 481 AATTTGAAACGGATTTATTTCTTAAAGTTGTCCCTTTCTTCATTAATAAAGCAAAGC 540
Db 481 AATTTGAAACGGATTTATTTCTTAAAGTTGTCCCTTTCTTCATTAATAAAGCAAAGC 540
QY 541 AATTTACACGCTTTCTTTCTTTAGAACCCGAGCTGTGACCTGTGTTATACGCGGCAAT 600
Db 541 AATTTACACGCTTTCTTTCTTTAGAACCCGAGCTGTGACCTGTGTTATACGCGGCAAT 600
QY 601 CTAGCTTGTAAACCTTTCTGGAAGCCTCGGAACCTGAACAACGAGCAATGAGCTCGAC 660
Db 601 CTAGCTTGTAAACCTTTCTGGAAGCCTCGGAACCTGAACAACGAGCAATGAGCTCGAC 660
QY 661 ATGCAAGTGTCTTTCGACCAACGACGACCAATTTGGGCTTCCGTTTCTTATTTCTTAC 720
Db 661 ATGCAAGTGTCTTTCGACCAACGACGACCAATTTGGGCTTCCGTTTCTTATTTCTTAC 720
QY 721 TACAAGCTCAAGACGAAAGGACCTTTCAAGCAAAAGACCTGTAAAGAGAGAGCAATACA 780
Db 721 TACAAGCTCAAGACGAAAGGACCTTTCAAGCAAAAGACCTGTAAAGAGAGAGCAATACA 780
QY 781 GAGACGACGAGCTGCTCTCTTCAAAAATGTTTCTCAGGGGATTAATAATTAGCTGTG 840
Db 781 GAGACGACGAGCTGCTCTCTTCAAAAATGTTTCTCAGGGGATTAATAATTAGCTGTG 840
QY 841 GATTACACTTAACAACAAGAAAGATGATGATTAATGCTTAAAGCAATGCACTCCCG 900
Db 841 GATTACACTTAACAACAAGAAAGATGATGATTAATGCTTAAAGCAATGCACTCCCG 900
QY 901 TGGGCGGGGCGCATGACGCAATGGGCATACAGTCCCACTGGTATGCAATGCGGATTC 960
Db 901 TGGGCGGGGCGCATGACGCAATGGGCATACAGTCCCACTGGTATGCAATGCGGATTC 960
QY 961 GCGACGCTCTTCACTGTGATGTGCGCAAGAACCAACAAGAAATATATTTACATTTA 1020
Db 961 GCGACGCTCTTCACTGTGATGTGCGCAAGAACCAACAAGAAATATATTTACATTTA 1020
QY 1021 GATGAAGAGAGCTGTGATGCTTCCATACATGACGACTCCCAAGAGAGAGCTCCCG 1080
Db 1021 GATGAAGAGAGCTGTGATGCTTCCATACATGACGACTCCCAAGAGAGAGCTCCCG 1080
QY 1081 CCGCGGCGGAAGGCTTTCTGCTGCTAATTCAGTAAAGATGGCCAGATACATGAATGTC 1140
Db 1081 CCGCGGCGGAAGGCTTTCTGCTGCTAATTCAGTAAAGATGGCCAGATACATGAATGTC 1140
QY 1141 GTCCAGTGTGTCCTACTTCTCCAGAGCTTGTGGCTGTGAGGTGGCTTGGACCTG 1200
Db 1141 GTCCAGTGTGTCCTACTTCTCCAGAGCTTGTGGCTGTGAGGTGGCTTGGACCTG 1200
QY 1201 TGGGAAGACTTCAAGCTCTGTAGAGAGGCAAGAGAAATGGGTCAATCCAGAAATCCAC 1260
Db 1201 TGGGAAGACTTCAAGCTCTGTAGAGAGGCAAGAGAAATGGGTCAATCCAGAAATCCAC 1260
QY 1261 GAGTCCCACTTCAATTTGTGTTTGTTCGAAAGATGAATGATCTTTGTGCAAGAA 1320
Db 1261 GAGTCCCACTTCAATTTGTGTTTGTTCGAAAGATGAATGATCTTTGTGCAAGAA 1320
QY 1261 GAGTCCCACTTCAATTTGTGTTTGTTCGAAAGATGAATGATCTTTGTGCAAGAA 1320
Db 1261 GAGTCCCACTTCAATTTGTGTTTGTTCGAAAGATGAATGATCTTTGTGCAAGAA 1320
QY 1321 AACTACAAACAAGAGAGGTGGCGAGGCTCGGGGAAAGAGAGCTTCTCGTGGGCG 1380
Db 1321 AACTACAAACAAGAGAGGTGGCGAGGCTCGGGGAAAGAGAGCTTCTCGTGGGCG 1380
QY 1381 GTGTGAGCATTGCGGAAAGCTCCGCAAGCCAGACAGATTCGTCCGCGGCGCTCAGC 1440
Db 1381 GTGTGAGCATTGCGGAAAGCTCCGCAAGCCAGACAGATTCGTCCGCGGCGCTCAGC 1440
QY 1441 AAGTTTATGCGCGTCACTTTGATTAATCTCTGGAAGAGAGAGCTCCCGGATATCTAGAC 1500
Db 1441 AAGTTTATGCGCGTCACTTTGATTAATCTCTGGAAGAGAGAGCTCCCGGATATCTAGAC 1500
QY 1501 CTGAGTACCAAGATACAGACTATGAGCAATCTTCTCAGCTGTGTTCCACCTGCACTCC 1560
Db 1501 CTGAGTACCAAGATACAGACTATGAGCAATCTTCTCAGCTGTGTTCCACCTGCACTCC 1560

QY 1561 CGAGACCAAGGCTCCAGAGAGCGGGGAGACACAGCGACAGGGGACAGAAAGAACTAC 1620
Db 1561 CGAGACCAAGGCTCCAGAGAGCGGGGAGACACAGCGACAGGGGACAGAAAGAACTAC 1620
QY 1621 TTCGGAGAGATGACAGGCGGCTCCATATGTCGCCATTTGCAACATGACCAAGTTATTT 1680
Db 1621 TTCGGAGAGATGACAGGCGGCTCCATATGTCGCCATTTGCAACATGACCAAGTTATTT 1680
QY 1681 GACGAGAGAGCCGAGCTGTGTAAGAAAGGTTGTTCCCTTCATCTCTCCACCTGCGC 1740
Db 1681 GACGAGAGAGCCGAGCTGTGTAAGAAAGGTTGTTCCCTTCATCTCTCCACCTGCGC 1740
QY 1741 TACCGGAGAGCCGAGCTGTGTAAGAAATTTGATTTGGGCTGGTTTAAATGATCAATGTC 1800
Db 1741 TACCGGAGAGCCGAGCTGTGTAAGAAATTTGATTTGGGCTGGTTTAAATGATCAATGTC 1800
QY 1801 AAACGAGGCTGAGAGATGACTTGTGCTTAAAGTGAAGGCGCTGTTCTTGGGGCAAC 1860
Db 1801 AAACGAGGCTGAGAGATGACTTGTGCTTAAAGTGAAGGCGCTGTTCTTGGGGCAAC 1860
QY 1861 GGAACGAGGCTGAGAGATGACTTGTGCTTAAAGTGAAGGCGCTGTTCTTGGGGCAAC 1920
Db 1861 GGAACGAGGCTGAGAGATGACTTGTGCTTAAAGTGAAGGCGCTGTTCTTGGGGCAAC 1920
QY 1921 CCGGCTGCTTGAAGGATGAGGCTGCGGCGCTGCAACCCCTGCTGCAACGCTGAAAGCGCGC 1980
Db 1921 CCGGCTGCTTGAAGGATGAGGCTGCGGCGCTGCAACCCCTGCTGCAACGCTGAAAGCGCGC 1980
QY 1981 AGCCCTCGGAGATGCGGGGAGCTCAAGGATCTATGACTGCTGTGCTGCTCATCCGAG 2040
Db 1981 AGCCCTCGGAGATGCGGGGAGCTCAAGGATCTATGACTGCTGTGCTGCTCATCCGAG 2040
QY 2041 CTGTCTTGCACATGAGAGAGATCTTGAAGGAGCAGACAGAAACGTTCTCCCTGACG 2100
Db 2041 CTGTCTTGCACATGAGAGAGATCTTGAAGGAGCAGACAGAAACGTTCTCCCTGACG 2100
QY 2101 GAGAGGATGCTCTCTCTTCAAGGCTGCGGAGAGAGAACTCTGCTGCTTCTTCCAG 2160
Db 2101 GAGAGGATGCTCTCTCTTCAAGGCTGCGGAGAGAGAACTCTGCTGCTTCTTCCAG 2160
QY 2161 CTCTCTCTTCTGAGGATGAGCAAGAGATCTTGGTGGCGGAGCTACATGATGAACTC 2220
Db 2161 CTCTCTCTTCTGAGGATGAGCAAGAGATCTTGGTGGCGGAGCTACATGATGAACTC 2220
QY 2221 CAGCGGATGCGGCTTTGTTAAACAAAGAGATGATGATGCACTTTAGCTGCTG 2280
Db 2221 CAGCGGATGCGGCTTTGTTAAACAAAGAGATGATGATGCACTTTAGCTGCTG 2280
QY 2281 CCTCCTCTGATTTCCCAAGCTCATCTCCTGCTGATGAGCCCATTTGAGCTGAGCTC 2340
Db 2281 CCTCCTCTGATTTCCCAAGCTCATCTCCTGCTGATGAGCCCATTTGAGCTGAGCTC 2340
QY 2341 CATACAAAGATATTTGAGATGAGAAATGCTGGCAATGCTTCTCCCTGCGGCAACCT 2400
Db 2341 CATACAAAGATATTTGAGATGAGAAATGCTGGCAATGCTTCTCCCTGCGGCAACCT 2400
QY 2401 TTACGAGATATCTTGAACAACCTCCCAATTTCTAATAATGATGAGCTGTGAAGGCA 2460
Db 2401 TTACGAGATATCTTGAACAACCTCCCAATTTCTAATAATGATGAGCTGTGAAGGCA 2460
QY 2461 TGTCAATAAGGCTGTGCAACAAGCTTGGCAATTTGGTTAGTCTTGGAGTCAAGCTGTT 2520
Db 2461 TGTCAATAAGGCTGTGCAACAAGCTTGGCAATTTGGTTAGTCTTGGAGTCAAGCTGTT 2520
QY 2521 GTGGAGAGTAAAGGAGAAATATGTAAGAAACAGAAAGATACGAGCACTAATCACTCA 2580
Db 2521 GTGGAGAGTAAAGGAGAAATATGTAAGAAACAGAAAGATACGAGCACTAATCACTCA 2580
QY 2581 GACTTCATTGAGCTGTGCAACCTTTGCTGTTGCTATTGGCTACCTGATTTGAATGTC 2640
Db 2581 GACTTCATTGAGCTGTGCAACCTTTGCTGTTGCTATTGGCTACCTGATTTGAATGTC 2640

QY 2641 TTTGTGAAAAAGGCACTTTTAACATCATAGCCACAGAAATCAAGTCCAGTCTATCTGG 2700
DB 2641 TTTGTGAAAAAGGCACTTTTAACATCATAGCCACAGAAATCAAGTCCAGTCTATCTGG 2700
QY 2701 AATCCATGTTGTATTTGCAAGATAATGTTCTCATTTATTTTGTGANGTAATTAACATTGCC 2760
DB 2701 AATCCATGTTGTATTTGCAAGATAATGTTCTCATTTATTTTGTGANGTAATTAACATTGCC 2760
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DB 2761 AAGGGGTTTAAATAGCTTTGAGTCAAAAGTCAAGAAAGTCAAGTAATATACAGTCACT 2820
QY 2821 TTTATGAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 2880
DB 2821 TTTATGAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 2880
QY 2881 CTCGAGGGGCCCAAGCTTACGCGTACCCAGCTTTCTTTGACAAAGTGTCCCTATAGTGA 2940
DB 2881 CTCGAGGGGCCCAAGCTTACGCGTACCCAGCTTTCTTTGACAAAGTGTCCCTATAGTGA 2940
QY 2941 GTCGTATTTAATAGCTAGGCACTGGCCGCTGTTTACAAAGTGTGATCGGAAAACTGCT 3000
DB 2941 GTCGTATTTAATAGCTAGGCACTGGCCGCTGTTTACAAAGTGTGATCGGAAAACTGCT 3000
QY 3001 AGCTTGGGATCTTTGTGAAGAACTTACTTCTGTGTGTGACATATTTGGAACAACCTAC 3060
DB 3001 AGCTTGGGATCTTTGTGAAGAACTTACTTCTGTGTGTGACATATTTGGAACAACCTAC 3060
QY 3061 CTACAGAGATTTAAAGCTCTTAC 3083
DB 3061 CTACAGAGATTTAAAGCTCTTAC 3083

RESULT 5

US-10-842-006-1
; Sequence 1, Application US/10842006
; Publication No. US20040235104A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Ruey-Bing
; TITLE OF INVENTION: A Novel Human SER Molecule and Uses
; FILE OF INVENTION: Therefore
; FILE REFERENCE: MP103-071PIRM
; CURRENT APPLICATION NUMBER: US/10/842, 006
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469522
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90) ... (2309)
US-10-842-006-1

Query Match 91.5%; Score 2822.4; DB 8; Length 4477;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2826; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TGGCTGGGGGAGGCGACGGCAATGAGCCCGTGGCTGACAGTCTGCTCCGCTCTTTAGG 60
DB 69 TGGCTGGGGGAGGCGACGGCAATGAGCCCGTGGCTGACAGTCTGCTCCGCTCTTTAGG 128
QY 61 GTCAAGCTGTCTCAACGGCTGCGACAGTGTGTGGCGCTGGCGGGTCCGGCCGCGG 120
DB 129 GTCAAGCTGTCTCAACGGCTGCGACAGTGTGTGGCGCTGGCGGGTCCGGCCGCGG 188
QY 121 TGGGAGCTGTGACAGCTGTGTGGCTGGAGGGAGGTGGGGCCAGCCAGCAAGAACTGGGCTG 180
DB 189 CCGGAGCGCGACAGCTGTGTGGCTGGAGGGAGGTGGGGCCAGCCAGCAAGAACTGGGCTG 248

QY 181 TACAACATCAGCTTCAAAATATGACAATTGTACACCACTACTTGAATTCAGTGGGGAAGCAT 240
DB 249 TACAACATCAGCTTCAAAATATGACAATTGTACACCACTACTTGAATTCAGTGGGGAAGCAT 308
QY 241 GTGATTGTGAGCGCCGAGAAATTCACATCAGCCAGTATGCTTGGCAAGCAAGTGGCA 300
DB 309 GTGATTGTGAGCGCCGAGAAATTCACATCAGCCAGTATGCTTGGCAAGCAAGTGGCA 368
QY 301 GTACACATCTTTGGGCCGAGGGGCCCTGGCATCGAATTCGTAAGAAATTTGGGGTA 360
DB 369 GTACACATCTTTGGGCCGAGGGGCCCTGGCATCGAATTCGTAAGAAATTTGGGGTA 428
QY 361 ATACTGAGAGAGCTGAGTGGAGGGAGAGACAGTGCACAACTGATTTCTAAAGATCCG 420
DB 429 ATACTGAGAGAGCTGAGTGGAGGGAGAGACAGTGCACAACTGATTTCTAAAGATCCG 488
QY 421 AAGCAGCTCAACAGTAGTCTTCAAAAGAACTGGAATGGAATTCACCTTTCTGAATATG 480
DB 489 AAGCAGCTCAACAGTAGTCTTCAAAAGAACTGGAATGGAATTCACCTTTCTGAATATG 548
QY 481 AATTTGAAAGGATTAATTTGTAAGGTGTCCCTTTCTTCCATTTAAAAAGAAAGC 540
DB 549 AATTTGAAAGGATTAATTTGTAAGGTGTGTCCCTTTCTTCCATTTAAAAAGAAAGC 608
QY 541 AATTACCACTTTCTTCTTTGAAACCGAGCTGTGACCTGTGTACAGCCGGACAAT 600
DB 609 AATTACCACTTTCTTCTTTGAAACCGAGCTGTGACCTGTGTACAGCCGGACAAT 668
QY 601 CTAGCTTGTAAACCTTTCTGAAAGCTTGGAACTGGAACATCAGCCAGCATGGCTGGAGC 660
DB 669 CTAGCTTGTAAACCTTTCTGAAAGCTTGGAACTGGAACATCAGCCAGCATGGCTGGAGC 728
QY 661 AAGCAGGTGCTCTTGGACACAGGACAGCAACTTGGCTTCCGTTCTTATCTAC 720
DB 729 AAGCAGGTGCTCTTGGACACAGGACAGCAACTTGGCTTCCGTTCTTATCTTAC 788
QY 721 TACAAGCTCAACAGAGAAAGACCTTTCAAGCGAAAGACCTGTGAAGAGCAAGCAACTACA 780
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QY 841 GATGACACTAACAACAAGAAAGTGAATGCAATTAATGCTTAAAGCAGTGCACCTCCCG 900
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QY 901 TGGGCGGGGCCCATGAGAGCCATGAGCCATCAGTGCACCTGGTATGCTATTCGGCATTC 960
DB 969 TGGGCGGGGCCCATGAGAGCCATGAGCCATCAGTGCACCTGGTATGCTATTCGGCATTC 1028
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DB 1209 GTCAAGTGTGTGCTTACTTCTTCCAGACTTCTGTGTGTGAGTGTGCTGTGACCTG 1268
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DB 1269 TGGGAAAGCTTACAGCTTGTGTGAAGAGGAGAGAAATGGGTATTCAGAAAGATCCAC 1328
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Db 1389 AACTTACAAACACAAAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGCG 1448
Qy 1381 GTGTGAGCCATTGGCCGAAAGCTCCGACAGGACAGAGTTCGTCCGGGGGCTCAGC 1440
Db 1449 GTGTGAGCCATTGGCCGAAAGCTCCGACAGGACAGAGTTCGTCCGGGGGCTCAGC 1508
Qy 1441 AAGTTTATGCGCGCTTACTTGTATTTCTTGCAGAGGAGACGTCGCCGATCTTAC 1500
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Qy 1501 CTGAGTACCAAGTACAGATCTATGACAAATCTTCTCAAGCTCTGTCCCACTGCACTCC 1560
Db 1569 CTGAGTACCAAGTACAGATCTATGACAAATCTTCTCAAGCTCTGTCCCACTGCACTCC 1628
Qy 1561 CGAGACCAAGGCTTCCAGAGGCGGGGACACACGACAGAGGACAGAGAAAGTAC 1620
Db 1629 CGAGACCAAGGCTTCCAGAGGCGGGGACACACGACAGAGGACAGAGAAAGTAC 1688
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Db 1689 TTCGAGAGCAAGTACAGGCGGCTCCCTTATAGTGCATTTGCAACATGACAGTTAT 1748
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Db 1869 AAACCAAGGCGCTGAGAGTGAATCTTGCCTTAAAGTAAAGGCGGCTGTTCTTGGGGCAAC 1928
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Db 2109 CTGTCTCTGCACTGATGAGAGATCTCGACCGACCAAGACAAAGTCTTCTCCAGC 2168
Qy 2101 GAGAGGTGTCTCTCTTCAAGGCTGTGAGAGAGAACCTTCGCTTCTTCCAG 2160
Db 2169 GAGAGGTGTCTCTCTTCAAGGCTGTGAGAGAGAACCTTCGCTTCTTCCAG 2228
Qy 2161 CTCTCTCTTCTGAGGATGCAAGAGATCTGTGTCGCGAGCTACATGATGAACTC 2220
Db 2229 CTCTCTCTTCTGAGGATGCAAGAGATCTGTGTCGCGAGCTACATGATGAACTC 2288
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Db 2289 CAGCGGATGCGCCCTTGTGTAACAAAGAGTCTAAGACTTGCACCTTATGCTGCTG 2348
Qy 2281 CTCTCTCTGATTCCTCAAGCTCATCTCTGTGTTGCAATGCGCACTTGAAGCTGAGGCT 2340
Db 2349 CTCTCTCTGATTCCTCAAGCTCATCTCTGTGTTGCAATGCGCACTTGAAGCTGAGGCT 2408
Qy 2341 CATACAGAGTATTTGAGAGTGAATGCTGCGCAGTACTTGTCTCCCTTCCCAACCT 2400

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Db 2409 CATACAGAGTATTTGAGTGAATGCTGCGCAGTACTTGTCTCCCTTGCCCAACCT 2468
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Db 2469 TTACCGGATATCTTGAACAACTCTCCAAATTTCTTAAATGATATGAGCTCTGAAGGCA 2528
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Qy 2761 ATGGGTGTTAATATAGCTTTGAGTCAAAAGTCAAGAAAGTACTGAATATACGTACCT 2820
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Db 2889 TTTTGAAGTGA 2900

RESULT 6
US-10-608-449-1
; Sequence 1, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Tsinghua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: 12003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 4477
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-608-449-1

Query Match      91.5%; Score 2822.4; DB 8; Length 4477;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2826; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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309 GTGATGTCGACGCCAGATATACCATCAGCCAGTATGCTTGCATGACCAAGTGGCA 368
Qy GTGATGTCGACGCCAGATATACCATCAGCCAGTATGCTTGCATGACCAAGTGGCA 360
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429 ATACTGAGAGAGTCGAGTGGAGGAGCAGTGGCAACATGATCTTAAAGATCCG 488
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609 AATTACCAACCTTCTTCTTGAACCCGAGCCTGTGACCTGTGTTAAGCCGGAACAT 668
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669 CTAGCTTGAACCTTCTTGAAGCCTCGGAACCTGAACATCAGCCAGATGGCTGGAC 728
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1809 TACCGGAGCCGCTTGGAGAAATTTGATTCGGGCTTGGTTTAAATGATGATGTC 1868
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2169 GAGAGCGTGTCTCTCTTCAAGGCTGGGTGAGAGAACTCTGCTTCTTCAAG 2228
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2349 CTCTCCTCTGATTTCCCAAGCTCATCTCTGTTCAGAGGCGCACTTGAAGTGAAGTCT 2408
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Db 2889 TTTATGAATGA 2900

RESULT 7

US-10-343-348-15
; Sequence 15, Application US/10343348
; Publication No. US20040038242A1
; GENERAL INFORMATION:
; APPLICANT: Edmonds, Brian
; APPLICANT: Micanovic, Radmila
; APPLICANT: Su, WeiJia
; APPLICANT: Su, Eric
; APPLICANT: Techang, Sheng-Hung
; APPLICANT: Wang, He
; TITLE OF INVENTION: No. US20040038242A1 secreted proteins and their uses
; FILE REFERENCE: X-14001
; CURRENT APPLICATION NUMBER: US/10/343,348
; CURRENT FILING DATE: 2003-01-29
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 4392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1662)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (82)..()
; OTHER INFORMATION:
; US-10-343-348-15

Query Match 89.4%; Score 2757.4; DB 7; Length 4392;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2805; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

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QY 82 TCGCAGCTGCTGTGGCCGCTGGCGGGTTCGGCGCGCGCTGGGGCGTGCACACTGTGGC 141
Db 61 TCGCAGCTGCTGTGGCCGCTGGCGGGTTCGGCGCGCGCTGGGGCGTGCACACTGTGGC 120

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Db 181 GACAAATTGTACCACTCACTTTGAATCCAGTGGGGAAGCATGTGTATGCTGACGCCGAAT 240
QY 262 ATCACCATGACGCGATATGCTTGCATGACCAAGTGGCAGTCCATTTCTTGTCCCA 321
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QY 322 GGGGCGCTTGGCATGCAATTTCTGAAAGATTTCCGGGTATTTCTGAGAGAGCTGAAGTGG 381
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Db 361 GAGGGAAGACAGTGCACACATGATTTTAAAGATCCGAAAGCTCAACAGTACCTTC 420
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QY 502 GTTAAAGTGTCCCTTTCTTCTTCAATTAAGAAAGCAATTTACACCTTCTCTT 561
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QY 562 AGAACCAGACCTGTGACCTGTGTTGTTACAGCGGACATCTAGCTTTAAACCTTCTGG 621
Db 541 AGAACCAGACCTGTGACCTGTGTTGTTACAGCGGACATCTAGCTTTAAACCTTCTGG 600
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RESULT 8
US-09-863-818A-9
Sequence 9, Application US//09863818A
Publication No. US20030092881A1
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
TITLE OF INVENTION: MALAYSIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX01170K
CURRENT APPLICATION NUMBER: US/09/863,818A
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/206,862
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patencin version 3.1
SEQ ID NO 9
LENGTH: 2786
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (194)..(194)
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RESULT 9
US-10-749-144-9

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; Publication No. US20040197306A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX01170K1
; CURRENT APPLICATION NUMBER: US/10/749,144
; PRIOR FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 60/206,862
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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Query Match 87.5%; Score 2696.6; DB 8; Length 2786;
Best Similarity 99.2%; Pred. No. 0;
Matches 2718; Conservative 0; Mismatches 20; Indels 3; Gaps 1;

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Qy      2461 TGTCCATAGTCTGACACACACTTGCCTCAATTTGGTTAGTCTTGGATCAGAGCTGTT 2520
Db      2506 TGTCCATAGTCTGACACACACTTGCCTCAATTTGGTTAGTCTTGGATCAGAGCTGTT 2565
Qy      2521 GTGGAGGTAGGAGGAATATGTAAGAAAGAAACAGAGAGATACCTGCACTAATCTCA 2580
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Qy      2581 GACTTCATTGAGCTCTGCAAACTTGCCTGTTGCTATTGCTACCTTAATTTGAATGC 2640
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Qy      2641 TTTGTGAAAAAGGCACTTTTAACATCATAGCACAAGAAATCAAGTCCAGTCTACTG 2700
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Qy      2701 AATCCATGTTGATGACATATATGTTCTCATTTATTTTG 2741
Db      2746 AATCCATGTTGATGACATATATGTTCTCATTTATTTTG 2786

RESULT 11
US-10-608-449-3
; Sequence 3, Application US/10608449
; Publication No. US20040265834A1
; GENERAL INFORMATION:
; APPLICANT: Tsinghua University
; TITLE OF INVENTION: Human Interleukin-17 Receptor Like Molecule
; FILE REFERENCE: 12003269C-US
; CURRENT APPLICATION NUMBER: US/10/608,449
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 4508
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-608-449-3

Query Match      87.1%; Score 2684.6; DB 8; Length 4508;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2690; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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2033 ACGGTAGCGGCGCTGCAACCTCTGTGACACAGGTGAAGCCGAGCCTCTGGAACA 2092
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2093 TGCCTCGGAGCTCAGGCAATCTATGACTGTCTGTGCTCTATCCGAGCTGTCTTGCCAC 2152
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 ; Sequence 42, Application US/10477714
 ; Publication No. US2005003018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LAL, Preeti G.; WARREN, Bridget A.;
 ; APPLICANT: XU, Yuming; DUGAN, Brendan M.;
 ; APPLICANT: HONCHIELL, Cynthia D.; KALLICK, Deborah A.;
 ; APPLICANT: BAUGHN, Mariah R.; TANG, Y. Tom;
 ; APPLICANT: YUE, Henry; BANDMAN, Olga;
 ; APPLICANT: JONES, Karen Anne; BECHTA, Shanya D.;
 ; APPLICANT: TRAN, Yuen K.; AU-YOUNG, Janice K.;
 ; APPLICANT: GRIFFIN, Jennifer A.; ZEBARADIAN, Yeganeh;
 ; APPLICANT: LEB, Ernestine A.; ELLIOTT, Vicki S.;
 ; APPLICANT: THANGAVELU, Kavitha; RAMKUMAR, Jayalaxmi;
 ; APPLICANT: LU, Yan; HAFALIA, April J.A.;
 ; APPLICANT: CHAMLA, Narinder K.; ISON, Craig H.;
 ; APPLICANT: THORNTON, Michael B.; SWARNAKAR, Anita;
 ; APPLICANT: YANG, Junming; RICHARDSON, Thomas W.;
 ; APPLICANT: EMERLING, Brooke M.; YAO, Monique G.;
 ; APPLICANT: COCKS, Benjamin G.; SANJANMALA, Bharati;
 ; APPLICANT: MASON, Patricia M.; GANDHI, Ameena R.;
 ; APPLICANT: LI, Joana X.; FORSYTHE, Ian J.;
 ; APPLICANT: GURUBAJAN, Rajagopal; GIETZEN, Kimberly J.
 ; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
 ; FILE REFERENCE: PF-0992 USN
 ; CURRENT APPLICATION NUMBER: US/10/477,714
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: PCT/US02/15899
 ; PRIOR FILING DATE: 2002-05-16
 ; PRIOR APPLICATION NUMBER: 60/292,197
 ; PRIOR FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: US 60/297,012
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/300,582
 ; PRIOR FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: US 60/300,495
 ; PRIOR FILING DATE: 2001-06-22
 ; PRIOR APPLICATION NUMBER: US 60/301,992
 ; PRIOR FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 60/340,542
 ; PRIOR FILING DATE: 2001-12-14
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PERL Program
 ; SEQ ID NO: 42
 ; LENGTH: 4450
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 6986529CB1
 US-10-477-714-42
 Query Match 85.1%; Score 2622.2; DB 8; Length 4450;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2624; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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US-10-302-172-125
; Sequence 125, Application US/10302172
; Publication No. US2004053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aldong J.
; APPLICANT: Dmanac, Radote T.
; TITLE OF INVENTION: No. US2004053250A1e1 Arginine-rich Protein-like Nucleic Acids an
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/10/302,172
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: PL_FU_genes Version 2.0
; SEQ ID NO 125
; LENGTH: 3948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (60)..(1844)
US-10-302-172-125

Query Match 78.7%; Score 2426.4; DB 7; Length 3948;

Best Local Similarity 99.8%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 457 GAATCTCAACCTTTCTGAAATATGAATTTGAAACGGAATTTTCTGAAAGCTTGCCCT 516
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Qy 517 TTTCTTCATTTAAAGAAAGCAATTTACCACTTTTCTTTTGAACCGAGGCTGT 576
Db 123 TTTCTTCATTTAAAGAAAGCAATTTACCACTTTTCTTTTGAACCGAGGCTGT 182
Qy 577 GACTGTGTTTACGCGGCAATCTAGCTTTGAAACCTTTCTGAAAGCTCTGGAACCTG 636
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Qy 637 AACATAGCCAGATGAGCTCTGCAATGCAAGGTCTCTTGAACGACGACCGCAACCTTC 696
Db 243 AACATAGCCAGATGAGCTCTGCAATGCAAGGTCTCTTGAACGACGACCGCAACCTTC 302

Qy 697 GCGTCCGTTTCTTCTATCTTCACTACAGCTCAAGCAAGAAAGCTTTCAAGCAAG 756
Db 303 GCGTCCGTTTCTTCTATCTTCACTACAGCTCAAGCAAGAAAGCTTTCAAGCAAG 362
Qy 757 ACCGTGAGCAGAGCAAACTACAGAGACGACGAGCTGCTCTTCAAAATGTTTCTCA 816
Db 363 ACCGTGAGCAGAGCAAACTACAGAGACGAGCTGCTCTTCAAAATGTTTCTCA 422
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RESULT 15

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US-09-912-157-7
; Sequence 7, Application US/09912157
; Patent No. US20020165348A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Kuestner, Rolf E.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Human Cytokine Receptor
; FILE REFERENCE: 00-49
; CURRENT APPLICATION NUMBER: US/09/912,157
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86) ... (2302)
US-09-912-157-7

Query Match      73.5%; Score 2267.4; DB 3; Length 2341;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2271; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Search completed: March 1, 2006, 07:50:41
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1994 TGGCGGGGAGCTCAGGCACTTAATGACTGCTGTGTGCTCATCCGAGCTGTCTGCGCAC 2053
2062 TGGCGGGGAGCTCAGGCACTTAATGACTGCTGTGTGCTCATCCGAGCTGTCTGCGCAC 2121
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Db 2023 TTGACCATGACACCGACAACCTTGCGCTTCCTTTCTTATCTGACATGACATCAAG 2082
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RESULT 7
 US-11-102-026A-6

Sequence 6, Application US/11102026A
 Publication No. US20060021087A1
 GENERAL INFORMATION:
 APPLICANT: Monsanto Technology LLC
 APPLICANT: Baum, James A
 APPLICANT: Gilbertson, Larry A
 APPLICANT: Kovalic, David K
 APPLICANT: LaRosa, Thomas J
 APPLICANT: Lu, Maolong
 APPLICANT: Munyikwa, Tichifa R. I.
 APPLICANT: Roberts, James K
 APPLICANT: Wu, Wei
 APPLICANT: Zhang, Bei
 TITLE OF INVENTION: Compositions and Methods for Control of Insect Infestations in Pl
 FILE REFERENCE: 38-21(53596)
 CURRENT APPLICATION NUMBER: US/11/102,026A
 CURRENT FILING DATE: 2005-04-08
 PRIOR APPLICATION NUMBER: 60560842
 PRIOR FILING DATE: 2004-04-09
 PRIOR APPLICATION NUMBER: 60565632
 PRIOR FILING DATE: 2004-04-27
 PRIOR APPLICATION NUMBER: 60579062
 PRIOR FILING DATE: 2004-06-11
 PRIOR APPLICATION NUMBER: 60603421
 PRIOR FILING DATE: 2004-08-20
 PRIOR APPLICATION NUMBER: 60617261
 PRIOR FILING DATE: 2004-10-11
 PRIOR APPLICATION NUMBER: 60669241
 PRIOR FILING DATE: 2005-04-07
 NUMBER OF SEQ ID NOS: 190
 SEQ ID NO 6
 LENGTH: 2656
 TYPE: DNA
 ORGANISM: Lygus hesperus
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(1)
 OTHER INFORMATION: n is a, c, g, or t
 US-11-102-026A-6

Query Match 3.9%; Score 118.8; DB 12; Length 2656;
 Best Local Similarity 61.1%; Pred. No. 2.8e-15;
 Matches 192; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 2770 AATAGCTTGTGACAAAGTCAAGAAAGTCACTAATATACAGTACCTTTTAA 2829
 Db 2083 AA 2142
 QY 2830 TGAAGAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCTCTAGATATCCCTCGAGGG 2889
 Db 2143 AAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCGCTCTTAAATCCCGCGGG 2202
 QY 2890 CCCAGCTTACGCGTACCCAGCTTCTGTACAAAGTGTCCCTATATGAGTGTATTA 2949
 Db 2203 GCCCAATTTTCCCGACCCCTTTTGTGAAAAAGGCGCGCCCTAAAGGCGGCTATTT 2262
 QY 2950 TAAGTAGGACAGTGGCGCTGTATTAACAGTGTACAGGAAAGTGTACTTCTGGA 3009
 Db 2263 AAAAGTAGGCGCGCGCGCGGTATTAACGCGCGGCGGAAATGTATTTTGGGA 2322
 QY 3010 TCTTTGGAAGAACTTCTCTGTGTGTGACATTAATTTGACAAACTACCTACAGAG 3069
 Db 2323 TTTTGTGGAAGAACCTTTTGTGGGCGGGAATATTGGGAAAAATCCCAAAAA 2382

QY 3070 TTTAAGCTTAAG 3083
 Db 2383 TTTAAGCTTTAAG 2396

RESULT 8
 US-09-925-065A-829666

Sequence 829666, Application US/09925065A
 Publication No. US20040181048A1
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single
 FILE REFERENCE: 108827.135
 CURRENT APPLICATION NUMBER: US/09/925,065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 829666
 LENGTH: 599
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-829666

Query Match 3.8%; Score 117.2; DB 6; Length 599;
 Best Local Similarity 97.5%; Pred. No. 3.8e-15;
 Matches 119; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 613 CCCTTGTGAGAGCTTGTGAACTGAAATGACGACGATGCTGGACATGCAAGTGTCC 672
 Db 478 CAGTGTGAGAGCTTGTGAACTGAAATGACGACGATGCTGGACATGCAAGTGTCC 537
 QY 673 TTGACCATGACACCGACAACCTTGCGCTTCCTTCTATCTTCACTAACAAGCTCAAG 732
 Db 538 TTGACCATGACACCGACAACCTTGCGCTTCCTTCTATCTTCACTAACAAGCTCAAG 597
 QY 733 CA 734
 Db 598 CA 599

RESULT 9
 US-10-991-285-284

Sequence 284, Application US/10991285
 Publication No. US20060041962A1
 GENERAL INFORMATION:
 APPLICANT: VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW
 TITLE OF INVENTION: GENES AND USES THEREOF TO MODULATE SECONDARY METABOLITE BIOSYNTHESIS
 FILE REFERENCE: DIN/SEM/V116
 CURRENT APPLICATION NUMBER: US/10/991,285
 CURRENT FILING DATE: 2004-11-16
 PRIOR APPLICATION NUMBER: EP02076973.3
 PRIOR FILING DATE: 2002-05-17
 NUMBER OF SEQ ID NOS: 901
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 284
 LENGTH: 1434
 TYPE: DNA
 ORGANISM: Nicotiana tabacum
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: MAP2
 US-10-991-285-284

Qy	2830	TGAAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCGCTAGAGTATCCCTCGAGGG	2889
Db	800	AAAAAAAAAAAAAAAAAAAAAAAAAAGGGGGGGGGGTTTAAATTTCCCGGGGGG	741
Qy	2890	CCCAAGCTTACGCGTACCAGCTTCTTGTA CAAGGTGCTCTATATGAGTGTATTA	2948
Db	740	GGCCAATTTTGGGCGCCCTCTTTTTTTTAAAAAGGGGGCCCCAAGGGGGGTTT	681
Qy	2950	TAAGCTAGGCACTGGCGGTGTTTACAAGTCGAGATGGGAAAACGTAGCTTGGGA	3008
Db	680	AAAAAAAAAGGGGGGGGGGGTTTTTAAACCGGGGGGGGAAAAATTTTTTGGGT	621
Qy	3010	TCCTTGTGAAGAACTTACTTCGTGTGTGACATTAATGGACAATACCTACAGAGA	3068
Db	620	TTTTTTTGGAAAAACACTTTTTTTGGGGGGGGTTTTTGGAAAAACCCCCCAGAAA	561
Qy	3070	TTTAAGCTCT	3080
Db	560	ATTTAGGCTT	550

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RESULT 13
US-11-193-750-1/c
; Sequence 1, Application US/11193750
; Publication No. US20050273873A1
; GENERAL INFORMATION:
; APPLICANT: Avigenics, Inc
; TITLE OF INVENTION: MODIFICATION OF THE GENOME BY INTRODUCTION OF LARGE NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: AVI-025CIP4
; CURRENT APPLICATION NUMBER: US/11/193,750
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: US/11/068,155
; PRIOR FILING DATE: 2005-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 6230
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pCMV-31int
US-11-193-750-1

Query Match          2.8%; Score 86; DB 12; Length 6230;
Best Local Similarity 100.0%; Pred. No. 3e-08;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2998  GCTAGCTTGGGATCTTTGTGAGGAACCTTACTTGTGTGTGTCATTAATTGACAAC 3057
          |||
DB      641  GCTAGCTTGGGATCTTTGTGAGGAACCTTACTTGTGTGTGTCATTAATTGACAAC 582

QY      3058  TACCTACGAGATTTAAAGCTCTAAG 3083
          |||
DB      581  TACCTACGAGATTTAAAGCTCTAAG 556

RESULT 14
US-11-096-622-20/c
; Sequence 20, Application US/11096622
; Publication No. US20050260643A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: DAY, CHI-PING
; APPLICANT: RAY, KUN-MING
; APPLICANT: XIE, XIAOMING
; APPLICANT: LI, ZHENG
; TITLE OF INVENTION: CANCER SPECIFIC PROMOTERS
; FILE REFERENCE: UTSC:845US
; CURRENT APPLICATION NUMBER: US/11/096,622
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: 60/559,111
; PRIOR FILING DATE: 2004-04-02

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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 8512
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-11-096-622-20

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Query March 2.7%; Score 83; DB 12; Length 8512;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
US-11-096-622--21/c
: Sequence 21, Application US/11096622
: Publication No. US20050260643A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: DAY, CHI-PING
APPLICANT: RAO, KUN-MING
APPLICANT: XIE, XIAOMING
APPLICANT: LI, ZHENG
TITLE OF INVENTION: CANCER SPECIFIC PROMOTERS
FILE REFERENCE: UTSC:845US
CURRENT APPLICATION NUMBER: US/11/096,622
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: 60/559,111
PRIOR FILING DATE: 2004-04-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 8565
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-096-622-21

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Query Match	2.7%	Score 83	DB 12	Length 8565
Best Local Similarity	100.0%	Pred. No. 1.4e-07		
Matches	83	Conservative 0	Mismatches 0	Indels 0
			Gaps 0	
Qy	3001	AGCTGGGACCTTGTGTAAGGAACCTTACTTGTGTGTGACATATATGACAACTAC	3060	
Db	567	AGCTGGGACCTTGTGTAAGGAACCTTACTTGTGTGTGACATATATGACAACTAC	508	
Qy	3061	CTACAGAGATTAAAGCTTAAG	3083	
Db	507	CTACAGAGATTAAAGCTTAAG	485	

Search completed: March 1, 2006, 11:15:43
Job time : 3282 secs

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494 ATTAATTCGTAAGGTGTGTCCTTTCTTTCATTAAAAAGAAAGCAATTACCCCTT 553
562 ATTATTTCTGTAAGGTGTGTCCTTTCTTTCATTAAAAAGAAAGCAATTACCCCTT 621
554 TCTTCTTTAGAACCCGAGCCTGTGACCTGTGTATGACCGGACAACTAGCTGTGAAC 613
622 TCTTCTTTAGAACCCGAGCCTGTGACCTGTGTATGACCGGACAACTAGCTGTGAAC 681
614 CCTTCTGGAAGCCTCGGAACCTGACATGACCGACATGGCTGGACATGCAAGTGTCTT 673
682 CCTTCTGGAAGCCTCGGAACCTGACATGACCGACATGGCTGGACATGCAAGTGTCTT 741
674 TCGAACACGACCGGACCAACTTGGGCTTCCGTTCTTCTTCACTCACTCAAGCTCAAG 733
742 TCGAACACGACCGGACCAACTTGGGCTTCCGTTCTTCTTCACTCACTCAAGCTCAAG 801
734 ACGAAGGACCTTTCAAGCGAAGACCTGTAAAGAGAGCAAACTACAGAGACGACGCT 793
802 ACGAAGGACCTTTCAAGCGAAGACCTGTAAAGAGAGCAAACTACAGAGATGACGAGCT 861
794 GCTCTCTTCAAAATGTTTCTCCAGGGGATTAATTAATGAGCTGTGTGATGACATTAACA 853
862 GCTCTCTTCAAAATGTTTCTCCAGGGGATTAATTAATGAGCTGTGTGATGACATTAACA 921
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922 CAACAAGAAAGATGATGATTAATGCTTAAAGCAGTGCATCCCGTGGGCGGGCCCA 981
914 TCAAGACCATGACATCAAGTGCATGCTGATGATTAATGAGATTCGCGACGCTTTCA 973
982 TCAAGACCATGACATCAAGTGCATGCTGATGATTAATGAGATTCGCGACGCTTTCA 1041
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1162 TCTTCTGTGCTAATTCAGTAAGATGGCCAGAAATCAATGAATGTGCTCAGTGTTCG 1221
1154 CCTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCTGAGCTGTGGGAAGACTTCA 1213
1222 CCTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCTGAGCTGTGGGAAGACTTCA 1281
1214 GCTCTGTGAGAGAGGAGAGAGATGGGTCAATCCAGAAATCCAGATCCAGTTCA 1273
1282 GCTCTGTGAGAGAGGAGAGAGATGGGTCAATCCAGAAATCCAGATCCAGTTCA 1341
1274 TCAATGTGTTGTTCCAAAGGTATGAAGTACTTTGTGCAACAAGAACTACAAACACA 1333
1342 TCAATGTGTTGTTCCAAAGGTATGAAGTACTTTGTGCAACAAGAACTACAAACACA 1401
1334 AAGGAGTGGCCGAGGCTCGGGGAAAGAGAGCTTCTGTGGTGGGGGTCAAGCATTTG 1393
1402 AAGGAGTGGCCGAGGCTCGGGGAAAGAGAGCTTCTGTGGTGGGGGTCAAGCATTTG 1461
1394 CCGAANAAGCTCGGCGAGGCAAGCAGAGTTGTCGCGGGGCTCAGCAAGTTTATGCGG 1453
1462 CCGAANAAGCTCGGCGAGGCAAGCAGAGTTGTCGCGGGGCTCAGCAAGTTTATGCGG 1521
1454 TCTACTTTGAATTAATTCCTGTGAGAGAGAGCTCCCGGTATCTTGAAGCTGAGTACCAAGT 1513
1522 TCTACTTTGAATTAATTCCTGTGAGAGAGAGCTCCCGGTATCTTGAAGCTGAGTACCAAGT 1581
1514 ACAAGACTATGAGCAATCTTCTCAGAGCTGTTCCTCACTGCACTCCCGAGACCAAGGCC 1573
1582 ACAAGACTATGAGCAATCTTCTCAGAGCTGTTCCTCACTGCACTCCCGAGACCAAGGCC 1641

1574 TCAAGAGCCGGGGAGACACACGACAGAGGAGCAAGAAAGAACTAATTCGAGCAAGT 1633
1642 TCAAGAGCCGGGGAGACACACGACAGAGGAGCAAGAAAGAACTAATTCGAGCAAGT 1701
1634 CAGGCGGCTCCTTAATGCTGCGCAATTTGCAATATGACCAAGTTTATTTGACAGAGACCCG 1693
1702 CAGGCGGCTCCTTAATGCTGCGCAATTTGCAATATGACCAAGTTTATTTGACAGAGACCCG 1761
1694 ACTGGTGGAAAAGAGTGTGCTCCCTTCATCCTCCTCACTGGGCTACCGGAGGACAG 1753
1762 ACTGGTGGAAAAGAGTGTGCTCCCTTCATCCTCCTCACTGGGCTACCGGAGGACAG 1821
1754 TCTTGGAGAAATTTGATTCGGGCTTGTGTTTAAATGATGATGATGCAAAACGAGGCTGTG 1813
1822 TCTTGGAGAAATTTGATTCGGGCTTGTGTTTAAATGATGATGATGCAAAACGAGGCTGTG 1881
1814 AAGTGAATTCCTGCTTAAAGGTGAGAGGCGCTGTTCTTGGGCAACCGGACCAAGCCGACT 1873
1882 AAGTGAATTCCTGCTTAAAGGTGAGAGGCGCTGTTCTTGGGCAACCGGACCAAGCCGACT 1941
1874 CCGAGACGAGAGTACGACATGGGGGCTTGGACCAAGAGGGGAGGCGGGGCTGCGCTTG 1933
1942 CCGAGACGAGAGTACGATGGGGGCTTGGACCAAGAGGGGAGGCGGGGCTGCGCTTG 2001
1934 ACGGTAGCGCGCGCTGCAACCCCTGTGCAACGAGTGAAGCCGAGACCCCTCGGACA 1993
2002 ACGGTAGCGCGCGCTGCAACCCCTGTGCAACGAGTGAAGCCGAGACCCCTCGGACA 2061
1994 TCCCGGGGACTCAGGCACTTAATGACTGTGTGTGCTCATCCGAGCTGTCTTGGCAC 2053
2062 TCCCGGGGACTCAGGCACTTAATGACTGTGTGTGCTCATCCGAGCTGTCTTGGCAC 2121
2054 TGATGGAAGGACTCTGACCGGACGACAGCAAGAAACGTTCCCTGACGGAAGCGTGTCT 2113
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2114 CCTCTTCAAGGCTGAGTGAAGAGAACTCTGCTGCTTCTTCAAGCTCTCTTCTG 2173
2182 CCTCTTCAAGGCTGAGTGAAGAGAACTCTGCTGCTTCTTCAAGGCTCTCTCTG 2241
2174 GGTCAATGCAAGCAATCTTGGTGTGCGGAGCTTACATGATGAATCCACGCGGTGCGCC 2233
2242 GGTCAATGCAAGCAATCTTGGTGTGCGGAGCTTACATGATGAATCCACGCGGTGCGCC 2301
2234 CTTTGTAAACAAACGAAAGAGCTTAAGCAATGSCAATTTAGCTGCTGCTCCCTGATT 2293
2302 CTTTGTAAACAAACGAAAGAGCTTAAGCAATGSCAATTTAGCTGCTGCTCCCTGATT 2361
2294 CCCAGCTCATCTCCCTGTTGCATGGCCCACTTGAAGCTGAGTCTCATACAGAGATAT 2353
2362 CCCAGCTCATCTCCCTGTTGCATGGCCCACTTGAAGCTGAGTCTCATACAGAGATAT 2421
2354 TTGAGTGAATATGCTGGCAGTACTTGTTCCTTGTGCCCAACCTTTAACGGATATT 2413
2422 TTGAGTGAATATGCTGGCAGTACTTGTTCCTTGTGCCCAACCTTTAACGGATATT 2481
2414 TGACAAACCTCCCAATTTCTTAAATGATATGAGAGCTGGAAGGCAATGCAATAAGTTC 2473
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2474 TGACAAACGCTTGCAAAATTTGTTAGTCTTGTGATCAGAGCCTGTTGTGGAGGTAGGG 2533
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2534 AAGAAATATGTAAGAAAGAAACGAGAAATATCTGCACTAATCATTCAGCTTCAATTGAGC 2593
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2594 TCTGCAACCTTGGCTGTTTGTGATTTGGTACTGCTTGAATTTGAAAGTCTTTGAAAGAAAG 2653
2662 TCTGCAACCTTGGCTGTTTGTGATTTGGTACTGCTTGAATTTGAAAGTCTTTGAAAGAAAG 2721
2654 GCACTTTTAACATCATAGCAAGAAATCAAGTGCAGTCTATCTGGAATCCATGTTGTA 2713

Db 2722 GACATTTTACATCATAGCCACAGAAATCAAGTGCAGCTCATCTGGAATCCATGTTGTA 2781
 Qy 2714 TTGCAGATTAATGTTCTCATTTATTTTGTAGTGAATTTTACATGGCATGGGTGTTAAAT 2773
 Db 2782 TTGCAGATTAATGTTCTCATTTATTTTGTAGTGAATTTTACATGGCATGGGTGTTAAAT 2841
 Qy 2774 AAGCTTTGATGTCAAAAGTCAAGAAAGTGAATGATATATACATGTCACCTTTTATG 2826
 Db 2842 AAGCTTTGATGTCAAAAGTCAAGAAAGTGAATGATATATACATGTCACCTTTTATG 2894

RESULT 2
 US-09-799-451-125
 ; Sequence 125, Application US/09799451
 ; Patent No. 6783969
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Goodrich, Ryle
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Ren, Feiyan
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Xue, Aidong J.
 ; APPLICANT: Zhao, Qiang A.
 ; APPLICANT: Wang, Jian-Rui
 ; APPLICANT: Ma, Yungqing
 ; APPLICANT: Yamazaki, Victoria
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wang, Dunrui
 ; APPLICANT: Yang, Yonghong
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Ghosh, Reena
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 803
 ; CURRENT APPLICATION NUMBER: US/09/799,451
 ; CURRENT FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 948
 ; SOFTWARE: pc FL_genes Version 2.0
 ; SEQ ID NO 125
 ; LENGTH: 3948
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (60)..(1844)
 ; US-09-799-451-125

Query Match 78.7%; Score 2426.4; DB 3; Length 3948;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2430; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 397 CACAACATGATTTCTAAGAGATCCGAAGCAGCTCAACAGTAGCTTCAAAAAGATGGAATG 456
 Db 3 CCACAACATGATTTCTAAGAGATCCGAAGCAGCTCAACAGTAGCTTCAAAAAGATGGAATG 62
 Qy 457 GAATCTCAACCTTTCTGTAATATGAATTTGAACGAGATATTTTGTAAAGTTGTCCT 516
 Db 63 GAATCTCAACCTTTCTGTAATATGAATTTGAACGAGATATTTTGTAAAGTTGTCCT 122
 Qy 517 TTTCCTTCATTAATAAGAAAGCAATTAACCACTTTCTTTTGAACCCGAGCTGT 576
 Db 123 TTTCCTTCATTAATAAGAAAGCAATTAACCACTTTCTTTTGAACCCGAGCTGT 182
 Qy 577 GACCTGTTGTTACAGCCGAGCAATCTAGCTTGAACCCCTTCTGAAGCCTCGAACTG 636
 Db 183 GACCTGTTGTTACAGCCGAGCAATCTAGCTTGAACCCCTTCTGAAGCCTCGAACTG 242
 Qy 637 AACATCAGCCACATGCTCGACATGCAAGGTGTCTTGGACCAAGCAGCAACTTC 696

Db 243 AACATCAGCCACATGCTCGACATGCAAGGTGTCTTGGACCAAGCAGCAACTTC 302
 Qy 697 GECTTCCTGTTTCTTATCTTCACTACAGCTCAAGCAAGAAAGACCTTCAAGCAAG 756
 Db 303 GECTTCCTGTTTCTTATCTTCACTACAGCTCAAGCAAGAAAGACCTTCAAGCAAG 362
 Qy 757 ACCTGTAAGCAGAGCAAACTACAGAGAGACAGCTGCTCTTCAAAATGTTTCTCA 816
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 Qy 877 GCTTAAAGCCAGTCACTCCCGTGGGCGGGCCCATCAAGCCATGACAGTG 936
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 Db 783 GECTGTAGTGTGCTCTGAGCTGTGAGAGACTTCAAGCTCTGTAGAGAGGAGCA 842
 Qy 1237 GAATGGTATCACAAGATCAAGATCCAGTTCATCATTTGTGTTTTCGCAAGGT 1296
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 Db 903 ATGAAGTACTTGTGTGAACAAGAACTACAAACAACAAGAGGTGCGGAGGCTCGGG 962
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 Db 1023 CAGAGTTCCTCCGCGGCGCTCAGCAAGTTATCGCGTCTACTTGAATTTCTGCGAG 1082
 Qy 1477 GAGAGCTGCTCCGCTGATCTTGAAGCTGAGTACCAAGTACAGACTCATGCAATCTTCT 1536
 Db 1083 GAGAGCTGCTCCGCTGATCTTGAAGCTGAGTACCAAGTACAGACTCATGCAATCTTCT 1142
 Qy 1537 CAGCTCTGTTCCACCTGCACTCCGAGACCAAGGCTCTCAGAGACCGGGGAGCAAG 1596
 Db 1143 CAGCTCTGTTCCACCTGCACTCCGAGACCAAGGCTCTCAGAGACCGGGGAGCAAG 1202
 Qy 1597 CGACAGGCGAGCAAGAACTACTTCCGAGCAAGTCAAGGCGGTCCTATACGTGCGC 1656
 Db 1203 CGACAGGCGAGCAAGAACTACTTCCGAGCAAGTCAAGGCGGTCCTATACGTGCGC 1262
 Qy 1657 ATTGCAACATGACCACTTATTTGAAGAAGCCGCACTGTTTGAAGAAAGCAATTCGT 1716
 Db 1263 ATTGCAACATGACCACTTATTTGAAGAAGCCGCACTGTTTGAAGAAAGCAATTCGT 1322
 Qy 1717 CCTTCATCTCTCTCACTGCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGC 1776
 Db 1323 CCTTCATCTCTCTCACTGCGCTACCGGAGCCAGTCTTGGAGAAATTTGATTCGGGC 1382

1777 TTGGTTTAAATGATGTCATGTGCAAAAGGAGCTGAGAGTGACTTGTGCTAAAGTGA 1836
1383 TTGGTTTAAATGATGTCATGTGCAAAAGGAGCTGAGAGTGACTTGTGCTAAAGTGA 1442
1837 GAGGGCGCTGTTCTTGGGGCAACCGGACCAAGCCGATCTCCAGACGAGAGTCAGATGAG 1896
1443 GAGGGCGCTGTTCTTGGGGCAACCGGACCAAGCCGATCTCCAGACGAGAGTCAGATGAG 1502
1897 GGCGCTGAGACAAAGGAGGAGGCGGCGCTTGAAGGTAGGCGCGCGCTGAGAACCC 1956
1503 GGCGCTGAGACAAAGGAGGAGGCGGCGCTTGAAGGTAGGCGCGCGCTGAGAACCC 1562
1957 CTGTGACACACGGGTGAAAGCCCGGACCGCTCGGACATGATCGCGGAGCTCAGGACATCTAT 2016
1563 CTGTGACACACGGGTGAAAGCCCGGACCGCTCGGACATGATCGCGGAGCTCAGGACATCTAT 1622
2017 GACTGCTGTGCGCTCATCCGAGCTGTCTTGACATGATGAGAGACTCTTGACGAGAC 2076
1623 GACTGCTGTGCGCTCATCCGAGCTGTCTTGACATGATGAGAGACTCTTGACGAGAC 1682
2077 CAGACAGAAAGCTCTTCCCTGACGAGAGCGGTCTCTCTCTTCAAGGCTTGGGTGAGAG 2136
1683 CAGACAGAAAGCTCTTCCCTGACGAGAGCGGTCTCTCTCTTCAAGGCTTGGGTGAGAG 1742
2137 GAACCTCTGCGCTTCTTCAAGCTCTCTTCTTGGGTGATGCAAAAGCAGATCTTGGT 2196
1743 GAACCTCTGCGCTTCTTCAAGCTCTCTCTTGGGTGATGCAAAAGCAGATCTTGGT 1802
2197 TGCCGAGCTACAGTATGAACTCAAGCGGTGCGCTTCTTGTAAACAAAGAGAGTC 2256
1803 TGCCGAGCTACAGTATGAACTCAAGCGGTGCGCTTCTTGTAAACAAAGAGAGTC 1862
2257 TGAAGATTGCGCACTTGAAGTGTGCTGCTCTGATTTCCCGAGCTATCTCCCTGTTGTC 2316
1863 TGAAGATTGCGCACTTGAAGTGTGCTGCTCTGATTTCCCGAGCTATCTCCCTGTTGTC 1922
2317 ATGGCCCACTTGAAGCTGAGTCTCATACAGGAATTTGAGTGAATGTCGAGTGA 2376
1923 ATGGCCCACTTGAAGCTGAGTCTCATACAGGAATTTGAGTGAATGTCGAGTGA 1982
2377 CTGTGTTCTTCCCTTGGCCCAACCTTTTACGGATATCTTGAACAACTCTCCAAATTTCTAA 2436
1983 CTGTGTTCTTCCCTTGGCCCAACCTTTTACGGATATCTTGAACAACTCTCCAAATTTCTAA 2042
2437 AATGATATGAGACTCTGAAAGGATCTCCATTAAGTCTGACAAAGCTTGCCTGCTTGGT 2496
2043 AATGATATGAGACTCTGAAAGGATCTCCATTAAGTCTGACAAAGCTTGCCTGCTTGGT 2102
2497 TTAGTCTTGAATCAGAGCTGTGTGGAGGTGAGGAGGAAATATGTAAAGAAAAACAG 2556
2103 TTAGTCTTGAATCAGAGCTGTGTGGAGGTGAGGAGGAAATATGTAAAGAAAAACAG 2162
2557 GAAATACCTGACCTATATCAGACTTCACTTATGAGCTCTGCAAACTTGTGCTTGGT 2616
2163 GAAATACCTGACCTATATCAGACTTCACTTATGAGCTCTGCAAACTTGTGCTTGGT 2222
2617 ATTGGCTACCTGATTTGAAAAGCTTGTGAAAAAGGCACTTTAACTCATAGGCAAA 2676
2223 ATTGGCTACCTGATTTGAAAAGCTTGTGAAAAAGGCACTTTAACTCATAGGCAAA 2282
2677 GAAATCAAGTGCAGCTATCTGAAATCCATGTTGATGAGATTAATGTTCTCATTTAT 2736
2283 GAAATCAAGTGCAGCTATCTGAAATCCATGTTGATGAGATTAATGTTCTCATTTAT 2342
2737 TTTTATGATGAGATTTTACATGTCATGCGATGGTGTAAATTAAGCTTGAAGTCAAG 2796
2343 TTTTATGATGAGATTTTACATGTCATGCGATGGTGTAAATTAAGCTTGAAGTCAAG 2402
2797 AAGTACATGATATACAGTACCTTTTATGAATGA 2832
2403 AAGTACATGATATACAGTACCTTTTATGAATGA 2438

RESULT 3
US-09-747-259-17
Sequence 17, Application US/09747259
Patent No. 6569645
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Hillan, Kenneth
APPLICANT: Tumas, Daniel
APPLICANT: Vanlookeren, Menno
APPLICANT: Vandlen, Richard
APPLICANT: Watanabe, Colin
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William
APPLICANT: Yansura, Daniel
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C1P1 (US)
CURRENT APPLICATION NUMBER: US/09/747,259
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/311,832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/172,096
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US 60/175,481
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/191,007
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/213,087
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: US 09/644,848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/242,837
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: US 60/253,646
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 17
LENGTH: 2319
TYPE: DNA
ORGANISM: Homo Sapien
US-09-747-259-17

Query Match 67.3%; Score 2075.6; DB 3; Length 2319;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 2130; Conservative 0; Mismatches 9; Indels 39; Gaps 1;
DB 135 CTGTGCTGAGAGGAGTGTGGGCGCAGCGAGAGAAAGTGGGCTGTACATCACTCTT 194
111 CAGTGAGAGCAGGAGAGTGTGGGCGCAGCGAGAGAAAGTGGGCTGTACATCACTCTT 170

QY 195 CAAATATGACAAATTTGACGACCTACTTGAATCCAGTGGGGAGAGATGTAATGCTGACGC 254
DB 171 CAAATATGACAAATTTGACGACCTACTTGAATCCAGTGGGGAGAGATGTAATGCTGACGC 230
QY 255 CCAGAAATATCAGCATCAGCCAGATATGCTTCCATGACCAAGTGGCAGTCACTCTTTG 314
DB 231 CCAGAAATATCAGCATCAGCCAGATATGCTTCCATGACCAAGTGGCAGTCACTCTTTG 290
QY 315 GTTCCCAAGGGGCTCTGCGCATTCGAATCTGAAAGATTTGGGTAATCTGAGAGAGCT 374
DB 291 GTTCCCAAGGGGCTCTGCGCATTCGAATCTGAAAGATTTGGGTAATCTGAGAGAGCT 350
QY 375 GAAGTGGAGGGAGAGACAGTGGCAACAACTGATTTCTTAAAGATCCGAGAGCTCAACAG 434
DB 351 GAAGTGGAGGGAGAGACAGTGGCAACAACTGATTTCTTAAAGATCCGAGAGCTCAACAG 410
QY 435 TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACGGA 494
DB 411 TAGCTTCAAAAGAACTGGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACGGA 470
QY 495 TTAATTTGTAAGGTTGTCTCTTTCTCTTCATTTAAAGCAAAAGCAATTAACAACCTTT 554
DB 471 TTAATTTGTAAGGTTGTCTCTTTCTCTTCATTTAAAGCAAAAGCAATTAACAACCTTT 530
QY 555 CTTCTTTAGAACCCGAGCCCTGTAACCTTGTGTAACAGCCGGAACAATCTTACTTGTAAAC 614
DB 531 CTTCTTTAGAACCCGAGCCCTGTAACCTTGTGTAACAGCCGGAACAATCTTACTTGTAAAC 590
QY 615 CTTCTGGAAGCTCTGGAACCTGGAACATCAGCCAGACAGTGTCTC----- 656
DB 591 CTTCTGGAAGCTCTGGAACCTGGAACATCAGCCAGACAGTGTCTC----- 650
QY 657 -----GGAATGCAAGTGTCTTTCGACCAAGCAAGCAACTT 695
DB 651 CGACCAAGCAAGCTGTGCTCGGACATGCAAGTGTCTTTCGACCAAGCAAGCAACTT 710
QY 696 CCGCTTCCGTTTCTTCTATCTTCACTAAGCTCAAGCAAGAGAGACTTTCAAGGAAA 755
DB 711 CCGCTTCCGTTTCTTCTATCTTCACTAAGCTCAAGCAAGAGAGACTTTCAAGGAAA 770
QY 756 GACCTTAAGCAGAGCAAACTACAGAGACGACAGTGTCTCTTCAAAATGTTCTCC 815
DB 771 GACCTTAAGCAGAGCAAACTACAGAGACGACAGTGTCTCTCTTCAAAATGTTCTCC 830
QY 816 AGGGGATTAATTAATTAAGTGTGATGACACTTAAACAACAAGAAAGTATGACTTA 875
DB 831 AGGGGATTAATTAATTAAGTGTGATGACACTTAAACAACAAGAAAGTATGACTTA 890
QY 876 TGCCTTAAGCCAGTGCATCTCCGCTGAGCCGAGCCCACTAGAGCCATGGCCATCAGAT 935
DB 891 TGCCTTAAGCCAGTGCATCTCCGCTGAGCCGAGCCCACTAGAGCCATGGCCATCAGAT 950
QY 936 GGCACCTGTATGATTAATGAGCATTTGCGGAGCTCTTCACTGATATGAGCGGCAAGAGCA 995
DB 951 GGCACCTGTATGATTAATGAGCATTTGCGGAGCTCTTCACTGATATGAGCGGCAAGAGCA 1010
QY 996 ACAAGAAATATAATTAATTAATTAAGTATGAGAGAGCTTGAAGCTTTCACATACACTGC 1055
DB 1011 ACAAGAAATATAATTAATTAATTAAGTATGAGAGAGCTTGAAGCTTTCACATACACTGC 1070
QY 1056 AGGACTTCCCAAGAGAGAGCTCCGCGCGCGCGAGAGCTTTTCTCTGCTATTCAGTAA 1115
DB 1071 AGGACTTCCCAAGAGAGAGCTCCGCGCGCGCGAGAGCTTTTCTCTGCTATTCAGTAA 1130
QY 1116 AGATGGCAGAAATCAATGAATGATGCTGAGTGTCTGCTACTCTTCCAGAGACTTCTG 1175
DB 1131 AGATGGCAGAAATCAATGAATGATGCTGAGTGTCTGCTACTCTTCCAGAGACTTCTG 1190
QY 1176 TGGCTGTGAGGTGCTCTGAGACCTGTGGAAGAACTTCAAGCTCTGTAGAGAGGGCAGAG 1235
DB 1191 TGGCTGTGAGGTGCTCTGAGACCTGTGGAAGAACTTCAAGCTCTGTAGAGAGGGCAGAG 1250

QY 1236 AGAATGGGTCAATCAGAAAGATCCAGAGTCCAGATTCAATCATTTGGTGTTCGAAAG 1295
DB 1251 AGAATGGGTCAATCAGAAAGATCCAGAGTCCAGATTCAATCATTTGGTGTTCGAAAG 1310
QY 1296 TATGAATATCTTGTGGAACAAGAACTACAAACAAGAGAGTGGCCGAGGCTCGGG 1355
DB 1311 TATGAATATCTTGTGGAACAAGAACTACAAACAAGAGAGTGGCCGAGGCTCGGG 1370
QY 1356 GAAAGAGAGCTTTCTCTGATGGCGGTGACGCAATTCGCCAAAGCTCCGCAAGCCAA 1415
DB 1371 GAAAGAGAGCTTTCTCTGATGGCGGTGACGCAATTCGCCAAAGCTCCGCAAGCCAA 1430
QY 1416 GCAGATGCTGCTCCGCGCGCTCAGCAAGTTTATGCGCGCTACTTGTGATTAATTCCTGCGA 1475
DB 1431 GCAGATGCTGCTCCGCGCGCTCAGCAAGTTTATGCGCGCTACTTGTGATTAATTCCTGCGA 1490
QY 1476 GGGAGAGCTCCCGGATATCTTAGACCTGAGTACAAAGTACAGACTATGAGCAATCTTCC 1535
DB 1491 GGGAGAGCTCCCGGATATCTTAGACCTGAGTACAAAGTACAGACTATGAGCAATCTTCC 1550
QY 1536 TCAAGCTGTCTCCACCTGCACTCCGAGACCAAGGCTTCAGAGCCGCGGAGCAGACAC 1595
DB 1551 TCAAGCTGTCTCCACCTGCACTCCGAGACCAAGGCTTCAGAGCCGCGGAGCAGACAC 1610
QY 1596 GGGAGAGGGGAGAGAAAGAACTACTTCCGAGCAAGTCAAGGCGGCTCCATATACGTCGC 1655
DB 1611 GGGAGAGGGGAGAGAAAGAACTACTTCCGAGCAAGTCAAGGCGGCTCCATATACGTCGC 1670
QY 1656 CATTTCGAACATGCAACAGTTTATTTAGACAGAGAGCCGCACTGTGTTGAAAGAGCTTCGT 1715
DB 1671 CATTTCGAACATGCAACAGTTTATTTAGACAGAGAGCCGCACTGTGTTGAAAGAGCTTCGT 1730
QY 1716 TCCCTTCATCTCTCTCACTGCGCTACCGGAGACCAAGTCTTGGAAATTTGATTCGGG 1775
DB 1731 TCCCTTCATCTCTCTCACTGCGCTACCGGAGACCAAGTCTTGGAAATTTGATTCGGG 1790
QY 1776 CTTGGTTTAAATGATGATGATGCAACAGGAGCCGAGAGTCACTTGCCTTAAAGT 1835
DB 1791 CTTGGTTTAAATGATGATGATGCAACAGGAGCCGAGAGTCACTTGCCTTAAAGT 1850
QY 1836 AGAGGCGCTGTCTTGGGGCAACCGGACAGCCGACTCCACAGACAGAGATCAGATGG 1895
DB 1851 AGAGGCGCTGTCTTGGGGCAACCGGACAGCCGACTCCACAGACAGAGATCAGATGG 1910
QY 1896 GGGCTGTGAACAAAGCGGGAGGCGCGGCTGTGACGTTGACGTTAGCGCCCTGCAACC 1955
DB 1911 GGGCTGTGAACAAAGCGGGAGGCGCGGCTGTGACGTTGACGTTAGCGCGCCCTGCAACC 1970
QY 1956 CCTGTGCAACAGGTAAAGCCGCGAGCCCTCTGGAATGCGCGGGGACTCAGGCAATCTA 2015
DB 1971 CCTGTGCAACAGGTAAAGCCGCGAGCCCTCTGGAATGCGCGGGGACTCAGGCAATCTA 2030
QY 2016 TGAAGCTGTGAGCTCTCATCCAGAGTGTCTGCACTGATGAGAGAGCTCTGACGGA 2075
DB 2031 TGAAGCTGTGAGCTCTCATCCAGAGTGTCTGCACTGATGAGAGAGCTCTGACGGA 2090
QY 2076 CCAGACAGAAAGCTTCTCCCTGACGAGAGCGGTCTCTCTTCAAGCCCTGGGTAGGA 2135
DB 2091 CCAGACAGAAAGCTTCTCCCTGACGAGAGCGGTCTCTCTTCAAGCCCTGGGTAGGA 2150
QY 2136 GGAAGCTCTGCGCTCTTCCCAAGCTCTCTCTTCTGAGTCAATGAAAGCAGATCTTGG 2195
DB 2151 GGAAGCTCTGCGCTCTTCCCAAGCTCTCTCTTCTGAGTCAATGAAAGCAGATCTTGG 2210
QY 2196 TTGCGCAGACTACATGATGAAGTCCAGCGGCTGCGCCCTTTGTAAACAAGAGAGT 2255
DB 2211 TTGCGCAGACTACATGATGAAGTCCAGCGGCTGCGCCCTTTGTAAACAAGAGAGT 2270
QY 2256 CTAAGCATTCGCACTTAA 2273
DB 2271 CTAAGCATTCGCACTTAA 2288

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RESULT 4
US-09-904-615-15
; Sequence 15, Application US/09904615
; Patent No. 6566325
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2278)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2290)
; OTHER INFORMATION: n equals a,t,g, or c
; US-09-904-615-15

Query Match
Best Local Similarity 89.2%; Score 194.6; DB 3; Length 2334;
Matches 222; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 2835 AAAAAAAAAAAAAAAAAAGGCGCGCGCTCTAGATATCCCTGAGGGGCCAA 2894
DB 1696 ACATAGAAAAAAAAAAAAAAAAAGGCGCGCGCTCTAGAGATCCCTGAGGGGCCAA 1755
QY 2895 GCTTACGCGTACCCAGCTTTCTGTACAAGTGTCCCTATAGTGTATTAAGC 2954
DB 1756 GCTTACGCGTGC--ATGCGAGCTCATAGCTCTCTCCATAGTGTATTAAGC 1812
QY 2955 TAGGACATGCGCGCTTTTACACGTCGTGACTGGGAAATGCTAGCTGGGATCTTT 3014
DB 1813 TAGGACATGCGCGCTTTTACACGTCGTGACTGGGAAATGCTAGCTGGGATCTTT 1872
QY 3015 GTGAAGAACTTACTTCTGTGTGTGACATTAATTGACAACTACTACAGATTTAA 3074
DB 1873 GTGAAGAACTTACTTCTGTGTGTGACATTAATTGACAACTACTACAGATTTAA 1932
QY 3075 AGCTCTAAG 3083
DB 1933 AGCTCTAAG 1941

RESULT 5
US-10-054-988-15
; Sequence 15, Application US/10054988
; Patent No. 6953667
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/10/054,988
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/904,615
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 2334
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2278)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (2290)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-054-988-15

Query Match
Best Local Similarity 89.2%; Score 194.6; DB 3; Length 2334;
Matches 222; Conservative 0; Mismatches 24; Indels 3; Gaps 1;

QY 2835 AAAAAAAAAAAAAAAAAAGGCGCGCGCTCTAGATATCCCTGAGGGGCCAA 2894
DB 1696 ACATAGAAAAAAAAAAAAAAAAAGGCGCGCGCTCTAGAGATCCCTGAGGGGCCAA 1755
QY 2895 GCTTACGCGTACCCAGCTTTCTGTACAAGTGTCCCTATAGTGTATTAAGC 2954
DB 1756 GCTTACGCGTGC--ATGCGAGCTCATAGCTCTCTCCATAGTGTATTAAGC 1812
QY 2955 TAGGACATGCGCGCTTTTACACGTCGTGACTGGGAAATGCTAGCTGGGATCTTT 3014
DB 1813 TAGGACATGCGCGCTTTTACACGTCGTGACTGGGAAATGCTAGCTGGGATCTTT 1872
QY 3015 GTGAAGAACTTACTTCTGTGTGTGACATTAATTGACAACTACTACAGATTTAA 3074
DB 1873 GTGAAGAACTTACTTCTGTGTGTGACATTAATTGACAACTACTACAGATTTAA 1932
QY 3075 AGCTCTAAG 3083
DB 1933 AGCTCTAAG 1941

RESULT 6
US-09-181-339-2
; Sequence 2, Application US/09181339
; Patent No. 6610827
; GENERAL INFORMATION:
; APPLICANT: Forsayeth, John R.
; APPLICANT: Zhao, Byron
; APPLICANT: Chavez, Raymond C.
; TITLE OF INVENTION: PORASSIUM CHANNEL SUBUNIT POLYPEPTIDE
; TITLE OF INVENTION: AND POLYNUCLEOTIDE COMPOSITIONS AND USES THEREFOR
; FILE REFERENCE: 5865-0033.30
; CURRENT APPLICATION NUMBER: US/09/181,339
; CURRENT FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 60/063,450
; PRIOR FILING DATE: 1997-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2799
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154) ... (1647)
; NAME/KEY: misc_feature
; LOCATION: (1) ... (2799)
; OTHER INFORMATION: n = A,T,C or G
; US-09-181-339-2

Query Match
Best Local Similarity 89.0%; Score 178.6; DB 3; Length 2799;
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Matches 203; Conservative 1; Mismatches 21; Indels 3; Gaps 1;

QY 2833 AAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCTCTAGACTATCCCTCGAGGGGCC 2892

DB 2575 AAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCTCTAGACTATCCCTCGAGGGGCC 2634

QY 2893 AAGCTTACCGCTGACCCAGCTTTCTGTACAAAGTGTGCTCCATAGTAGAGTCGATTTATA 2952

DB 2635 AAGCTTACCGCTGAC---GCGACGCTATAGCTCTCTCCCTATAGTAGAGTCGATTTATA 2691

QY 2953 GCTAGGCACTGGCGCGCTTTTACAACTGCTGACTGGGAAACTGCTAGCTTGGGATCT 3012

DB 2692 GCTAGGCACTGGCGCGCTTTTACAACTGCTGACTGGGAAACTGCTAGCTTGGGATCT 2751

QY 3013 TTGTGAAGAACTTACTTCTGTGTGTGTGATTAATTGACAACTAC 3060

DB 2752 TTGTGAAGAACTTACTTCTGTGTGTGTGATTAATTGACAACTAC 2799

RESULT 7

US-09-620-312D-12

; Sequence 12, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yongshong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yungting

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghaast

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6569662el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/09/620,312D

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1105

; SOFTWARE: pc FL_genes Version 1.0

; SEQ ID NO 12

; LENGTH: 2243

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (216)..(2129)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(2243)

; OTHER INFORMATION: n = a,t,c or g

US-09-620-312D-12

Query Match 3.7%; Score 113; DB 3; Length 2243;

Best Local Similarity 88.7%; Pred. No. 9.9e-19;

Matches 133; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 2832 AAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCTCTAGAGTATCCCTCGAGGGGCC 2891

DB 2088 AAGGAGAAAGAAAAAAAAAAAAAAAAAGGCGCGCTCTAGAGTATCCCTCGAGGGGCC 2147

QY 2892 CAAGCTTACCGCTACCCAGCTTTCTGTACAAAGTGTGCTCCATAGTAGAGTCGATTTATA 2951

DB 2148 CAAGCTTACCGCTACCCAGCTTTCTGTACAAAGTGTGCTCCATAGTAGAGTCGATTTATA 2206

QY 2952 AAGCTTACCGCTGACCCAGCTTTTACAACT 2981

DB 2207 AAGCTTACCGCTGACCCAGCTTTTACAACT 2236

RESULT 8

US-09-620-312D-968/c

; Sequence 968, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyan

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yongshong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yungting

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghaast

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6569662el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/09/620,312D

; PRIOR FILING DATE: 2000-07-19

; PRIOR APPLICATION NUMBER: 09/552,317

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1105

; SOFTWARE: pc FL_genes Version 1.0

; SEQ ID NO 968

; LENGTH: 1277

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (736)..(1014)

US-09-620-312D-968

Query Match 3.6%; Score 111.8; DB 3; Length 1277;

Best Local Similarity 98.3%; Pred. No. 1.5e-18;

Matches 113; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2833 AAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCTCTAGAGTATCCCTCGAGGGGCC 2892

DB 153 AAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCTCTAGAGTATCCCTCGAGGGGCC 94

QY 2893 AAGCTTACCGCTGACCCAGCTTTCTGTACAAAGTGTGCTCCATAGTAGAGTCGAT 2947

DB 93 AAGCTTACCGCTGACCCAGCTTTCTGTACAAAGTGTGCTCCATAGTAGAGTCGAT 39

RESULT 9

US-09-620-312D-108

; Sequence 108, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

```

; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 108
; LENGTH: 2265
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (79)..(1614)
US-09-620-312D-108
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Query Match      3.5%; Score 108.4; DB 3; Length 2265;
Best Local Similarity 98.4%; Pred. No. 1.6e-17;
Matches 120; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY 2841 AAAAAAAAAAAGGGGCGCGCTAGAGTATCCCTCGAGGGGCCCAAGCTTAC 2900
DB 2116 AAAAAAAAAAAGGGGCGCGCGCTTAGAGTATCCCTCGAGGGGCCCAAGCTTAC 2175
QY 2901 GCGTACCCAGCTTCTTGTGACAAAGTGTCCTATAGTAGTCGATTATTAAGCTAGGCA 2960
DB 2176 GCGTACCCAGCTTCTTGTGACAAAGTGTCCTATAGTAGTCGTA-TATAAGCTAGGCA 2234
QY 2961 CT 2962
DB 2235 GT 2236
```

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RESULT 10
US-09-620-312D-109
; Sequence 109, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
```

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; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 109
; LENGTH: 2349
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (79)..(1698)
US-09-620-312D-109
```

```

Query Match      3.5%; Score 108.4; DB 3; Length 2349;
Best Local Similarity 98.4%; Pred. No. 1.6e-17;
Matches 120; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```

QY 2841 AAAAAAAAAAAGGGGCGCGCTAGAGTATCCCTCGAGGGGCCCAAGCTTAC 2900
DB 2200 AAAAAAAAAAAGGGGCGCGCGCTTAGAGTATCCCTCGAGGGGCCCAAGCTTAC 2259
QY 2901 GCGTACCCAGCTTCTTGTGACAAAGTGTCCTATAGTAGTCGATTATTAAGCTAGGCA 2960
DB 2260 GCGTACCCAGCTTCTTGTGACAAAGTGTCCTATAGTAGTCGTA-TATAAGCTAGGCA 2318
QY 2961 CT 2962
DB 2319 GT 2320
```

```

RESULT 11
US-09-620-312D-964
; Sequence 964, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunding
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 964
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Homo sapiens
```


FEATURE:
-; NAME/KEY: CDS
; LOCATION: (149)..(778)
US-09-620-312D-964

Query Match 3.5%; Score 106.8; DB 3; Length 1476;
Best Local Similarity 90.5%; Pred. No. 3.2e-17;
Matches 114; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2822 TATGAAATGAAAAAAGGGCGCGCGCTTAGAGTATCCC 2881
DB 1311 TATGAAATGCTTAATCTCAACAAACAAAAAGGGCGCGCTTAGAGTATCCC 1370
QY 2882 TCGAGGGGCCCAAGCTTACCCGCTTCTTGTACAAAGTGTCTTATAGTAG 2941
DB 1371 TCGAGGGGCCCAAGCTTACCCGCTTCTTGTACAAAGTGTCTTATAGTAG 1430
QY 2942 TCGTAT 2947
DB 1431 TCGTAT 1436

RESULT 12
US-09-620-312D-348
; Sequence 348, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Auendi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 348
; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25)..(2976)
US-09-620-312D-348

Query Match 2.9%; Score 90.8; DB 3; Length 4062;
Best Local Similarity 93.1%; Pred. No. 7.6e-13;
Matches 95; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2827 AATGAAAAAAGGGCGCGCGCTTAGAGTATCCCTCGAG 2886
DB 3961 AATGAAATTACAGATTAAGAAAAAAGGGCGCGCGCTTAGAGTATCCCTCGAG 4020
QY 2887 GGGCCCAAGCTTACCGCTTCTTGTACAAAGTGG 2928

DB 4021 GGGCCCAAGCTTACCGCTTCTTGTACAAAGTGG 4062

RESULT 13
US-09-620-312D-742
; Sequence 742, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Auendi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP28
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_FL_genes Version 1.0
; SEQ ID NO 742
; LENGTH: 1912
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (340)..(1176)
US-09-620-312D-742

Query Match 2.9%; Score 89.8; DB 3; Length 1912;
Best Local Similarity 97.8%; Pred. No. 9.5e-13;
Matches 91; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2836 AAAAAAAGGGCGCGCGCTTAGAGTATCCCTCGAGGGGCCAAG 2895
DB 1820 ACATAAAAAAGGGCGCGCGCTTAGAGTATCCCTCGAGGGGCCAAG 1879
QY 2896 CTTACCGCTTACCGCTTCTTGTACAAAGTGG 2928
DB 1880 CTTACCGCTTACCGCTTCTTGTACAAAGTGG 1912

RESULT 14
US-09-620-312D-100/C
; Sequence 100, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Auendi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.

```
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungting
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaest
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 100
; LENGTH: 2275
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (770)..(2230)
; US-09-620-312D-100
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Query Match 2.9%; Score 89.4; DB 3; Length 2275;
Best Local Similarity 98.9%; Pred. No. 1.3e-12;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2838 AAAAAAAAAAAAAAAAAAGGCGCGCTAGAGTATCCCTGAGGGGCCCAAGCT 2897
DB 91 AAAAAAAAAAAAAAAAAAGGCGCGCTAGAGTATCCCTGAGGGGCCCAAGCT 32
QY 2898 TAGCGTACCGAGCTTCTTGTAACAAGTGG 2928
DB 31 TAGCGTACCGAGCTTCTTGTAACAAGTGG 1
```

```
RESULT 15
US-09-620-312D-101/c
; Sequence 101, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungting
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghaest
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
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; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 101
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (770)..(2359)
; US-09-620-312D-101
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Query Match 2.9%; Score 89.4; DB 3; Length 2817;
Best Local Similarity 98.9%; Pred. No. 1.5e-12;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2838 AAAAAAAAAAAAAAAAAAGGCGCGCTAGAGTATCCCTGAGGGGCCCAAGCT 2897
DB 91 AAAAAAAAAAAAAAAAAAGGCGCGCTAGAGTATCCCTGAGGGGCCCAAGCT 32
QY 2898 TAGCGTACCGAGCTTCTTGTAACAAGTGG 2928
DB 31 TAGCGTACCGAGCTTCTTGTAACAAGTGG 1
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Search completed: March 1, 2006, 09:01:00
Job time : 535 secs
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Db 1561 CGAGACCAAGGCTCCAGAGAGCGGGGCAACACGAGACAGGGGACAGAAAGAACTAC 1620
Qy 1621 TTCGGAGACAGTCAAGCGGCTCCCTAATACGTGCCATTGGCAACATGACCAAGTTATT 1680
Db 1621 TTCGGAGACAGTCAAGCGGCTCCCTAATACGTGCCATTGGCAACATGACCAAGTTATT 1680
Qy 1681 GAGGAGAGCGGAGCTGGTTGGAAGAGATGGTCCCTTCCATCCTCTCCATGCGGC 1740
Db 1681 GAGGAGAGCGGAGCTGGTTGGAAGAGATGGTCCCTTCCATCCTCTCCATGCGGC 1740
Qy 1741 TACCGGAGACGATCTTGAGAAATTTGATTGCGGCTTGGTTTAAATGATCATGTGC 1800
Db 1741 TACCGGAGACGATCTTGAGAAATTTGATTGCGGCTTGGTTTAAATGATCATGTGC 1800
Qy 1801 AAACAGAGGCTGAGAGTGAATTCTGCTAAAGATAGAGGCGCTGTTCTTGGGGCAAC 1860
Db 1801 AAACAGAGGCTGAGAGTGAATTCTGCTAAAGATAGAGGCGCTGTTCTTGGGGCAAC 1860
Qy 1861 GAGACCAAGGCTCCAGACAGAGTCAAGATGAGGAGGCTTGGACCAAGCGGGAGGCG 1920
Db 1861 GAGACCAAGGCTCCAGACAGAGTCAAGATGAGGAGGCTTGGACCAAGCGGGAGGCG 1920
Qy 1921 CGGCTGAGGCTTGAAGGATAGCGGCGGCTGCAACCCCTGCTGCAACGAGTGAAGCGGC 1980
Db 1921 CGGCTGAGGCTTGAAGGATAGCGGCGGCTGCAACCCCTGCTGCAACGAGTGAAGCGGC 1980
Qy 1981 AGCCCTCGAGACATGCGCGGGAATCAAGGATATGATCTGCTGCTGCTCATCGAG 2040
Db 1981 AGCCCTCGAGACATGCGCGGGAATCAAGGATATGATCTGCTGCTGCTCATCGAG 2040
Qy 2041 CTGTCTCTGCACTGATGAGAGATCTTGAACGACCAAGCAAGAAAGTCTTCCCTGAGC 2100
Db 2041 CTGTCTCTGCACTGATGAGAGATCTTGAACGACCAAGCAAGAAAGTCTTCCCTGAGC 2100
Qy 2101 GAGAGGCTGCTCTCTCTTCAAGGCTGAGTGAAGAGAACTCTCTGCGCTTCCCTCAAG 2160
Db 2101 GAGAGGCTGCTCTCTCTTCAAGGCTGAGTGAAGAGAACTCTCTGCGCTTCCCTCAAG 2160
Qy 2161 CTCTCTCTCTTCTGGGTCATGCAAGAGATCTTGGTTCGCGAGCTACATGATGAACTC 2220
Db 2161 CTCTCTCTCTTCTGGGTCATGCAAGAGATCTTGGTTCGCGAGCTACATGATGAACTC 2220
Qy 2221 CAGCGGCTGCGGCTTGTGAACAAAGAAAGTCTAGACATGGCACTTTCAGTCTG 2280
Db 2221 CAGCGGCTGCGGCTTGTGAACAAAGAAAGTCTAGACATGGCACTTTCAGTCTG 2280
Qy 2281 CCTCCCTCTGATTCCTCCAGCTCATCTCCCTGATGCAATGSCCATTTGAGCTGAGGTC 2340
Db 2281 CCTCCCTCTGATTCCTCCAGCTCATCTCCCTGATGCAATGSCCATTTGAGCTGAGGTC 2340
Qy 2341 CATACAGAGATATTTGAGAGTGAATGCTGCGCAGTACTTGTCTTCCCTTCCCAACCT 2400
Db 2341 CATACAGAGATATTTGAGAGTGAATGCTGCGCAGTACTTGTCTTCCCTTCCCAACCT 2400
Qy 2401 TTAACCGATATCTTGAACAACTCTCAATTTCTAAATATGATGAGCTTGAAGGCA 2460
Db 2401 TTAACCGATATCTTGAACAACTCTCAATTTCTAAATATGATGAGCTTGAAGGCA 2460
Qy 2461 TGTCCATTAAGGCTGCAACAGCTTGCATTTGGTATGCTTGGATGAGAGGCTGTT 2520
Db 2461 TGTCCATTAAGGCTGCAACAGCTTGCATTTGGTATGCTTGGATGAGAGGCTGTT 2520
Qy 2521 GTGGAGAGTGAAGAGAAATATATTAAGAAAGAGAGATGCTGCACTAATCAATTC 2580
Db 2521 GTGGAGAGTGAAGAGAAATATATTAAGAAAGAGAGATGCTGCACTAATCAATTC 2580
Qy 2581 GACTTCAATGAGCTTGCACAACTTTGCTGTTGCTATGCTTGAATTTGAATGC 2640
Db 2581 GACTTCAATGAGCTTGCACAACTTTGCTGTTGCTATGCTTGAATTTGAATGC 2640
Qy 2641 TTGTGAAAAAGGCACTTTAATCATATGCAAGAAATCAAGTGCATATCTG 2700

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Db 2641 TTGTGAAAAAGGCACTTTAATCATATGCAAGAAATCAAGTGCATATCTG 2700
Qy 2701 AATCCATGTTGATATGCAATATGTTCTCATTTATTTTGTATGATTAATTACATTGCC 2760
Db 2701 AATCCATGTTGATATGCAATATGTTCTCATTTATTTTGTATGATTAATTACATTGCC 2760
Qy 2761 ATGGGTTTAAATTAAGCTTTGAGTCAAAAGTCAAGAAATGACTGAATATACAGTCACT 2820
Db 2761 ATGGGTTTAAATTAAGCTTTGAGTCAAAAGTCAAGAAATGACTGAATATACAGTCACT 2820
Qy 2821 TTATGAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGTATCC 2880
Db 2821 TTATGAAATGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGTATCC 2880
Qy 2881 CTGAGAGGCGCAAGCTTACGGTACCGGCTTCTTGTATCAAAAGTGTCCCTATATGTA 2940
Db 2881 CTGAGAGGCGCAAGCTTACGGTACCGGCTTCTTGTATCAAAAGTGTCCCTATATGTA 2940
Qy 2941 GTGATATTAAGCTAGGACCTGGCGGCTTTTACAAAGTGTGACTGGAAAACTGCT 3000
Db 2941 GTGATATTAAGCTAGGACCTGGCGGCTTTTACAAAGTGTGACTGGAAAACTGCT 3000
Qy 3001 AGCTTGGATCTTTGTGAAGAACTTACTTCTGTGTGTGACATATTTGACAAACTAC 3060
Db 3001 AGCTTGGATCTTTGTGAAGAACTTACTTCTGTGTGTGACATATTTGACAAACTAC 3060
Qy 3061 CTACAGAGATTTAAAGCTCTTAAG 3083
Db 3061 CTACAGAGATTTAAAGCTCTTAAG 3083

```

```

RESULT 2
ADU69243
ID ADU69243 standard; DNA; 3083 BP.
XX
AC ADU69243;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human SEF gene variant SEQ ID NO:3.
XX
KW da; fibroblast growth factor; SEF; similar expression of FGF genes;
KW cytostatic; cardiovascular-gen.; antiarteriosclerotic; cardiant;
KW vasotropic; hypotensive; nephrotropic; gene therapy; diagnosis;
KW prognosis; proliferative disorders; cardiovascular disorders;
KW renal disease; glomerular disease; gene.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 22..2241
FT /tag= a
FT /product= "SEF"
XX
PN US2004235104-A1.
XX
PD 25-NOV-2004.
XX
PF 07-MAY-2004; 2004US-00842006.
XX
PR 08-MAY-2003; 2003US-0469522P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Yang R;
XX
DR WPI; 2004-821320/81.
XX
DR P-PSDB; ADU69244.
XX
PT New isolated SEF nucleic acid and polypeptide, useful for monitoring,
PT treating, or diagnosing proliferative and/or differentiative disorders,
PT e.g. ovarian cancer, breast cancer, or cardiovascular disorder including
PT arteriosclerosis.

```

XX Disclosure; SEQ ID NO 3; 46bp; English.
XX
XX The invention relates to a novel isolated SEF (similar expression of RGE
CC gene) nucleic acid molecule (1). An SEF of the invention has cytoskeletal,
CC cardiovascular-gen., antiarteriosclerotic, cardiant, vasotrophic,
CC hypotensive, and nephrotropic activity, and may have a use in gene
CC therapy. The SEF nucleic acids and polypeptides can be used for
CC diagnostic assays, prognostic assays, and monitoring clinical trials.
CC They can also be used for treating a subject at risk of or susceptible to
CC a disorder or having a disorder associated with aberrant or unwanted SEF
CC expression or activity. The SEF molecules can also be used for
CC monitoring, treating, or diagnosing proliferative and/or differentiative
CC disorders, e.g. ovarian cancer, breast cancer, colon cancer, prostatic
CC cancer, RGE related disorder, cardiovascular disorder including
CC arteriosclerosis, coronary artery disease, ischemia, reperfusion injury,
CC restenosis, arterial inflammation, hypertension, endothelial disorders,
CC and a kidney disorder, e.g. glomerulonephritis, vascular nephropathy,
CC renal failure, or glomerular disease. The SEF molecules can also be used
CC as markers of disorders or disease states, as markers for precursors of
CC disease states, as markers for predisposition of disease states, as
CC markers of drug activity, or as markers of the pharmacogenomic profile of
CC a subject. The present sequence represents a variant of the SEF nucleic
CC acid shown in ADU69241.
XX
SQ Sequence 3083 BP; 782 A; 807 C; 767 G; 727 T; 0 U; 0 Other;
Query Match 100.0%; Score 3083; DB 13; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TGGCTGGGCGAGCGACGCGATGCGCGCTGCGTGCAGCTGCTCCGCTCTTAAAG 60
1 TGGCTGGGCGAGCGACGCGATGCGCGCTGCGTGCAGCTGCTCCGCTCTTAAAG 60
61 GTCAACGCTGCTCAACGCGCTGCGAGCTGCGTGTGCGCGTGGCGGCTCGCGCG 120
61 GTCAACGCTGCTCAACGCGCTGCGAGCTGCGTGTGCGCGTGGCGGCTCGCGCG 120
121 TGGGGGCTGACACCTGTGCTGAGAGGAGAGTGGGGCCGACGAGAAACAGTGGGCTG 180
121 TGGGGGCTGACACCTGTGCTGAGAGGAGAGTGGGGCCGACGAGAAACAGTGGGCTG 180
121 TGGGGGCTGACACCTGTGCTGAGAGGAGAGTGGGGCCGACGAGAAACAGTGGGCTG 180
181 TCAACATCACTCTTAATATGACATTTGACCACTTGAATCAGTGGGGAAGCAT 240
181 TCAACATCACTCTTAATATGACATTTGACCACTTGAATCAGTGGGGAAGCAT 240
181 TCAACATCACTCTTAATATGACATTTGACCACTTGAATCAGTGGGGAAGCAT 240
241 GTGATTGCTGACGCGCAGAAATATCACATCAAGCAGATATGCTTCCATGACCAAGTGGCA 300
241 GTGATTGCTGACGCGCAGAAATATCACATCAAGCAGATATGCTTCCATGACCAAGTGGCA 300
301 GTCAACATCTTTGTGTGCTCCCAAGGCGCTCGCATGAAATCTTGAAAGATTTCCGGTAA 360
301 GTCAACATCTTTGTGTGCTCCCAAGGCGCTCGCATGAAATCTTGAAAGATTTCCGGTAA 360
361 ATACTGGAGAGCTGAAGTCCGAGGAGAGCAGTGCACCACTGATTTCTTAAAGATCCG 420
361 ATACTGGAGAGCTGAAGTCCGAGGAGAGCAGTGCACCACTGATTTCTTAAAGATCCG 420
421 AAGCAGCTCAACAGTATCTTCAAAAGAACTGAAATGAAATCTCAACCTTTCGTATATG 480
421 AAGCAGCTCAACAGTATCTTCAAAAGAACTGAAATGAAATCTCAACCTTTCGTATATG 480
481 AAATTGAAACGAGTATTTCTTAAAGGTTTCCCTTTCTTCAATTTAAAGAAAGC 540
481 AAATTGAAACGAGTATTTCTTAAAGGTTTCCCTTTCTTCAATTTAAAGAAAGC 540
541 AATTACACCTCTTCTTGAACCGAGCTGACCTGTGTTTACAGCGGCAAT 600
541 AATTACACCTCTTCTTGAACCGAGCTGACCTGTGTTTACAGCGGCAAT 600
601 CTAGCTTGTAAACCTTCTGAAAGCTCGAACTGTAAATCAAGCAGCATGCTCGAGC 660
601 CTAGCTTGTAAACCTTCTGAAAGCTCGAACTGTAAATCAAGCAGCATGCTCGAGC 660

DB 601 CTAGCTTGTAAACCTTCTGAAAGCTCGAACTGTAAATCAAGCAGCATGCTCGAGC 660
QY 661 ATGCAAGTGTCTTGGACACGACGACAACTTCGCGCTTCGTTCTTATCTTAC 720
DB 661 ATGCAAGTGTCTTGGACACGACGACAACTTCGCGCTTCGTTCTTATCTTAC 720
QY 721 TCAAGCTCAACGAGAGGAGCTTTCAGCGAAAGACTGTAGCAGAGCAAACTACA 780
DB 721 TCAAGCTCAACGAGAGGAGCTTTCAGCGAAAGACTGTAGCAGAGCAAACTACA 780
QY 781 GAGACGACCACTGCTCTCTTAAATGTTTCTCAAGGAGATTAATTAATGAGTGGT 840
DB 781 GAGACGACCACTGCTCTCTTAAATGTTTCTCAAGGAGATTAATTAATGAGTGGT 840
QY 841 GATGACCTTAACAACAAGAAAGATGATTAATGCTTAAGCCAGTGCATCCCG 900
DB 841 GATGACCTTAACAACAAGAAAGATGATTAATGCTTAAGCCAGTGCATCCCG 900
QY 901 TGGCGCGGCGCCATGAGAGCCATGAGCATACAGTGCATGCTGTATGATCGGCAATTC 960
DB 901 TGGCGCGGCGCCATGAGAGCCATGAGCATACAGTGCATGCTGTATGATCGGCAATTC 960
QY 961 GCGAGCTCTTCACTGTGATGTGCGCAAGAGCAACAAGAAATATATATTCACATTTA 1020
DB 961 GCGAGCTCTTCACTGTGATGTGCGCAAGAGCAACAAGAAATATATATTCACATTTA 1020
QY 1021 GATGAAGAGAGCTGAGCTTCCACATACCTGAGACCTCCAGAGAGAGGCTCCGG 1080
DB 1021 GATGAAGAGAGCTGAGCTTCCACATACCTGAGACCTCCAGAGAGAGGCTCCGG 1080
QY 1081 CCGCGGCGAAGGCTTCTCTGCTATTCAGTAAAGATGCGAGAAATCACATGATGTC 1140
DB 1081 CCGCGGCGAAGGCTTCTCTGCTATTCAGTAAAGATGCGAGAAATCACATGATGTC 1140
QY 1141 GTCCAGTGTGCTTCTTCTTCCAGACCTTCTGTGCTGTGAGTGGCTCTGACCTG 1200
DB 1141 GTCCAGTGTGCTTCTTCTTCCAGACCTTCTGTGCTGTGAGTGGCTCTGACCTG 1200
QY 1201 TGGGAAGACTTCAAGCTCTGTGAGAGGAGGAGAGATGGGTATCAGAAAGATCCAC 1260
DB 1201 TGGGAAGACTTCAAGCTCTGTGAGAGGAGGAGAGATGGGTATCAGAAAGATCCAC 1260
QY 1261 GAGTCCAGTTCATATGTTGTTGTTCCAAAGATATGATGTTGTGACCAAGAG 1320
DB 1261 GAGTCCAGTTCATATGTTGTTGTTCCAAAGATATGATGTTGTGACCAAGAG 1320
QY 1321 AACTCAAAACAACAAGAGAGTGGCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGCG 1380
DB 1321 AACTCAAAACAACAAGAGAGTGGCGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGCG 1380
QY 1381 GGTGAGCACTTGGCGAAAGCTCGGCAAGGCAAGAGTGGTCCGCGCGCTCAGC 1440
DB 1381 GGTGAGCACTTGGCGAAAGCTCGGCAAGGCAAGAGTGGTCCGCGCGCTCAGC 1440
QY 1441 AAGTTTATGCGCGTCTATCTTGAATATTCCTGCGAGGAGAGCTGCCGATCTTAC 1500
DB 1441 AAGTTTATGCGCGTCTATCTTGAATATTCCTGCGAGGAGAGCTGCCGATCTTAC 1500
QY 1501 CTGAGTACCAAGTACAGACTATGAGCAATCTTCTCAGCTCTGTTCCACTGACATCC 1560
DB 1501 CTGAGTACCAAGTACAGACTATGAGCAATCTTCTCAGCTCTGTTCCACTGACATCC 1560
QY 1561 CGAGACCAAGGCTTCCAGAGGCGCGGAGCAACGCGACAGGCGAGAGAACTAC 1620
DB 1561 CGAGACCAAGGCTTCCAGAGGCGCGGAGCAACGCGACAGGCGAGAGAACTAC 1620
QY 1621 TTCGGAAGCAAGTCAAGGCGGCTCTATATGCTGCGCACTTTCACATGACCAAGTTTAT 1680
DB 1621 TTCGGAAGCAAGTCAAGGCGGCTCTATATGCTGCGCACTTTCACATGACCAAGTTTAT 1680
QY 1681 GACGAGAGGCGGAGCTGGTTCGAAAGAGATTCCTTCCATCTCTCAGCTGCGC 1740
DB 1681 GACGAGAGGCGGAGCTGGTTCGAAAGAGATTCCTTCCATCTCTCAGCTGCGC 1740

Qy	1741	TACGGGAGCCAGGCTTGTGAGAAATTTGATTCGGGCTGGTTTAAATGAGTCAATGGC	1800
Db	1741	TACGGGAGCCAGGCTTGTGAGAAATTTGATTCGGGCTGGTTTAAATGAGTCAATGGC	1800
Qy	1801	AAACCAAGGGCTTGAGAGTGAAGTCTTGCTGCTAAAGGTAGAGGGCGCTGTTCTTGGGGCAAC	1860
Db	1801	AAACCAAGGGCTTGAGAGTGAAGTCTTGCTGCTAAAGGTAGAGGGCGCTGTTCTTGGGGCAAC	1860
Qy	1861	GGACCAAGCCGACTCCCAAGACAGAGGTAGCAATGGGGGCTGTGACCAAGACGGGGAGGCC	1920
Db	1861	GGACCAAGCCGACTCCCAAGACAGAGGTAGCAATGGGGGCTGTGACCAAGACGGGGAGGCC	1920
Qy	1921	CGGCTGCGCTTGTGACGTGTAGCGCGCCCTGTGAAACCCTGTGACACAGGTGAAAAGCCGGC	1980
Db	1921	CGGCTGCGCTTGTGACGTGTAGCGCGCCCTGTGAAACCCTGTGACACAGGTGAAAAGCCGGC	1980
Qy	1981	AGCCCTCTGGACATGCGCGGGGACTCAGGCACTATATGACTGTGTGCTCCCTCACG	2040
Db	1981	AGCCCTCTGGACATGCGCGGGGACTCAGGCACTATATGACTGTGTGCTCCCTCACG	2040
Qy	2041	CTGTCTCTGCACTGATGGAAGGACCTCTCGACGGGCGACAGAAAGGTCTTCCCTGACG	2100
Db	2041	CTGTCTCTGCACTGATGGAAGGACCTCTCGACGGGCGACAGAAAGGTCTTCCCTGACG	2100
Qy	2101	GAGAGCGTGTCTCTCTTTCAGGCGCTGGGTGAGAGGAACTCTGCTTCTTCCAG	2160
Db	2101	GAGAGCGTGTCTCTCTTTCAGGCGCTGGGTGAGAGGAACTCTGCTTCTTCCAG	2160
Qy	2161	CTCCTCTCTTCTGGGTCAATGCAAAAGCAGATCTTGTTGCCGACGTACATGATGAATC	2220
Db	2161	CTCCTCTCTTCTGGGTCAATGCAAAAGCAGATCTTGTTGCCGACGTACATGATGAATC	2220
Qy	2221	CACGCGGTGCGCCCTTGTGTAAACAAACGAAAGAGCTAGAGATTGGCCACTTATAGCTGTG	2280
Db	2221	CACGCGGTGCGCCCTTGTGTAAACAAACGAAAGAGCTAGAGATTGGCCACTTATAGCTGTG	2280
Qy	2281	CCTCCCTCTGATTCGCCAGCTCATCTCCTGTGTGCAATGCGCCCACTTGAAGCTAGGTCT	2340
Db	2281	CCTCCCTCTGATTCGCCAGCTCATCTCCTGTGTGCAATGCGCGCCCACTTGAAGCTAGGTCT	2340
Qy	2341	CATTCAGAGGATTTTGTGAGTAAATAGCTGGGCAAGTACTGTTCTCCCTGTGCCCCAACCT	2400
Db	2341	CATTCAGAGGATTTTGTGAGTAAATAGCTGGGCAAGTACTGTTCTCCCTGTGCCCCAACCT	2400
Qy	2401	TTACCGGATATCTTGACAAACTCTCCAAATTTCTTAAATGATATGAGCTCTGAAAGGCA	2460
Db	2401	TTACCGGATATCTTGACAAACTCTCCAAATTTCTTAAATGATATGAGCTCTGAAAGGCA	2460
Qy	2461	TGTGCAATAAGCTCTGACAAACAGCTTGGCAATTTGGTTAGTCTTGTGATTCAGAGCTGT	2520
Db	2461	TGTGCAATAAGCTCTGACAAACAGCTTGGCAATTTGGTTAGTCTTGTGATTCAGAGCTGT	2520
Qy	2521	GTGGGAGGTAGGAGGAATATGTATTAAGAAAACAGAAAGATACCTGCATATCATTTCA	2580
Db	2521	GTGGGAGGTAGGAGGAATATGTATTAAGAAAACAGAAAGATACCTGCATATCATTTCA	2580
Qy	2581	GACTTCATTTAGCTCTGCAAACTTGTGCTGTGTTGCTATTGGCTACTTGATTTGAATGC	2640
Db	2581	GACTTCATTTAGCTCTGCAAACTTGTGCTGTGTTGCTATTGGCTACTTGATTTGAATGC	2640
Qy	2641	TTTGTGAAAAGGACCTTTTAACTATCAATAGCACAAATCAAGTGCACATCTATCTGG	2700
Db	2641	TTTGTGAAAAGGACCTTTTAACTATCAATAGCACAAATCAAGTGCACATCTATCTGG	2700
Qy	2701	AATCCAGTGTGATATGCAATATGTTCTCAATTTATTTTGTAGTGAATTTTACATTGCC	2760
Db	2701	AATCCAGTGTGATATGCAATATGTTCTCAATTTATTTTGTAGTGAATTTTACATTGCC	2760
Qy	2761	ATGGGTGTAAATATAGCTTTAGTCAAAAGTCAAGAAAGTACGTAAATATACAGTCACT	2820
Db	2761	ATGGGTGTAAATATAGCTTTAGTCAAAAGTCAAGAAAGTACGTAAATATACAGTCACT	2820

Qy	2821	TTTATGAAATGAAAAAAAAAAAAAAAAAAGGCGCCGCTTAGAGTATCC	2880
Db	2821	TTTATGAAATGAAAAAAAAAAAAAAAAAAGGCGCCGCTTAGAGTATCC	2880
Qy	2881	CTCAGAGGCGCCAAAGCTTACGCGTACCAAGCTTCTTGTAACAAAGTGTCCCTTATAGTA	2940
Db	2881	CTCAGAGGCGCCAAAGCTTACGCGTACCAAGCTTCTTGTAACAAAGTGTCCCTTATAGTA	2940
Qy	2941	GTGCTATTATTAAGCTAGGCACTGGCGGTGTTTACAACGTCTGGACTGGGAAAACTGCT	3000
Db	2941	GTGCTATTATTAAGCTAGGCACTGGCGGTGTTTACAACGTCTGGACTGGGAAAACTGCT	3000
Qy	3001	AGCTTGGGATCTTGTGTGAAGAACCTTACTTCTGTGTGTGACATTAATTGGACAAACTAC	3060
Db	3001	AGCTTGGGATCTTGTGTGAAGAACCTTACTTCTGTGTGTGACATTAATTGGACAAACTAC	3060
Qy	3061	CTACAGAGATTTAAGGCTTAAG	3083
Db	3061	CTACAGAGATTTAAGGCTTAAG	3083

XX	ADU69241	standard; DNA; 4477 BP.
XX	ADU69241;	
XX	10-FEB-2005	(first entry)
XX	Human SEF gene SEQ ID NO:1.	
XX	ds; gene; fibroblast growth factor; SEF; similar expression of FGF genes;	
KW	cytostatic; cardiovascular-gen.; antiarteriosclerotic; cardiant;	
KW	vasotropic; hypotensive; nephrotropic; gene therapy; diagnosis;	
KW	prognosis; proliferative disorders; cardiovascular disorders;	
KW	renal disease; glomerular disease.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	CDS	90..2309
FT		/*tag= a
FT		/product= "SEF"
XX	US2004235104-A1.	
XX	25-NOV-2004.	
XX	07-MAY-2004; 2004US-00842006.	
XX	08-MAY-2003; 2003US-0469522P.	
XX	(MILL-) MILLENNIUM PHARM INC.	
XX	Yang R;	
XX	WPI; 2004-821320/81.	
XX	P-PSDB; ADU69242.	
XX	New isolated SEF nucleic acid and polypeptide, useful for monitoring,	
XX	treating, or diagnosing proliferative and/or differentiative disorders,	
XX	e.g. ovarian cancer, breast cancer, or cardiovascular disorder including	
XX	arteriosclerosis.	
XX	Claim 1; SEQ ID NO 1; 46pp; English.	
XX	The invention relates to a novel isolated SEF (similar expression of FGF	
XX	genes) nucleic acid molecule (I). An SEF of the invention has cytostatic,	
XX	cardiovascular-gen., antiarteriosclerotic, cardiant, vasotropic,	
XX	hypotensive, and nephrotropic activity, and may have a use in gene	
XX	therapy. The SEF nucleic acids and polypeptides can be used for	
XX	diagnostic assays, prognostic assays, and monitoring clinical trials.	
XX	They can also be used for treating a subject at risk of or susceptible to	

D	b	1929	GGACACGCCCACTCCACGACGAGAGTACAGATGGGGGCTGGACCAAGACGGGAGGCC	1988
Q	y	1921	CGGCTTCGCTTGACGGTAGCGCGGCTTGCAACCCTTGCGACACGGTAGAAACCGGGC	1980
D	b	1989	CGGCTTCGCTTGACGGTAGCGCGGCTTGCAACCCTTGCGACACGGTAGAAACCGGGC	2048
Q	y	1981	AGCCCTTCGGACATGCGCGGGGACTCAGAGCATCTATGACTGGTCTGTGCCCTCATCCGAG	2040
D	b	2049	AGCCCTTCGGACATGCGCGGGGACTCAGAGCATCTATGACTGGTCTGTGCCCTCATCCGAG	2108
Q	y	2041	CTGTCTCTGCGACATGATGGAAGGACTCTGCAACGACACAGAAACGCTTCCCTGACG	2100
D	b	2109	CTGTCTCTGCGACATGATGGAAGGACTCTGCAACGACACAGAAACGCTTCCCTGACG	2168
Q	y	2101	GAGAGCGGTCTCTCTCTTTCAGAGCGCTGGGTGAGAGGAACTCTGCCCTTCTTCCAG	2160
D	b	2169	GAGAGCGGTCTCTCTCTTTCAGAGCGCTGGGTGAGAGGAACTCTGCCCTTCTTCCAG	2228
Q	y	2161	CTCCTCTCTTCGGGGTCAATGAAAGCAGATCTTGTTGCCGACGTACATGATGAATC	2220
D	b	2229	CTCCTCTCTTCGGGGTCAATGAAAGCAGATCTTGTTGCCGACGTACATGATGAATC	2288
Q	y	2221	CACCGGGTCGCGCTTGTGTAACAAAACGAAAGAGCTAGAGATTGGCCACTTAAAGTGTG	2280
D	b	2289	CACCGGGTCGCGCTTGTGTAACAAAACGAAAGAGCTAGAGATTGGCCACTTAAAGTGTG	2348
Q	y	2281	CTCTCTCTGTATCCCAAGCTCATCTCTCCGTGTGCAAGGCCCACTTGGAGCTAGAGTCT	2340
D	b	2349	CTCTCTCTGTATCCCAAGCTCATCTCTCCGTGTGCAAGGCCCACTTGGAGCTAGAGTCT	2408
Q	y	2341	CATCAAGGATATTTGAGTGAAATATCGGGCAGATCTGTTCTTCCTTGGCCCCAACCT	2400
D	b	2409	CATCAAGGATATTTGAGTGAAATATCGGGCAGATCTGTTCTTCCTTGGCCCCAACCT	2468
Q	y	2401	TTACCGGATATCTTGACAAACTCTCAATTTCTTAAATGATATGAGACTCTGAAAGGCA	2460
D	b	2469	TTACCGGATATCTTGACAAACTCTCAATTTCTTAAATGATATGAGACTCTGAAAGGCA	2528
Q	y	2461	TGTCATATAGGTCCTGACAAACAGCTTGCCAAATTTGGTTAGTCTTGATCAAGCTGTT	2520
D	b	2529	TGTCATATAGGTCCTGACAAACAGCTTGCCAAATTTGGTTAGTCTTGATCAAGCTGTT	2588
Q	y	2521	GTGGAGGTTAGGGAGGAAATATGTAAAGAAACAGAAAGATACCTGACATATCATCTCA	2580
D	b	2589	GTGGAGGTTAGGGAGGAAATATGTAAAGAAACAGAAAGATACCTGACATATCATCTCA	2648
Q	y	2581	GACTTCATTGAGCTCTGCAAACTTGGCTGTGTTCTATTTGACTACCTGATTTGAAATGC	2640
D	b	2649	GACTTCATTGAGCTCTGCAAACTTGGCTGTGTTCTATTTGACTACCTGATTTGAAATGC	2708
Q	y	2641	TTTGTGAAAAAGGCACTTTTAAATCATCATACGACAGAAATCAAGTGCAGTCTATCTGG	2700
D	b	2709	TTTGTGAAAAAGGCACTTTTAAATCATCATACGACAGAAATCAAGTGCAGTCTATCTGG	2768
Q	y	2701	AATTCAGTTGTATATGAGATTAAGTCTCATAGTTATTTTGAATGAAATTTTAATATGGC	2760
D	b	2769	AATTCAGTTGTATATGAGATTAAGTCTCATAGTTATTTTGAATGAAATTTTAATATGGC	2828
Q	y	2761	ATGGGTATTAATATAGCTTTGAGTCAAAAGTCAAGAAAGTGAATATCAAGTCACT	2820
D	b	2829	ATGGGTATTAATATAGCTTTGAGTCAAAAGTCAAGAAAGTGAATATCAAGTCACT	2888
Q	y	2821	TTTATGAAATGA 2832	
D	b	2889	TTTATGAAATGA 2900	

RESULT	4
ID	ADW23599
XX	ADW23599 standard; DNA; 4477 BP
AC	ADW23599;

[illegible]

Db 369 GTCAACATTCCTTGTGATCCCCAGGGGCCCTCGGCATCGAAATTCCTGAAGAGATTCGAGTA 428
Qy 361 ATACTGAGAGAGCTGAAGTGCAGAGGAGAGACAGTGCACAACATCGATTCTTAAGATCCG 420
Db 429 ATACTGAGAGAGCTGAAGTGCAGAGGAGAGACAGTGCACAACATCGATTCTTAAGATCCG 488
Qy 421 AAGCAGCTCAACAGTAGTCTTCAAAAGACTGGAATGGAAATCTCAACCTTTCCTGAATATG 480
Db 489 AAGCAGCTCAACAGTAGTCTTCAAAAGACTGGAATGGAAATCTCAACCTTTCCTGAATATG 548
Qy 481 AATTTGAAACGGAATTAATTCGTAAAGTTCCTTTCCTTCCATTTAAAAAGAAAC 540
Db 549 AATTTGAAACGGAATTAATTCGTAAAGTTCCTTTCCTTCCATTTAAAAAGAAAC 608
Qy 541 AATTACCAACCTTCTTCTTTAAGACCCGAGCCTGTGACCTGTGTTTACAGCCGGAACAT 600
Db 609 AATTACCAACCTTCTTCTTTAAGACCCGAGCCTGTGACCTGTGTTTACAGCCGGAACAT 668
Qy 601 CTAGCTTGTAAACCTTCTTGAAGCCTCGGAACCTGAAACATCAGCCAGATGGCTCGAC 660
Db 669 CTAGCTTGTAAACCTTCTTGAAGCCTCGGAACCTGAAACATCAGCCAGATGGCTCGAC 728
Qy 661 ATGCAAGTGTCTTTCGACACGACGACGACACTTGGGCTTCCTTCTTATCTTAC 720
Db 729 ATGCAAGTGTCTTTCGACACGACGACGACACTTGGGCTTCCTTCTTATCTTAC 788
Qy 721 TACAAGCTCAAGACGAAAGGACCTTCAAGCGAAAGACTGTAAAGAGAGAGCAATACA 780
Db 789 TACAAGCTCAAGACGAAAGGACCTTCAAGCGAAAGACTGTAAAGAGAGAGCAATACA 848
Qy 781 GAGACGACGAGCTGCTCTTCAAAATGTTTCTCAAGGGGATTAATAATGAGCTGTG 840
Db 849 GAGATACCAAGCTGCTCTTCAAAATGTTTCTCAAGGGGATTAATAATGAGCTGTG 908
Qy 841 GATGACACTTAACCAACAGAAAGATGATGATTAATGCTTAAAGCAGTGCCTCCG 900
Db 909 GATGACACTTAACCAACAGAAAGATGATGATTAATGCTTAAAGCAGTGCCTCCG 968
Qy 901 TGGGCGGGGCCCATGAGAGCATGGCCATGACAGTGCACCTGGTATGATATGCGGATTC 960
Db 969 TGGGCGGGGCCCATGAGAGCATGGCCATGACAGTGCACCTGGTATGATATGCGGATTC 1028
Qy 961 GCGACGCTCTTCACTGTGATGTGCGCAAGAGCAACAGAAATATATATTCACATTTA 1020
Db 1029 GCGACGCTCTTCACTGTGATGTGCGCAAGAGCAACAGAAATATATATTCACATTTA 1088
Qy 1021 GATGAAGAGAGCTCTGATGCTTCAACATACATGACACTCCCAAGAGAGAGCTCCG 1080
Db 1089 GATGAAGAGAGCTCTGATGCTTCAACATACATGACACTCCCAAGAGAGAGCTCCG 1148
Qy 1081 CCGCGGCGGAAGTCTTCTCTGCTATTCAGTAAAGATGGCCAGAAATCATGAATGTC 1140
Db 1149 CCGCGGCGGAAGTCTTCTCTGCTATTCAGTAAAGATGGCCAGAAATCATGAATGTC 1208
Qy 1141 GTTCAGTGTTCGCTTACTTCTCAAGAACTTCTGTGCTGTGAGGTGCTTGAACCTG 1200
Db 1209 GTTCAGTGTTCGCTTACTTCTCAAGAACTTCTGTGCTGTGAGGTGCTTGAACCTG 1268
Qy 1201 TGGGAAGACTTCAAGCTCTGTAGAAGAGGCAAGAGAAATGGCTATCCAGAAATCCAC 1260
Db 1269 TGGGAAGACTTCAAGCTCTGTAGAAGAGGCAAGAGAAATGGCTATCCAGAAATCCAC 1328
Qy 1261 GAGTCCAGTTCATCATTTGTGTTTGTTCAAAGATGGAAGATCTTGTGGAAGAAAG 1320
Db 1329 GAGTCCAGTTCATCATTTGTGTTTGTTCAAAGATGGAAGATCTTGTGGAAGAAAG 1388
Qy 1321 AACTACAAACAAAGAGAGGTGCGAGGCTCGGGGAAAGAGAGCTTCTGTGAGCG 1380
Db 1389 AACTACAAACAAAGAGAGGTGCGAGGCTCGGGGAAAGAGAGCTTCTGTGAGCG 1448
Qy 1381 GTGTCAAGCATTTGCGGAAAGCTCGGCAAGGCGCAAGCAAGATTCGTTCGCGGCGCTCAGC 1440
Db 1449 GTGTCAAGCATTTGCGGAAAGCTCGGCAAGGCGCAAGCAAGATTCGTTCGCGGCGCTCAGC 1508

Qy 1441 AAGTTATGCGCGTCTACTTTGATTAATTCCTGAGAGAGAGAGTCCCGGTATCCTAGAC 1500
Db 1509 AAGTTATGCGCGTCTACTTTGATTAATTCCTGAGAGAGAGAGTCCCGGTATCCTAGAC 1568
Qy 1501 CTGAGTACCAAGTACAGACTTACAGAACTTCTCTCAAGCTCTGTTCCTGACCTGCCTCC 1560
Db 1569 CTGAGTACCAAGTACAGACTTACAGAACTTCTCTCAAGCTCTGTTCCTGACCTGCCTCC 1628
Qy 1561 CGAGACCAAGGCTCGAGAGCGGGGAGCAGCGGACAGGGGAGAGAGAACTAC 1620
Db 1629 CGAGACCAAGGCTCGAGAGCGGGGAGCAGCGGACAGGGGAGAGAGAACTAC 1688
Qy 1621 TTCCGAGAGAGTCAAGCGCGGTCCCTATACGTCCGCAATTTGCAACATGACCAAGTTAT 1680
Db 1689 TTCCGAGAGAGTCAAGCGCGGTCCCTATACGTCCGCAATTTGCAACATGACCAAGTTAT 1748
Qy 1681 GACGAGAGCCCGACTGTGTGAAAGAGTTCCTTCCATCTCTCTCACTGCGC 1740
Db 1749 GACGAGAGCCCGACTGTGTGAAAGAGTTCCTTCCATCTCTCTCACTGCGC 1808
Qy 1741 TACCGGAGCGAGTCTGAGAAATTTGATTTGGGCTTGTAAATGATGATGTC 1800
Db 1809 TACCGGAGCGAGTCTGAGAAATTTGATTTGGGCTTGTAAATGATGATGTC 1868
Qy 1801 AAACAGGCGCTGAGAGTGAATTCCTGCTTAAAGTAGAGGCGCTGTTCTTGCGGCAAC 1860
Db 1869 AAACAGGCGCTGAGAGTGAATTCCTGCTTAAAGTAGAGGCGCTGTTCTTGCGGCAAC 1928
Qy 1861 GGAACAGCGGACTCCAGACGAGAGTCAAGATGGGGGCTTGAACAGCGGAGGCTC 1920
Db 1929 GGAACAGCGGACTCCAGACGAGAGTCAAGATGGGGGCTTGAACAGCGGAGGCTC 1988
Qy 1921 GGGCGTGGCTTGAAGGTAGGCGCGCCGCAACCTGTGTCACAGCGGTGAAGCGGCGC 1980
Db 1989 GGGCGTGGCTTGAAGGTAGGCGCGCCGCAACCTGTGTCACAGCGGTGAAGCGGCGC 2048
Qy 1981 AGCCCTCGGACATGCGCGGAGCTCAAGCATCTATGACTCTGTGTGCTCATTCGAG 2040
Db 2049 AGCCCTCGGACATGCGCGGAGCTCAAGCATCTATGACTCTGTGTGCTCATTCGAG 2108
Qy 2041 CTGTCTCTGCACTGATGGAAGAGACTTGCAGGACCAAGCAAGAAACGTCTTCCGTACG 2100
Db 2109 CTGTCTCTGCACTGATGGAAGAGACTTGCAGGACCAAGCAAGAAACGTCTTCCGTACG 2168
Qy 2101 GAGACGTGTCTCTCTTCAAGCCCTGGGTGAGAGAACTCTCGCCCTTCCCAAG 2160
Db 2169 GAGACGTGTCTCTCTTCAAGCCCTGGGTGAGAGAACTCTCGCCCTTCCCAAG 2228
Qy 2161 CTCTCTCTTCTGAGTCAATGCAAGCAGATCTTGGTTGCGGAGCTACATGATGATC 2220
Db 2229 CTCTCTCTTCTGAGTCAATGCAAGCAGATCTTGGTTGCGGAGCTACATGATGATC 2288
Qy 2221 CAGCGGTGCGCCCTTTGTAACAAACGAAAGATGAAAGCTTGCACCTTATAGCTGTG 2280
Db 2289 CAGCGGTGCGCCCTTTGTAACAAACGAAAGATGAAAGCTTGCACCTTATAGCTGTG 2348
Qy 2281 CCTCCCTGATTTCCCAAGCTCATCTCCCTGGTTCAGAGCCCACTGAGAGCTGAT 2340
Db 2349 CCTCCCTGATTTCCCAAGCTCATCTCCCTGGTTCAGAGCCCACTGAGAGCTGAT 2408
Qy 2341 CATACAAAGATTTTGAAGTGAATGCTGCGCAGATCTTGTCTCCCTTGCCCAACCT 2400
Db 2409 CATACAAAGATTTTGAAGTGAATGCTGCGCAGATCTTGTCTCCCTTGCCCAACCT 2468
Qy 2401 TTACGGATATCTTGAACAACTCTCCAAATTTTCTAAATGATAGAGCTCTGAAGGCA 2460
Db 2469 TTACGGATATCTTGAACAACTCTCCAAATTTTCTAAATGATAGAGCTCTGAAGGCA 2528
Qy 2461 TGTCCATTAAGTCTGACACAGCTTGCAGAAATTTGATAGTCTTGGATCAGAGCTGT 2520
Db 2529 TGTCCATTAAGTCTGACACAGCTTGCAGAAATTTGATAGTCTTGGATCAGAGCTGT 2588

QY 2521 GTGGAGTAGGAGGAGAAATATGTAAAGAAAACAGGAGATCTGCACTAATCATTC 2580
 DB 2589 GTGGAGTAGGAGGAGAAATATGTAAAGAAAACAGGAGATCTGCACTAATCATTC 2648
 QY 2581 GACTTCATTGAGCTGCAAACTTCTGTTTGTATTGCTACCTTGAATTTGAATGC 2640
 DB 2649 GACTTCATTGAGCTGCAAACTTCTGTTTGTATTGCTACCTTGAATTTGAATGC 2708
 QY 2641 TTTTGAAAAAAGGACCTTTTAACATCAACGACAGAAATCAAGGCCAGTCTAATCTG 2700
 DB 2709 TTTTGAAAAAAGGACCTTTTAACATCAACGACAGAAATCAAGGCCAGTCTAATCTG 2768
 QY 2701 AATCCATGTTGATTGTCAGATAATGTTCTCATTTATTTTGTAGATGAATTAATCATTC 2760
 DB 2769 AATCCATGTTGATTGTCAGATAATGTTCTCATTTATTTTGTAGATGAATTAATCATTC 2828
 QY 2761 ATGGGTTTAAATTAACCTTTGAGTCAAAAGTCAAGAAAGTCAATTAATCAAGTCACT 2820
 DB 2829 ATGGGTTTAAATTAACCTTTGAGTCAAAAGTCAAGAAAGTCAATTAATCAAGTCACT 2888
 QY 2821 TTTTATGAATGA 2832
 DB 2889 TTTATGAATGA 2900
 RESULT 5
 ABK62082
 ID ABK62082 standard; cDNA; 4392 BP.
 AC ABK62082;
 XX
 DT 18-JUN-2002 (first entry)
 DE Human cDNA encoding novel secreted protein LP253.
 XX
 KM Human; ss; gene; secreted protein; cancer; autoimmune disease; arthritis;
 KM osteoporosis; Alzheimer's disease; Parkinson's disease; meningitis;
 KM encephalitis; neoplasia; trauma; ischemia; infection; mania; stroke;
 KM cardiovascular disease; atherosclerosis; sepsis; anaemia;
 KM rheumatoid arthritis; hypothyroidism; allergic response; liver failure;
 KM multiple sclerosis; haemorrhage; paranoia; obsessive compulsive disorder;
 KM autism; panic disorder; learning disability; feeding disorder;
 KM sleep pattern disorder; balance; perception; Th1-dependent insulinitis;
 KM adult respiratory distress syndrome; ARDS.
 OS Homo sapiens.
 PN WO200214358-A2.
 PD 21-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US021124.
 PR 11-AUG-2000; 2000US-0224642P.
 PR 19-OCT-2000; 2000US-0241779P.
 XX
 PA (ELIL) LILLY & CO ELI.
 PI Edmonds BT, Micanovic R, Ou W, Su EW, Tschang SR, Wang H;
 DR MPI: 2002-304057/34.
 DR P-PSDB; AA091330.
 XX
 PT Novel polypeptides and polynucleotides of secreted proteins useful for
 PT treating various diseases such as multiple sclerosis, cancer, autoimmune
 PT diseases, osteoporosis, Alzheimer's disease and Parkinson's disease.
 XX
 PS Claim 1; Page 166-171; 235p; English.
 CC The invention relates to a novel human secreted polypeptide having
 CC sequence 90% identical to the polypeptide sequences of LP105, LP161,
 CC LP224, LP239(a), LP243(a), LP243(b), LP253, LP251(a),
 CC LP252, LP259(b), LP223(a), LP255(a), LP244, LP186, LP251(b), LP255(b), or

CC LP223(b). Also included are the nucleic acids encoding the LP proteins
 CC (including complement, fragments encoding mature forms of the polypeptide
 CC or variant), a vector comprising the nucleic acid, a host cell comprising
 CC the vector, the preparation of the protein, an anti-LP antibody,
 CC ant/agonists of LP and anti-LP-encoding mRNA ribozymes. The secreted
 CC protein or its agonist is useful in the manufacture of a medicament for
 CC treating a mammal suffering from a disease (and in diagnosis), condition
 CC or disorder associated with aberrant levels of the secreted protein e.g.
 CC cancer, autoimmune diseases, arthritis, osteoporosis, Alzheimer's
 CC disease, Parkinson's disease, meningitis, encephalitis, neoplasia,
 CC trauma, ischaemia and infection, mania, stroke, cardiovascular disease,
 CC atherosclerosis, rheumatoid arthritis, hypothyroidism, anaemia, sepsis,
 CC allergic responses, multiple sclerosis, liver failure, haemorrhages,
 CC paranoia, obsessive compulsive disorder, autism, panic disorder, learning
 CC disabilities, ALS (amyotrophic lateral sclerosis) psychoses, disorders
 CC in feeding, sleep patterns, balance, and perception, Th1-dependent
 CC insulinitis, adult respiratory distress syndrome (ARDS). The secreted
 CC protein is further useful for identifying compounds that bind to the
 CC secreted protein. The present sequence encodes a novel secreted protein
 CC of the invention
 CC
 SQ Sequence 4392 BP; 1125 A; 1050 C; 1101 G; 1116 T; 0 U; 0 Other;
 XX
 Query Match 89.4%; Score 2757.4; DB 6; Length 4392;
 Best Local Similarity 99.6%; Pred. No. 0; Mismatches 6; Indels 4; Gaps 4;
 Matches 2805; Conservative 0; Mismatches 6; Indels 4; Gaps 4;
 QY 22 ATGGCCCCGTGCTGAGCTGCTCCGTCCTTTTACCGTCAAGCCCTGCTCAAGCGC 81
 DB 1 ATGGCCCCGTGCTGAGCTGCTCCGTCCTTTTACCGTCAAGCCCTGCTCAAGCGC 60
 QY 82 TGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 141
 DB 61 TGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 QY 142 TGGAGGGGAGTGGGGGCGAGCCAGAGAAACAGTGGGCTGTACAAACATCACTTCAAAAT 201
 DB 121 TGGAGGGGAGTGGGGGCGAGCCAGAGAAACAGTGGGCTGTACAAACATCACTTCAAAAT 180
 QY 202 GACAAATTGTACCACTTACTTGAATCCAGTGGGAAAGCATGTATGCTGACGCCAGAA 261
 DB 181 GACAAATTGTACCACTTACTTGAATCCAGTGGGAAAGCATGTATGCTGACGCCAGAA 240
 QY 262 ATCACCATGACGCAATGCTTCCATGACCAAGTGGCAGTCACTTTTGGTCCCA 321
 DB 241 ATCACCATGACGCAATGCTTCCATGACCAAGTGGCAGTCACTTTTGGTCCCA 300
 QY 322 GGGGGCTCGGATGGAATTCCTGAAAGGATTCGGGTAATCTGGAGGAGCTGAAGTGG 381
 DB 301 GGGGGCTCGGATGGAATTCCTGAAAGGATTCGGGTAATCTGGAGGAGCTGAAGTGG 360
 QY 382 GAGGAGAGCAGTGGCAACACTGATTTCTAAAGATCCGAGACAGCTCAAGTAGCTTC 441
 DB 361 GAGGAGAGCAGTGGCAACACTGATTTCTAAAGATCCGAGACAGCTCAAGTAGCTTC 420
 QY 442 AAAAGACTGGAATGGAATTCACCTTTCTGAAATATGAAATTGAAAAGGATTAATTC 501
 DB 421 AAAAGACTGGAATGGAATTCACCTTTCTGAAATATGAAATTGAAAAGGATTAATTC 480
 QY 502 GTAAAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 561
 DB 481 GTAAAGTGTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 540
 QY 562 AGAACCCGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 621
 DB 601 AAGCTCGGAGACTGGAATGATGAGCAGATGGCTGAGACATGAGTGTCTTCCAGCAT 660
 QY 662 AAGCTCGGAGACTGGAATGATGAGCAGATGGCTGAGACATGAGTGTCTTCCAGCAT 681
 DB 601 AAGCTCGGAGACTGGAATGATGAGCAGATGGCTGAGACATGAGTGTCTTCCAGCAT 660
 QY 682 GGACGGCAACCTTGGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 741

Db 661 GACCGCACAACTTCGGCTTCGGTTCTTCTATCTTCACTAAGACTCAAGACGAGGA 720
Qy 742 CCTTTAGCGAAGAAGCCTGTAGACGAGCAAACTACAGAGACGACGAGCTGCTCTT 801
Db 721 CCTTTAGCGAAGAAGCCTGTAGACGAGCAAACTACAGAGACGAGCTGCTCTT 780
Qy 802 CAAAATGTTTCTTCAGGGGATTAATTAATTGAGCTGTGTGATGACATTAACAACAAGA 861
Db 781 CAAAATGTTTCTTCAGGGGATTAATTAATTGAGCTGTGTGATGACATTAACAACAAGA 840
Qy 862 AAGGTATGATTAATGCTTTAAAGCCAGTGCATCCCGGTGGGCGGGCCATCAGAGCC 921
Db 841 AAGGTATGATTAATGCTTTAAAGCCAGTGCATCCCGGTGGGCGGGCCATCAGAGCC 900
Qy 922 ATGGCATCAAGTGCATGTAATCATATCGGCAATTCGCGACGCTCTTCACTGTATG 981
Db 901 GTGGCATCAAGTGCATGTAATCATATCGGCAATTCGCGACGCTCTTCACTGTATG 960
Qy 982 TGCCGCAAGAGCAACAAGAAATATATATTCATTTAGATGAGAGCTGTAGTCT 1041
Db 961 TGCCGCAAGAGCAACAAGAAATATATATTCATTTAGATGAGAGCTGTAGTCT 1020
Qy 1042 TCACATTAACCTGACAGCTCCCAAGAGAGGCTCCGCGCGCGAAAGTCTTTCTC 1101
Db 1021 TCACATTAACCTGACAGCTCCCAAGAGAGGCTCCGCGCGCGAAAGTCTTTCTC 1080
Qy 1102 TGCTATTCAGTAAAGATGGCGAATCAATGAATGTGTCCAGTTTCCGCTACTTC 1161
Db 1081 TGCTATTCAGTAAAGATGGCGAATCAATGAATGTGTCCAGTTTCCGCTACTTC 1140
Qy 1162 CTCACAGACTTCTGTGGCTGTGAGTGGCTCTGGAACCTGTGGAGACCTTCAAGCTCTGT 1221
Db 1141 CTCACAGACTTCTGTGGCTGTGAGTGGCTCTGGAACCTGTGGAGACCTTCAAGCTCTGT 1200
Qy 1222 AAGAAAGGCGAGAGAAATGGGTCAATCCAGAAATCCAGATTCAGATTCATCATTTG 1281
Db 1201 AAGAAAGGCGAGAGAAATGGGTCAATCCAGAAATCCAGATTCAGATTCATCATTTG 1260
Qy 1282 GTTTGTTCCAAAGGTATGAATCTTGTGGAACAAGAACTAACAAACAAGAGGT 1341
Db 1261 GTTTGTTCCAAAGGTATGAATCTTGTGGAACAAGAACTAACAAACAAGAGGT 1320
Qy 1342 GGCAGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGCGGTGCAGCCATTGCCAAAAG 1401
Db 1321 GGCAGAGGCTCGGGGAAAGAGAGCTCTTCTGTGGCGGTGCAGCCATTGCCAAAAG 1380
Qy 1402 CTCGCCAGGCCAAGAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATGCGCGCTTACTTT 1461
Db 1381 CTCGCCAGGCCAAGAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATGCGCGCTTACTTT 1440
Qy 1462 GATTATTCCTGAGAGGGAACGTCGCCGATTCCTAGACTGAGTACCAAGTACAGACTTC 1521
Db 1441 GATTATTCCTGAGAGGGAACGTCGCCGATTCCTAGACTGAGTACCAAGTACAGACTTC 1500
Qy 1522 ATGACAATC-TTCCCTCAGCTCTGTCCAC-CTGCACTCCGAGACCAAGGCTCCAG 1579
Db 1501 ATGACAATCCTTTCTCAGCTCTGTCCACCTGTGACCTCCGAGACCAAGGCTCCAG 1560
Qy 1580 AGCCGGGGGCA-GCACAAGGCAAGGCA-GCAGAAAGAACTACTTCGAGAGCAAGTCAG 1637
Db 1561 AGCCGGGGGCAAGCAAGGCAAGGCAAGGCAAGAAAGAACTACTTCGAGAGCAAGTCAG 1620
Qy 1638 CCGGTCCCTAATCGTCGCAATTTGCAACTGCAACGTTTATTTGAGAGAGCCGACCTG 1697
Db 1621 CCGGTCCCTAATCGTCGCAATTTGCAACTGCAACGTTTATTTGAGAGAGCCGACCTG 1680
Qy 1698 GTTCAAAAAGCAGTTCCTTCCCTTCCATCTCTCCATCGCGTACCGGAGCAGTCTT 1757
Db 1681 GTTCAAAAAGCAGTTCCTTCCCTTCCATCTCTCCATCGCGTACCGGAGCAGTCTT 1740
Qy 1758 GGAGAAATTTGATCGGGCTTGTTTAAATGATGATGTCATGTCAAACCAAGGCTGAGAG 1817
Db 1741 GGAGAAATTTGATCGGGCTTGTTTAAATGATGATGTCATGTCAAACCAAGGCTGAGAG 1800

Qy 1818 TGACTTCTGCTTAAAGGTAGAGGCGCTGTCTTGGGGCAACCGGACAGCCGACTCCCA 1877
Db 1801 TGACTTCTGCTTAAAGGTAGAGGCGGCTGTCTTGGGGCAACCGGACAGCCGACTCCCA 1860
Qy 1878 GCAAGAGTCAAGCATGAGGGGCTGTGACCAAGACGAGAGGCGCGGCTGCTTGAAGCG 1937
Db 1861 GCAAGAGTCAAGCATGAGGGGCTGTGACCAAGACGAGAGGCGCGGCTGCTTGAAGCG 1920
Qy 1938 TAGCCCGGCTGTGCAACCCCTGTGCAACGCTGTGAAGCGCGGACCCCTCCGACATGCG 1997
Db 1921 TAGCCCGGCTGTGCAACCCCTGTGCAACGCTGTGAAGCGCGGACCCCTCCGACATGCG 1980
Qy 1998 GCGGACTCAGGCACTATGACTGTGTGCTGTGCTCATCCAGCTGTCTCTGCACTGAT 2057
Db 1981 GCGGACTCAGGCACTATGACTGTGTGCTGTGCTCATCCAGCTGTCTCTGCACTGAT 2040
Qy 2058 GGAAGGACTCTGACGAGACAGACAGAAACGTCCTTCCCTGACGAGAGCGTCTCTC 2117
Db 2041 GGAAGGACTCTGACGAGACAGACAGAAACGTCCTTCCCTGACGAGAGCGTCTCTC 2100
Qy 2118 TTCAAGCTGTGGTGAAGAGAACTCTGCTCTTCTTCCAAAGCTCTCTTCTGAGTCTC 2177
Db 2101 TTCAAGCTGTGGTGAAGAGAACTCTGCTCTTCTTCCAAAGCTCTCTTCTGAGTCTC 2160
Qy 2178 ATGCAAGCAGATCTTGTGTCGAGACTCACTGATGAATCCACGCGGTGCGCCCTT 2237
Db 2161 ATGCAAGCAGATCTTGTGTCGAGACTCACTGATGAATCCACGCGGTGCGCCCTT 2220
Qy 2238 GTACAAAAAGAAAGATCTTAAGACTTGCACATTTAGCTGTCTGCTCTCTGATTCGC 2297
Db 2221 GTACAAAAAGAAAGATCTTAAGACTTGCACATTTAGCTGTCTGCTCTCTGATTCGC 2280
Qy 2298 AGCTCATCTCCGTGTGATGAGGCCCATTTGAGAGCTGAGGTCATACAGGATATTGG 2357
Db 2281 AGCTCATCTCCGTGTGATGAGGCCCATTTGAGAGCTGAGGTCATACAGGATATTGG 2340
Qy 2358 AGTGAATGCTGGGCAAGTACTGTTCTCCCTTGGCCCAACCTTAAACGGATATCTGAG 2417
Db 2341 AGTGAATGCTGGGCAAGTACTGTTCTCCCTTGGCCCAACCTTAAACGGATATCTGAG 2400
Qy 2418 AAACCTCTCAATTTTCTAAATGATATGAGAGCTGTGAAGGATGCTCAATAGCTCTGAC 2477
Db 2401 AAACCTCTCAATTTTCTAAATGATATGAGAGCTGTGAAGGATGCTCAATAGCTCTGAC 2460
Qy 2478 AACAGCTTGCATTTGTTGTTAGTCTTGTGATCAGAGCTGTGTGAGAGGAGAGGA 2537
Db 2461 AACAGCTTGCATTTGTTGTTAGTCTTGTGATCAGAGCTGTGTGAGAGGAGAGGA 2520
Qy 2538 AATATGTAAGAAACAGGAAGATACCTGACATTAATCAATCAAGCTTCAATTGAGCTGTG 2597
Db 2521 AATATGTAAGAAACAGGAAGATACCTGACATTAATCAATCAAGCTTCAATTGAGCTGTG 2580
Qy 2598 CAAACTTGTGCTGTTGCTATTTGCTACTGATTTGAAATGCTTTGAAAAAAGGAC 2657
Db 2581 CAAACTTGTGCTGTTGCTATTTGCTACTGATTTGAAATGCTTTGAAAAAAGGAC 2640
Qy 2658 TTTTAACATCATAGCCACAGAAATCAAGTCCAGTCTATCTGGAATCATGTTGATTGC 2717
Db 2641 TTTTAACATCATAGCCACAGAAATCAAGTCCAGTCTATCTGGAATCATGTTGATTGC 2700
Qy 2718 AGATATGTTCTCATTTATTTTGTGATGTAAGAAATTAATTCATTCAGTGTAAATAAGC 2777
Db 2701 AGATATGTTCTCATTTATTTTGTGATGTAAGAAATTAATTCATTCAGTGTAAATAAGC 2760
Qy 2778 TTTGAGTCAAAAAGTCAAAAAGTGAAGTGAATATACAGTCACTTTTATGAATGA 2832
Db 2761 TTTGAGTCAAAAAGTCAAAAAGTGAAGTGAATATACAGTCACTTTTATGAATGA 2815

RESULT 6
AAS18134
ID AAS18134 standard; cDNA; 2786 BP.

OY	1321	AACTTCAAAACAAGAGAGGTGGCCGAGGCTCTGGGGGAAAAGAGACTCTTCCTGTGGGC	1380
Db	1366	AACCTCAAAACAAGAGAGGTGGCCGAGGCTGGGGGAAAAGAGACTCTTCCTGTGGGC	1425
OY	1381	GTGTACAGCCATTCGCGAAAAGCTCCGCCAGGCGCAAGCAGATTCTCTCGCGCGCTCAGC	1440
Db	1426	GTGTACAGCCATTCGCGAAAAGCTCCGCCAGGCGCAAGAGATTCTCTCGCGCGCTCAGC	1485
OY	1441	AAGTTTATCGCGCTACTTTGATTTATCTCGAGGGAGAGAGTCCCGGTATCTTAGAC	1500
Db	1486	AAGTTTATCGCGCTACTTTGATTTATCTCTCGAGGGAGAGAGTCCCGGTATCTTAGAC	1545
OY	1501	CMGAGTACCAATGACAGACTCAATGACAATCTTCCCAAGCTCTGTTTCCACCTGACATCC	1566
Db	1546	CTGAGTACCAATGACAGACTCAATGACAATCTTCTCAAGCTCTGTTTCCACCTGACATCC	1605
OY	1561	CGAGACCAACGCGCTCCAGGAGCCGGGGGAGCAACGCGCACAGGGGAGAGAGAAGAACTAC	1620
Db	1606	CGAGACCAACGCGCTCCAGGAGCCGGGGGAGCAACGCGCACAGGGGAGAGAGAAGAACTAC	1665
OY	1621	TTCCGGAGCAAGTCAAGCCGGTCCCTATACGTCCCATTTTGCAATGCAACCAATTATTT	1680
Db	1666	TTCCGGAGCAAGTCAAGCCGGTCCCTATACGTCCCATTTTGCAATGCAACCAATTATTT	1725
OY	1681	GACGAGAGAGCCCGGACTGTGTGCAAAAAGCAGTTCCTTCCTTCATCTCTCCATCTGGC	1740
Db	1726	GACGAGAGAGCCCGGACTGTGTTCAAAAAGCAGTTCCTTCCTTCATCTCTCCATCTGGC	1785
OY	1741	TACCGGGAGCCAGTCTTGGAGAAATTTGATTCCGGGCTTGTTTAAATGATGATCATGAGC	1800
Db	1786	TACCGGGAGCCAGTCTTGGAGAAATTTGATTCCGGGCTTGTTTAAATGATGATCATGAGC	1845
OY	1801	AAACCAAGGCGCTTGAGAGTGACTTCTGCTTAAAGGTAAAGAGCGCGCTGTTCTTGCGGCAAC	1866
Db	1846	AAACCAAGGCGCTTGAGAGTGACTTCTGCTTAAAGGTAAAGAGCGCGCTGTTCTTGCGGCAAC	1905
OY	1861	GGAACCAAGCGACTCCCAAGACAGAGAGTCAAGCATTTGGGGGCTTGAGACCAAGAGCGGAGCGC	1920
Db	1906	GGAACCAAGCGACTCCCAAGACAGAGAGTCAAGCATTTGGGGGCTTGAGACCAAGAGCGGAGCGC	1965
OY	1921	CGGCGTGGCTCTTGAAGGTAGCGCGCGCCCTGCAACCCCTGCTGCAACGAGGTAAAGCGGCG	1980
Db	1966	CGGCGTGGCTCTTGAAGGTAGCGCGCGCCCTGCAACCCCTGCTGCAACGAGGTAAAGCGGCG	2025
OY	1981	AGCCCTCGGACATGCGCGGGGACTCAAGCATCTATGACTGTCTGTGCCCTCATCTCCAG	2040
Db	2026	AGCCCTCGGACATGCGCGGGGACTCAAGCATCTATGACTGTCTGTGCCCTCATCTCCAG	2085
OY	2041	CTGTCTCTGCACTGATGAGAGAGACTCTCTGACGACACAGACAGAAAGTCTTCCCTGACG	2100
Db	2086	CTGTCTCTGCACTGATGAGAGAGACTCTCTGACGACACAGACAGAAAGTCTTCCCTGACG	2145
OY	2101	GAGAGCGGTCTCTCGCTTCAAGCGCGGGGTGAGAGAAAGCTCCGCGCCTTCTCTTCCAG	2166
Db	2146	GAGAGCGGTCTCTCGCTTCAAGCGCGGGGTGAGAGAAAGCTCTCCGCGCCTTCTCTTCCAG	2205
OY	2161	CTCTCTCTTCTTGGGTCAATGCAAGACAGATCTTGCTTGGCCGAGGCTACACTGATGAATCTC	2220
Db	2206	CTCTCTCTTCTTGGGTCAATGCAAGACAGATCTTGCTTGGCCGAGGCTACACTGATGAATCTC	2265
OY	2221	CAGCGCGGTGCGCCCTTTGTAAACAAACGAAAGAGTCTAAGCATTTGACACTTTAGTGTGTG	2280
Db	2266	CAGCGCGGTGCGCCCTTTGTAAACAAACGAAAGAGTCTAAGCATTTGACACTTTAGTGTGTG	2325
OY	2281	CTCTCCCTCTGATTTCCCGACGCTCATCTCCCTGTGTTGCAATGCGCCCACTTGGAGTGAAGTCT	2340
Db	2326	CTCTCCCTCTGATTTCCCGACGCTCATCTCCCTGTGTTGCAATGCGCCCACTTGGAGTGAAGTCT	2395
OY	2341	CATTAACAAGATTTTGGAGTGAATAATGCTGGCAGATGACTTGTCTCCCTTGCGCCCAACCT	2400
Db	2386	CATTAACAAGATTTTGGAGTGAATAATGCTGGCAGATGACTTGTCTCTCTTGCGCCCAACCT	2445
OY	2401	TTACCGGATATCTTGACAACTCTCCAAATTTTCTTAAATGATATGAGACTGTGAAGGCA	2460

Db	2446	TTACCGATATCTTGACAAACTCTCCAAATTTCTTAAATGATATGAGCTCTGAAAGCA	2505
Qy	2461	TGTCATTAAGGTCGTGACAAACAGCTTGCCAAATTTGGTTAGTCCTTGGATCAGACCTGTT	2520
Db	2506	TGTCATTAAGGCTGTGACAAACAGCTTGCCAAATTTGGTTAGTCCTTGGATCAGACCTGTT	2565
Qy	2521	GTGGAGGTGGGAGGAAATATGTAAAGAAAACAGAAAGTACTCTCATAATCATTTCA	2580
Db	2566	GTGGAGGTGGGAGGAAATATGTAAAGAAAACAGAAAGTACTCTCATAATCATTTCA	2625
Qy	2581	GACTTCATTGAGCTCTGCAAACTTTGCTGTGTTGCTATTGGCTACTTGATTTGAAATGC	2640
Db	2626	GACTTCATTGAGCTCTGCAAACTTTGCTGTGTTGCTATTGGCTACTTGATTTGAAATGC	2685
Qy	2641	TTTGTGAAAAAGGCACTTTTAACTATATAGCCACAGAAATCAAGTCCAGTCTATCTGG	2700
Db	2686	TTTGTGAAAAAGGCACTTTTAACTATATAGCCACAGAAATCAAGTCCAGTCTATCTGG	2745
Qy	2701	AATCAGTTGTGATTTGAGATTAATGTTCTCATTTAATTTTTG	2741
Db	2746	AATCAGTTGTGATTTGAGATTAATGTTCTCATTTAATTTTTG	2786

Result	7
AEBS5653	AEBS5653
ID	AEBS5653 standard; cDNA; 2786 BP.
XX	
AC	AEBS5653;
XX	
DT	22-SEP-2005 (first entry)
XX	
DE	Human DCSR8 polypeptide encoding cDNA.
XX	
KW	Protein engineering; cytokine receptor; DNAX cytokine receptor subunit;
KW	DCS8; interleukin-17C; IL-17C; psoriasis; inflammatory bowel disorder;
KW	interstitial lung disorder; asthma; allergy; atherosclerosis;
KW	gastrintestinal-gen.; antiinflammatory; antiasthmatic; antiallergic;
KW	antiproliferic; antiatherosclerotic; respiratory-gen.; immunosuppressive;
KW	antitumor; DCSR9 agonist; DCSR9 antagonist; IL-17C antagonist;
XX	IL-17C agonist; human; DCSR8; gene; ss; antitense therapy; RNAI therapy.
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
EH	70..2286
FT	CDS
FT	/*cag= b
FT	/product= "DCSR8"
PT	/transl_except= (pos: 169..171, aa: Xaa)
FT	/transl_except= (pos: 193..195, aa: Xaa)
FT	/transl_except= (pos: 442..444, aa: Xaa)
FT	/transl_except= (pos: 475..478, aa: Xaa)
FT	/transl_except= (pos: 517..519, aa: Xaa)
FT	/note= "Xaa = unknown"
FT	70..117
FT	/*cag= a
FT	118..2283
FT	/*cag= c
XX	
XX	mat_peptide
XX	
XX	sig_peptide
XX	
XX	70..117
XX	/*cag= a
XX	118..2283
XX	/*cag= c
XX	
XX	WO2005065711-A2.
XX	
XX	21-JUL-2005.
XX	
XX	22-DEC-2004; 2004WO-US042935.
XX	
XX	29-DEC-2003; 2003US-00749144.
XX	
XX	(SCHE) SCHERING CORP.
XX	
XX	Gorman DM;
XX	
XX	WP1; 2005-506792/51.
XX	
XX	P-PSDB; AEBS5654.
XX	

Db	1786	TACCGGAGCCAGTCTTGAGAAATTTGATTCCGGCTTGTTTAAATGATGTCATGTGC	1845
Qy	1801	AAACCAAGGCTGAGAGTGACTTCTGCTTAAAGGTAGAGCGCTGTTCTTGAGGCAAC	1866
Db	1846	AAACCAAGGCTGAGAGTGACTTCTGCTTAAAGGTAGAGCGGCTGTTCTTGAGGCAAC	1905
Qy	1861	GGACCAAGCCGACTCCCAACAGAGGTAGCATGGGGGCTGGACCAAGACGGGGAGGCG	1920
Db	1906	GGACCAAGCCGACTCCCAACAGAGGTAGCATGGGGGCTGGACCAAGACGGGGAGGCG	1965
Qy	1921	CGGCTGCGCTTGAACGATAGCGCGCCCTGCAACCCCTGCTGCACACGGTGAAGCCGGC	1980
Db	1966	CGGCTGCGCTTGAACGATAGCGCGCCCTGCAACCCCTGCTGCACACGGTGAAGCCGGC	2025
Qy	1981	AGCCCTTGAGACATGCGCGCGGAGCTCAGGCACTTATGACTGTCGTGTCGCTCATCCGAG	2040
Db	2026	AGCCCTTGAGACATGCGCGCGGAGCTCAGGCACTTATGACTGTCGTGTCGCTCATCCGAG	2085
Qy	2041	CTGTCTCTGCACTGATGGAAGGACTCTCGACGAGCAGACAGAAACGTTCTCCCTGACG	2100
Db	2086	CTGTCTCTGCACTGATGGAAGGACTCTCGACGAGCAGACAGAAACGTTCTCCCTGACG	2145
Qy	2101	GAGAGCGTGTCTCTCTCTTCAAGCGCTGGGTAGAGAGAACTCTGCTTCCTTCCAG	2166
Db	2146	GAGAGCGTGTCTCTCTCTTCAAGCGCTGGGTAGAGAGAACTCTGCTTCCTTCCAG	2205
Qy	2161	CTCCTCTCTTCTGGGTCAATGCAAAAGCAATCTGGTTGCGCAGCTACACTGATGAATC	2220
Db	2206	CTCCTCTCTTCTGGGTCAATGCAAAAGCAATCTGGTTGCGCAGCTACACTGATGAATC	2265
Qy	2221	CAGCGCGTCCGCTTGTGTAACAAAAGCAAGAGCTTAAAGCATTGCCACTTTAGCTGTG	2280
Db	2266	CAGCGCGTCCGCTTGTGTAACAAAAGCAAGAGCTTAAAGCATTGCCACTTTAGCTGTG	2325
Qy	2281	CCTCCCTCTGATTCGCCAGCTCATCTCCCTGGTTGCAAGGCCACTTGGAGCTAGAGTCT	2340
Db	2326	CCTCCCTCTGATTCGCCAGCTCATCTCCCTGGTTGCAAGGCCACTTGGAGCTAGAGTCT	2385
Qy	2341	CATACAAAGATATTGAGTGAATGCTGGCAAGTACTGTTCTCCCTTGGCCCAACCT	2400
Db	2386	CATACAAAGATATTGAGTGAATGCTGGCAAGTACTGTTCTCCCTTGGCCCAACCT	2445
Qy	2401	TTACCGGATATCTTGACAACTCTGCCAATTTTCTTAAATGATATGAGACTCTGAAGGCA	2466
Db	2446	TTACCGGATATCTTGACAACTCTGCCAATTTTCTTAAATGATATGAGACTCTGAAGGCA	2505
Qy	2461	TGTCATTAAGGCTGACAAACAGCTTGCCAAATTTGGTTAGTCTTGATTCAGAGCTGT	2520
Db	2506	TGTCATTAAGGCTGACAAACAGCTTGCCAAATTTGGTTAGTCTTGATTCAGAGCTGT	2555
Qy	2521	GTGGAGGTAGGAGAGAAATGTATMAAGAAACAGAAAGTACTGCACTAATCATCA	2580
Db	2566	GTGGAGGTAGGAGAGAAATGTATMAAGAAACAGAAAGTACTGCACTAATCATCA	2625
Qy	2581	GACTTCATGAGCTCTGCAAACTTGGCTGTGCTATTGGCTATCTTGATTTGAATGC	2640
Db	2626	GACTTCATGAGCTCTGCAAACTTGGCTGTGCTATTGGCTATCTTGATTTGAATGC	2685
Qy	2641	TTTGTGAAAAAAGCACTTTTAACTATAGCACAAGAAATCAAGTGCAGTCTATCTGG	2700
Db	2686	TTTGTGAAAAAAGCACTTTTAACTATAGCACAAGAAATCAAGTGCAGTCTATCTGG	2745
Qy	2701	AATCCATGTTGATTTGCAATPATGTTCTCATTTATTTTG	2741
Db	2746	AATCCATGTTGATTTGCAATPATGTTCTCATTTATTTTG	2786

RESULT 8	.
ID	ADW76619
XX	ADW76619
AC	ADW76619
	standard; DNA; 4508 BP

XX	24-MAR-2005	(first entry)
DT		
XX		
DE	Human interleukin-17 (IL-17) receptor DNA.	
XX		
KW	interleukin-17 receptor; IL-17 receptor; ds; gene.	
XX		
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
FT	CDS	553..2340
FT		/tag= a
FT		/product= "Human interleukin-17 (IL-17) receptor protein"
XX		
PN	CN1465592-A.	
XX		
PD	07-JAN-2004.	
XX		
PF	01-JUL-2002; 2002CN-00123540.	
XX		
PR	01-JUL-2002; 2002CN-00123540.	
XX		
XX	(UYQI) UNIV QINGHUA.	
PA		
PI	Xiong S, Chang Z, Fu X;	
XX		
DR	WPI: 2004-248799/24.	
XX		
DR	P-PSDB; ADW76620.	
XX		
PT	Human interleukin-17 receptor sample protein, coding gene and its uses.	
XX		
PS	Claim 3; SEQ ID NO 1; 14bp; Chinese.	
XX		
CC	The invention relates to a novel human interleukin-17 (IL-17) receptor	
CC	protein, the coding gene and application. The current sequence is that of	
CC	the human interleukin-17 receptor DNA of the invention.	
XX		
SQ	Sequence 4508 BP; 1175 A; 1061 C; 1141 G; 1131 T; 0 U; 0 Other;	

	Query Match	Best Local Similarity	Match 2690; Conservative	97.1%; 99.7%;	Score 2684.6;	DB 13;	Length 4508;
					Pred. No. 0;	Mismatches 9;	Indels 0; Gaps 0
Qy	134	CCCTGTGCTGAGGGAGTGGGGCCAGCCAGCAGAGAA	CAGTGGCTGTACATCACT	193			
Db	233	CTGTGGCTTGGCAGGGAGTGGGGCCAGCCAGAGAAA	CAGTGGCTGTACATCACT	292			
Qy	194	TCAATATGACAAATTGTATCACTTACTTGAATCC	AGTGGAGCATGTGATTTGTCGACG	253			
Db	293	TCAAAATATGACAAATTGTATCACTTACTTGAATCC	AGTGGAGCATGTGATTTGTCGACG	352			
Qy	254	CCGAGATATATCACCATCAGCCAGTATGCTGCGATG	ACCAATGTCCTTT	313			
Db	353	CCGAGATATATCACCATCAGCCAGTATGCTGCGATG	ACCAATGTCCTTT	412			
Qy	314	GGTCCCAAGGGGCCCTCGGCATCGAATTCCTGAA	AGATTCGGGTATATCTGGAGAGC	373			
Db	413	GGTCCCAAGGGGCCCTCGGCATCGAATTCCTGAA	AGATTCGGGTATATCTGGAGAGC	472			
Qy	374	TGAAGTCGAGGGGAGACAGTGCACAACTGATTTCT	TAAGATCCGAGCAGCTCAACA	433			
Db	473	TGAAGTCGAGGGGAGACAGTGCACAACTGATTTCT	TAAGATCCGAGCAGCTCAACA	532			
Qy	434	GTAAGCTTCAAAAGAACTGGATATGGAATCCAA	CTTTCTGAAATATGAAATTTGAAACGG	493			
Db	533	GTAAGCTTCAAAAGAACTGGATATGGAATCCAA	CTTTCTGAAATATGAAATTTGAAACGG	592			
Qy	494	ATTATTTCTGTAAGGTTGTCTCCCTTTCTCTTCA	TTAAAGAAAGCAATTAACAACCTT	553			
Db	593	ATTATTTCTGTAAGGTTGTCTCCCTTTCTCTTCA	TTAAAGAAAGCAATTAACAACCTT	652			
Qy	554	TCTTCTTTAGAACCGAGCCTGTGACCTGTGTTG	TACGCGGACCAATCTAGCTGTAAAC	613			

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Db 653 TCTTCTTAGAACCCGAGCCTGTGACCTGTGTTTACAGCCGGACAACTTAGCTTGTAAAC 712
Qy 614 CCTTCTGGAAGCCTCGGAACCTGGAACATGACCCAGATGGCTCGACATGCAAGTGTCTT 673
Db 713 CCTTCTGGAAGCCTCGGAACCTGGAACATGACCCAGATGGCTCGACATGCAAGTGTCTT 772
Qy 674 TCGACACGACCGGACCACTTCGCTCGTTCCTTCTATCTTCACTTCAAGCTCAAG 733
Db 773 TCGACACGACCGGACCACTTCGCTCGTTCCTTCTATCTTCACTTCAAGCTCAAG 832
Qy 734 ACGAAGACCTTTCAGACGAAAGACCTGTAAAGCAGGACAACTACAGACGACGAGCT 793
Db 833 ACGAAGACCTTTCAGACGAAAGACCTGTAAAGCAGGACAACTACAGACGACGAGCT 892
Qy 794 GCCTCTTCAAAATGTTTCTCCAGGGGATTTATTAATTGAGCTGTGATGACCTTACA 853
Db 893 GCCTCTTCAAAATGTTTCTCCAGGGGATTTATTAATTGAGCTGTGATGACCTTACA 952
Qy 854 CAACAAGAAAGTGTATGATTAAGCTTAAAGCAGTGAACCTCCCGTGGGCGGGCCCA 913
Db 953 CAACAAGAAAGTGTATGATTAAGCTTAAAGCAGTGAACCTCCCGTGGGCGGGCCCA 1012
Qy 914 TCAGAGCCATGGCCATCAGATGCACTGTAGTCAATCGGCATTCGGAGCCTTTCA 973
Db 1013 TCAGAGCCATGGCCATCAGATGCACTGTAGTCAATCGGCATTCGGAGCCTTTCA 1072
Qy 974 CTGTATGTGCGGCAAGAACAAAGAAATATATATTTACATTTAATGTAAGAGCT 1033
Db 1073 CTGTATGTGCGGCAAGAACAAAGAAATATATATTTACATTTAATGTAAGAGCT 1132
Qy 1034 CTGAGCTTTCCACATACATGAGCACTCCCAAGAGAGGCTCCGGCGGGCCGCAAG 1093
Db 1133 CTGAGCTTTCCACATACATGAGCACTCCCAAGAGAGGCTCCGGCGGGCCGCAAG 1192
Qy 1094 TCTTCTCTGCTATTCAGATTAAGATGCGCAGATCACTGAATGTCCTCAGTGTTCG 1153
Db 1193 TCTTCTCTGCTATTCAGATTAAGATGCGCAGATCACTGAATGTCCTCAGTGTTCG 1252
Qy 1154 CCTACTTCTCCAGACCTTCTGTGCTGTGAGGTGCTGTGACCTGTGGAAAGACTTCA 1213
Db 1253 CCTACTTCTCCAGACCTTCTGTGCTGTGAGGTGCTGTGACCTGTGGAAAGACTTCA 1312
Qy 1214 GCTCTGTGAGAAAGGCGAGAGAAATGGCTATCCAGAAATCCAGAGTCCCACTTCA 1273
Db 1313 GCTCTGTGAGAAAGGCGAGAGAAATGGCTATCCAGAAATCCAGAGTCCCACTTCA 1372
Qy 1274 TCATTGTGTTGTTCCAAAGGTAATGAAGTACTTGTGACAAAGAACTACAAACACA 1333
Db 1373 TCATTGTGTTGTTCCAAAGGTAATGAAGTACTTGTGACAAAGAACTACAAACACA 1432
Qy 1334 AAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTTTCCTGTGGCGGTGTCAAGCCATTG 1393
Db 1433 AAGAGGTGGCCGAGGCTCGGGGAAAGAGAGCTTTCCTGTGGCGGTGTCAAGCCATTG 1492
Qy 1394 CGGAAAGGCTCGGCGCAGGCGCAAGCAGAGTTCCTCCGGCGGCTCAGCAATTTATGCCG 1453
Db 1493 CGGAAAGGCTCGGCGCAGGCGCAAGCAGAGTTCCTCCGGCGGCTCAGCAATTTATGCCG 1552
Qy 1454 TCTACTTTGAATTAATTCCTGCGAGGGGAGAGTCCCGGATTCCTAGACCTGAGTACCAAGT 1513
Db 1553 TCTACTTTGAATTAATTCCTGCGAGGGGAGAGTCCCGGATTCCTAGACCTGAGTACCAAGT 1612
Qy 1514 ACAGACTCATGACATCTTCTCAGCTGTGTTCCCACTGCACTCCCGAGACAGCGGC 1573
Db 1613 ACAGACTCATGACATCTTCTCAGCTGTGTTCCCACTGCACTCCCGAGACAGCGGC 1672
Qy 1574 TCGAGAGGCGGGGCGAGCAAGCGGACAGGGGACAGAAAGAACTTCTCCGAGCAAT 1633
Db 1673 TCGAGAGGCGGGGCGAGCAAGCGGACAGGGGACAGAAAGAACTTCTCCGAGCAAT 1732
Qy 1634 CAGGCGGGCTCCATATGTCGCAATTTGCAACATGACAGTTTATGACAGAGAGCCCG 1693
Db 1733 CAGGCGGGCTCCATATGTCGCAATTTGCAACATGACAGTTTATGACAGAGAGCCCG 1792

Qy 1694 ACTGGTTCGAAAAGAGATTCGTTCCCTTCATCTCTCCATCGGCTTACCGGGAGCCAG 1753
Db 1793 ACTGGTTCGAAAAGAGATTCGTTCCCTTCATCTCTCCATCGGCTTACCGGGAGCCAG 1852
Qy 1754 TCTTGAAGAAATTTTATTCGGGCTTGTTTTAAATGATGTCATGTGCAAAACGAGGCTG 1813
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Db 1913 AGAGTGACTTCTGCTTAAAGGTAGAGGCGGCTGTTCTTGGGGCAACCGGACAGCCGACT 1972
Qy 1874 CCCAGACGAGAGTCAAGCATGGGGGCTGTGACCAAGAGGGGAGGCCCGGCTGCTTGG 1933
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Db 2033 ACGGTAGCGCGCCCTGCAACCCCTGTGCAACGCGTGAAGCCCGGACGCCCTCGGACA 2092
Qy 1994 TCCCGGGGACTCAGGCACTATGACTGTCGTGCTGCTCATCGAGCTGTCTTGCCAC 2053
Db 2093 TCCCGGGGACTCAGGCACTATGACTGTCGTGCTGCTCATCGAGCTGTCTTGCCAC 2152
Qy 2054 TGAATGAAGACTCTCGACGCAAGCAAGCAAGAAAGCTTTCCTTGACGAGAGCTGTCTT 2113
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Db 2213 CCTCTTACGGCCTGGGTGAGAGGAACCTCCGCTTCTTCAAGCTCTCTCTTCTG 2272
Qy 2174 GGTCAATGCAAAAGCAAGCTTGTGTTCCGCAAGCTTACATGATGAATCCACGCGGTGCCC 2233
Db 2273 GGTCAATGCAAAAGCAAGCTTGTGTTCCGCAAGCTTACATGATGAATCCACGCGGTGCCC 2332
Qy 2234 CTTTGTAAACAAAAGAAAGAGCTTAAGACTTTCCTTGTGCTGCTCTCTGAT 2293
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Db 2513 TGACAAACTCTCCAAATTTTCTAAATGATATGAGCTGTGAAGGCAATCATTAAGTCT 2572
Qy 2474 TGACAAAGCTTGGCCAAATTTTGTATGTCCTTGAATTCAGAGCTTGTGGAGAGTATGGG 2533
Db 2573 TGACAAAGCTTGGCCAAATTTTGTATGTCCTTGAATTCAGAGCTTGTGGAGAGTATGGG 2632
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Db 2633 AGGAATATGTAAGAAAGAAAGCAAGAAATACCTGCACTATCATTCAGACTTATGAGC 2692
Qy 2594 TCTGCAAACTTGGCTGTGTTGCTATGTCATCTTGAATGCTTGTGAAAAAG 2653
Db 2693 TCTGCAAACTTGGCTGTGTTGCTATGTCATCTTGAATGCTTGTGAAAAAG 2752
Qy 2654 GCACTTTTAACTATTAAGCCAGAAATCAAGTGCAGCTATCTGGAATCCATGTGTA 2713
Db 2753 GCACTTTTAACTATTAAGCCAGAAATCAAGTGCAGCTATCTGGAATCCATGTGTA 2812
Qy 2714 TTGCAGATTAATGTTCTCATTTTATTTTGTATGATGAATTTTACATTCGCAATGGGTGTAAT 2773
Db 2813 TTGCAGATTAATGTTCTCATTTTATTTTGTATGATGAATTTTACATTCGCAATGGGTGTAAT 2872
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OY 2774 AACCTTTGAGTCAAAAAGTCAAGAAAGTGACTGATATATACAGTCACCTTTTATGAAATGA 2832
 DB 2873 AAGCTTTGAGTCAAAAAGTCAAGAAAGTGACTGATATATACAGTCACCTTTTATGAAATGA 2931

RESULT 9
 ADB63275
 ID ADB63275 standard; cDNA; 2894 BP.
 XX

AC ADB63275;

DT 04-DEC-2003 (first entry)

DE Human cDNA encoding clone TESTI20046540.

XX Human; 88; gene; pharmaceutical; diagnostic; gene therapy;
 KW tissue regeneration; cell regeneration; membrane protein;
 KW signal transduction-related protein; transcription-related protein;
 KW osteoporosis; neurological disease; cancer; tumour.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 123..2309
 FT /tag= a
 FT /product= "Clone TESTI20046540 protein"

XX EPI308459-A2.

XX 07-MAY-2003.

XX 28-MAR-2002; 2002EP-00007401.

XX 05-NOV-2001; 2001JP-00379298.
 XX 25-JAN-2002; 2002US-00350978.

XX (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Iwogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
 PI Yamamoto J, Isono Y, Otsuka K, Nagai K, Irie R, Tamechika I,
 PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;

XX MPI: 2003-450961/43.
 DR P-PSDB; ADB65245.

XX New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.

XX Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesizing the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a cDNA of the invention. Note: Some of the sequence

CC data for this patent is not represented in the printed specification, but
 CC is based on sequence information supplied by the European Patent Office.
 XX

XX Sequence 2894 BP; 735 A; 751 C; 730 G; 678 T; 0 U; 0 Other;

Query Match 86.9%; Score 2678.6; DB 10; Length 2894;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2684; Conservative 9; Indels 0; Gaps 0;

OY 134 CCTGCGCTGAGGGGAGTGGGGCCAGCAGAGAAACAGTGGGCTGATCAATCACTACT 193
 DB 202 CCTGGCCTTGGAGGAGTGGGGCCAGCAGAGAAACAGTGGGCTGATCAATCACTACT 261
 OY 194 TCAATATATGACAAATTGTACCACTTGTAAATCCAGTGGGAGAGATGATTTGTCGACG 253
 DB 262 TCAATATATGACAAATTGTACCACTTGTAAATCCAGTGGGAGAGATGATTTGTCGACG 321
 OY 254 CCCAGAAATATGACCAATGACCAAGTATGCTTGCATGACCAAGTGGCACTCACTTTCTT 313
 DB 322 CCCAGAAATATGACCAATGACCAAGTATGCTTGCATGACCAAGTGGCACTCACTTTCTT 381
 OY 314 GGTCCCGCAGGGGCGCTCGGCATTCGAATTCCTGAAAGATTTGGGTATATCTGAGAGAC 373
 DB 382 GGTCCCGCAGGGGCGCTCGGCATTCGAATTCCTGAAAGATTTGGGTATATCTGAGAGAC 441
 OY 374 TGAAGTCGAGGAGAGAGACAGTGGCCAAACATGATCTTAAAGATTCGAAAGAGCTCAACA 433
 DB 442 TGAAGTCGAGGAGAGAGACAGTGGCCAAACATGATCTTAAAGATTCGAAAGAGCTCAACA 501
 OY 434 GTAGCTTCAAAAGAACTGGAATGGAATCTCAACTTTCTGATATGAAATTTGAAACGG 493
 DB 502 GTAGCTTCAAAAGAACTGGAATGGAATCTCAACTTTCTGATATGAAATTTGAAACGG 561
 OY 494 ATTATTTTGTAAAGTGTGCTTTTCTTCTTCATTTAAAGCAATTAACCACTTCTT 553
 DB 562 ATTATTTTGTAAAGTGTGCTTTTCTTCTTCATTTAAAGCAATTAACCACTTCTT 621
 OY 554 TCTTCTTTAGAACCCGAGCGTGTGACTGTTGTTACAGCCGAGCAATCTAGCTTTGAAAC 613
 DB 622 TCTTCTTTAGAACCCGAGCGTGTGACTGTTGTTACAGCCGAGCAATCTAGCTTTGAAAC 681
 OY 614 CTTTCTGAGAGCGCTCGGAACCTGGAACATGACGACAGTGTCTCGAGCATGCAAGTGTCT 673
 DB 682 CTTTCTGAGAGCGCTCGGAACCTGGAACATGACGACAGTGTCTCGAGCATGCAAGTGTCT 741
 OY 674 TCGACCAAGCAGCGACGCAACTTGGCTTCCGTTTCTTCTTATTTTCACTACAGCTCAACG 733
 DB 742 TCGACCAAGCAGCGACGCAACTTGGCTTCCGTTTCTTCTTATCTTCACTACAGCTCAACG 801
 OY 734 ACGAAGAACCTTTCAAGGAGAAAGACTGTAAAGCAGAGCAAACTACAGAGCAAGCAAGCT 793
 DB 802 ACGAAGAACCTTTCAAGGAGAAAGACTGTAAAGCAGAGCAAACTACAGAGCAAGCAAGCT 861
 OY 794 GCGTCTCTTCAAAATGTTTCTCCAGGGGATTAATTAATTAATTAATTAATTAATTAATTA 853
 DB 862 GCGTCTCTTCAAAATGTTTCTCCAGGGGATTAATTAATTAATTAATTAATTAATTAATTA 921
 OY 854 CAACAAAGAAAGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 913
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 OY 914 TCAGAGCAATGCGCATTCACAGTGCATGATGATTAATTAATTAATTAATTAATTAATTAAT 973
 DB 982 TCAGAGCAATGCGCATTCACAGTGCATGATGATTAATTAATTAATTAATTAATTAATTAAT 1041
 OY 974 CTGTATATGCGCGCAAGAGCAACAAAGAAATATATATTAATTAATTAATTAATTAATTAAT 1033
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 OY 1034 CTGAGCTTTTCAATCACTGACAGCACTTCCCAAGAGAGAGCTCCGCGCGCGCGAGAGG 1093
 DB 1102 CTGAGCTTTTCAATCACTGACAGCACTTCCCAAGAGAGAGAGCTCCGCGCGCGCGAGAGG 1161

1094 TCTTCTCTGCTATTCAGATTAAGATGCGCAGATCATGATGTCTGCTAGTGTTCG 1153
 1162 TCTTCTCTGCTATTCAGATTAAGATGCGCAGATCATGATGTCTGCTAGTGTTCG 1221
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 1214 GCTCTGTAGAGAGAGGAGAGAGATGTGCTCATCCAGAGATCCAGATCCAGATTC 1273
 1282 GCTCTGTAGAGAGAGGAGAGAGATGTGCTCATCCAGAGATCCAGATCCAGATTC 1341
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 1342 TCAATGTGTGTGTTCCTCAAGGATGATGATCTTTGTGACAAAGAACTACAAACACA 1401
 1334 AAGAGAGTGGCGAGGCTCGGAGAAAGAGAGCTCTTCTGTGAGGCTGACCATTTG 1393
 1402 AAGAGAGTGGCGAGGCTCGGAGAAAGAGAGCTCTTCTGTGAGGCTGACCATTTG 1461
 1394 CGGAAAAGCTCCGCGCCAGAGCAGAGATGCTCTCGCGCGCTCAGCAAGTTATGCGG 1453
 1462 CGGAAAAGCTCCGCGCCAGAGCAGAGATGCTCTCGCGCGCTCAGCAAGTTATGCGG 1521
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 1522 TCTACTTGAATTAATTCGAGAGAGAGAGTCCCGGATTCCTGAGCTGAGTACCAAGT 1581
 1514 ACAGACTCATGACATCTTCTCCTCAGCTCTGTCCACCTGCACTCCGAGACACAGGCG 1573
 1582 ACAGACTCATGACATCTTCTCCTCAGCTCTGTCCACCTGCACTCCGAGACACAGGCG 1641
 1574 TCCAGAGAGCCGCGGAGCAGCAGCAGCAGGAGCAGCAGAGAACTACTTCCGAGCAAGT 1633
 1642 TCCAGAGAGCCGCGGAGCAGCAGCAGCAGGAGCAGCAGAGAACTACTTCCGAGCAAGT 1701
 1634 CAGGCGCGCTCCATTCGTGCGCATTTGCAATGACAGATTAATGACAGAGAGCCG 1693
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 1694 ACTGTTTCAGAAAAGAGTCTGTTCCCTTCATCTCTCCTCAGCTGCGCTACCGGAGCCAG 1753
 1762 ACTGTTTCAGAAAAGAGTCTGTTCCCTTCATCTCTCCTCAGCTGCGCTACCGGAGCCAG 1821
 1754 TCTTGAAGAAATTTGATTCGGGCTGTGTTTAAATGATGATGCAAAACAGGCGCTTG 1813
 1822 TCTTGAAGAAATTTGATTCGGGCTGTGTTTAAATGATGATGCAAAACAGGCGCTTG 1881
 1814 AAGAGTACTTCTGCTTAAAGCTAGAGGCGCTGTTTGTGGGCGCAACCGAGCCGAGCT 1873
 1882 AAGAGTACTTCTGCTTAAAGCTAGAGGCGCTGTTTGTGGGCGCAACCGAGCCGAGCT 1941
 1874 CCGAGCAGAGAGTCAAGATGAGGAGCTGTGAGACCAAGAGGAGGCGCGGCTGCGCTTG 1933
 1942 CCGAGCAGAGAGTCAAGATGAGGAGCTGTGAGACCAAGAGGAGGCGCGGCTGCGCTTG 2001
 1934 ACGGTAGCCGCGCTGCAACCCCTGCTGCAACCGGTGAAGAGCCGCGAGCCCTCGGACA 1993
 2002 ACGGTAGCCGCGCTGCAACCCCTGCTGCAACCGGTGAAGAGCCGCGAGCCCTCGGACA 2061
 1994 TGGCGGAGAGCTCAGAGATCTATGATCTGCTGTGCTCTCATTCGAGCTGTCTGTGCAAC 2053
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 2054 TGAATGAGAGAGCTCTGAGAGAGCAGACAGAAAGCTCTTCCCTGAGAGAGAGGCTGCT 2113
 2122 TGAATGAGAGAGCTCTGAGAGAGCAGACAGAAAGCTCTTCCCTGAGAGAGAGGCTGCT 2181
 2114 CCTCTTCAAGGCTCTGAG 2173
 2182 CCTCTTCAAGGCTCTGAG 2241
 2174 GGTGATGCAAGAGATCTTGGTGGCGAGCTACACTGATGAATCTCAAGCGGCTGCGCC 2233

2242 GGTGATGCAAGAGATCTTGGTGGCGAGCTACACTGATGAATCCAGCGGCTGCGCC 2301
 2234 CTTTGTAAACAAACGAAAGAGCTTAAGCATTTGCGCTTAAAGCTTCTGCTGATTT 2293
 2302 CTTTGTAAACAAACGAAAGAGCTTAAGCATTTGCGCTTAAAGCTTCTGCTGATTT 2361
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 2362 CCCAGCTCATCTCCCTGCTGATGAGCCCATTTGAGCTGAGTCTCATACAGAGATAT 2421
 2354 TTGAGTGAATGCTGCGCAGTACTTGTCTCTTCCCAACCTTTTACCGGATATCT 2413
 2422 TTGAGTGAATGCTGCGCAGTACTTGTCTCTTCCCAACCTTTTACCGGATATCT 2481
 2414 TGAACAACTCTCAATTTCTTAAATGATGAGAGCTGGAAGAGATCTCATAGATTC 2473
 2482 TGAACAACTCTCAATTTCTTAAATGATGAGAGCTGGAAGAGATCTCATAGATTC 2541
 2474 TGAACAACTCTCAATTTGTTAGTCTTGATCAGAGCTGTTGTGAGAGTATG 2533
 2542 TGAACAACTCTCAATTTGTTAGTCTTGATCAGAGCTGTTGTGAGAGTATG 2601
 2534 ACGAAATATGTAAGAAAGAGAGAGATCTGCACTATCATTCAGACTTATGAGC 2593
 2602 ACGAAATATGTAAGAAAGAGAGAGATCTGCACTATCATTCAGACTTATGAGC 2661
 2594 TCTGCAACTTTCCTGTTGCTATTTGCTATTTGCTATTTGAAATCTTTGAAAAAG 2653
 2662 TCTGCAACTTTCCTGTTGCTATTTGCTATTTGCTATTTGAAATCTTTGAAAAAG 2721
 2654 GCACTTTTAAACATATGCAAGAGAGAGATGCAAGTCACTGAGATCCATGTTGTA 2713
 2722 GCACTTTTAAACATATGCAAGAGAGAGATGCAAGTCACTGAGATCCATGTTGTA 2781
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 2782 TTGAGATATATGTTCTCATTTTATTTTGTAGATGAAATTTACATTCAGATGTTTAAAT 2841
 2774 AAGCTTGAATCAAAAGTCAAGAAAGTGAATGATATACAGTCACTTTTATG 2826
 2842 AAGCTTGAATCAAAAGTCAAGAAAGTGAATGATATACAGTCACTTTTATG 2894

RESULT 10
 AAD51235
 ID AAD51235 standard; cDNA; 4450 BP.
 XX
 AC AAD51235;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human REMAP-16 cDNA.
 XX
 KW Human; receptor and membrane-associated protein; REMAP; arteriosclerosis;
 KW cell proliferative disorder; atherosclerosis; polycythemia vera; cancer;
 KW cirrhosis; hepatitis; paroxysmal nocturnal haemoglobinuria; psoriasis;
 KW primary chromocytopenia; developmental disorder; mental retardation;
 KW renal tubular acidosis; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; anemia; reproductive disorder; autoimmune disorder;
 KW infertility; inflammatory disorder; acquired immune deficiency syndrome;
 KW AIDS; epilepsy; allergy; asthma; autoimmune thyroiditis; Crohn's disease;
 KW contact dermatitis; diabetes mellitus; glomerulonephritis; osteoporosis;
 KW Goodpasture's syndrome; gout; Graves' disease; Hashimoto's thyroiditis;
 KW irritable bowel syndrome; multiple sclerosis; Reiter's syndrome; uveitis;
 KW osteoarthritis; pancreatitis; rheumatoid arthritis; Sjogren's syndrome;
 KW gene therapy; viricide; protozoacide; fungicide; gene; ss.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT 512..2299
 CDS /*tag= a

/product= "Human REMAP-16 protein"

WT 0020294990-A2.

XX 28-NOV-2002.

XX 16-MAY-2002; 2002WO-US015899.

XX 18-MAY-2001; 2001US-0292197P.

XX 08-JUN-2001; 2001US-0297012P.

XX 21-JUN-2001; 2001US-0300582P.

XX 22-JUN-2001; 2001US-0300495P.

XX 28-JUN-2001; 2001US-0301922P.

XX 14-DEC-2001; 2001US-0340542P.

XX (INCYTE GENOMICS INC.

XX Lai PG, Warren BA, Xu Y, Duggan BM, Honchell CD, Kallick DA,

XX Baughn MR, Tang YT, Yue H, Bandman O, Jones KA, Becha SD, Tran UK,

XX Au-Young JK, Griffin JA, Zebardjian Y, Lee EA, Elliott VS;

XX Thangavelu K, Raskumar J, Lu Y, Hafalla AJA, Walla NK, Ison CH,

XX Thonon M, Swarnakar A, Yang J, Richardson TW, Emerling BM, Yao MG,

XX Cocks BG, Sanjanwala B, Mason PM, Gandhi AR, Li JK, Forsythe JD,

XX Gururajan R, Gietzen KJ;

XX MPI: 2003-129423/12.

XX P-PSDB; AAE33485.

XX New human receptors and membrane-associated proteins and nucleic acids,

XX useful for diagnosing, treating or preventing inflammatory disorder, e.g.,

XX hepatitis.

XX Claim 97; Col 232-233; 243pp; English.

XX The present invention relates to human receptor and membrane-associated

XX proteins (REMP) and polynucleotides encoding such proteins. Sequences of

XX the invention are useful for diagnosing, treating or preventing disorders

XX associated with aberrant expression of REMAP, particularly cell

XX proliferative disorders (e.g. arteriosclerosis, atherosclerosis,

XX cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia

XX vera, psoriasis), primary thrombocytopaenia or cancer), developmental

XX disorders (e.g. renal tubular acidosis, anaemia or mental retardation),

XX neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or

XX epilepsy), reproductive disorders (e.g. infertility or a disruption in

XX the menstrual cycle) or autoimmune/inflammatory disorders (e.g. AIDS,

XX allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's

XX disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,

XX gout, Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,

XX multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's

XX syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis) or viral,

XX bacterial, fungal, parasitic, protozoan or helminthic infections. They

XX are also useful in gene therapy. The present sequence is human REMAP-16

XX cDNA

XX Sequence 4450 BP; 1151 A; 1046 C; 1086 G; 1167 T; 0 U; 0 Other;

XX

XX Query Match 85.1%; Score 2672.2; DB 8; Length 4450;

XX Best Local Similarity 99.9%; Pred. No. 0;

XX Matches 2624; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX

XX 206 ATTGACCACTTGAATCCAGTGGGGAACATGCTGATCCAGCCCGCAATATCA 265

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XX 264 ATTGACCACTTGAATCCAGTGGGGAACATGCTGATCCAGCCCGCAATATCA 323

XX |

XX 266 CCATGACCAATATCTGATCCATGACCAAGTGGAGTCCATCTTTGGTCCCAAGGG 325

XX |

XX 324 CCATGACCAATATCTGATCCATGACCAAGTGGAGTCCATCTTTGGTCCCAAGGG 383

XX |

XX 326 CCCTGGCAATGATCTGTAAGAGATTTGGGTAACTGAGAGAGCTGAAGTGGAGG 385

XX |

XX 384 CCCTGGCAATGATCTGTAAGAGATTTGGGTAACTGAGAGAGCTGAAGTGGAGG 443

386 GAAAGACAGTCCCACTGATTTCTAAAGATCCGAGAGCTCAACAGTACTTCAAA 445

444 GAAAGACAGTCCCACTGATTTCTAAAGATCCGAGAGCTCAACAGTACTTCAAA 503

446 GAACTGGAATGGAATCTCAACTTTCTGATATGAAATTGGAACGATTATTTGCTA 505

504 GAACTGGAATGGAATCTCAACTTTCTGATATGAAATTGGAACGATTATTTGCTA 563

506 AGGTGTCCCTTTTCTTCCATTAAGAAAGAAATTAACACCTTTCTTCTTGA 565

564 AGGTGTCCCTTTTCTTCCATTAAGAAAGAAATTAACACCTTTCTTCTTGA 623

566 CCCGAGCTGTGACCTGTGTTTACAGCCGCAATCTGATCTGTAAACCTTTGGAAGC 625

624 CCCGAGCTGTGACCTGTGTTTACAGCCGCAATCTGATCTGTAAACCTTTGGAAGC 683

626 CTGGACCTGAAACATCAAGCCAGATGCTGGACATGCAAGTGTCTTTCAGCAGCAGC 685

684 CTGGACCTGAAACATCAAGCCAGATGCTGGACATGCAAGTGTCTTTCAGCAGCAGC 743

686 CGCAACTGTTGGCTTCCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 745

744 CGCAACTGTTGGCTTCCGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 803

746 TCAAGCAAGAAAGCTGTAAAGCAGAGCAAACTACAGAGCAAGCTGCTCTTCAAA 805

804 TCAAGCAAGAAAGCTGTAAAGCAGAGCAAACTACAGAGCAAGCTGCTCTTCAAA 863

806 ATGTTTCTCCAGGGGATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 865

864 ATGTTTCTCCAGGGGATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTA 923

866 TGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 925

924 TGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 983

926 CCATGACAGTGCACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 985

984 CCATGACAGTGCACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1043

986 GCAAGAGCAACAGAAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1045

1044 GCAAGAGCAACAGAAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTA 1103

1046 CATACATGACACTCCCAAGAGAGAGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1105

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1164 ATTCAAGTAAAGATGAGCCAGATCAATGAATGCTGCAAGTGTTCGCTTACTTCTTCC 1223

1166 AGGACTTGTGGCTGTAGAGTGGCTGTGACCTGTGGAAGAGACTTCAAGCTTGTAGAG 1225

1224 AGGACTTGTGGCTGTAGAGTGGCTGTGACCTGTGGAAGAGACTTCAAGCTTGTAGAG 1283

1226 AAGGCAAGAGAGATGAGTCAATCCAGAGATCCAGAGATCCAGATTCATATGAGTGT 1285

1284 AAGGCAAGAGAGATGAGTCAATCCAGAGATCCAGAGATCCAGATTCATATGAGTGT 1343

1286 GTTCCAAAGTATGAAGTATTTGAGCAAGAGAGCTTCAAAACAAAGAGAGTGGCC 1345

1344 GTTCCAAAGTATGAAGTATTTGAGCAAGAGAGCTTCAAAACAAAGAGAGTGGCC 1403

1346 GAGGCTCGGGAAAGAGAGCTTCTCTGTGGCGGTGTCAGCAATGCGGAAAGCTCC 1405

1404 GAGGCTCGGGAAAGAGAGCTTCTCTGTGGCGGTGTCAGCAATGCGGAAAGCTCC 1463

1406 GCGAGGCAAGAGAGTGTGTCGCGGCGCTCAAGAAATTTATGCGCTTACTTGTGAT 1465

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1466 ATTCTGTGAGAGAGAGCTCCCGGTATCTTGAAGCTGAGTACCAAGTACAGACTCATGG 1525

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Db 1884 GCGTAAAGGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1943
Qy 1886 GTGACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1945
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Qy 1946 CCCTGGAACCCCTGCTGCAACAGGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2005
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Db 2844 AAAAGTCAAGAAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2890

RESULT 11
ABZ11243
ID ABZ11243 standard; cDNA; 3948 BP.
XX
AC ABZ11243;
XX
DT 20-JUN-2003 (first entry)
XX
DE Human polynucleotide SEQ ID NO 125.
XX
XX Human: genome mapping; gene therapy; food supplement; virus; fungus;
XX cell-proliferative disorder; neurodegenerative disease; bacterial;
XX Parkinson's disease; Alzheimer's disease; autoimmune disease;
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
XX arthritis; cytostatic; immunomodulator; neoplastic; neuroprotective;
XX antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
XX haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
XX antithrptic; gene; ss.
XX
OS Homo sapiens.
XX
PN MO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF -05-MAR-2002; 2002MO-US005095.
XX
PR -05-MAR-2001; 2001US-00799451.
XX
PA (HYSB-) HYSBQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F,
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M,
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
XX
DR P-PDB; ABP69026.
XX
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
XX
PS Claim 1; SEQ ID NO 125; 1012bp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising a
XX nucleotide sequence selected from any of 948 sequences (ABZ1119-
XX ABZ12066) or their mature protein coding portion, active domain coding
XX protein or complementary sequences. The polynucleotides are useful for
XX identifying expressed genes or for physical mapping of human genome. The
XX encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX markers, as a food supplement, for generating antibodies, in medical
XX imaging, screening and diagnostic assays and for treating cell-
XX proliferative disorders (cancer), neurodegenerative diseases (Parkinson's

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or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, meloid or lymphoid disorders, CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritits, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at http://wipo.int/pub/publshd_pct_sequences

Sequence 3948 BP; 1013 A; 938 C; 975 G; 1022 T; 0 U; 0 Other;

Query Match 78.7%; Score 2426.4; DB 6; Length 3948;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2430; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 397 CAACAACGATCTTAAAGGATCCGAGAGAGCTCAACAGTAGCTTCAAAAGAACTGGAATG 456
DB 3 CCAACAATGATCTTAAGGATCCGAGAGAGCTCAACAGTAGCTTCAAAAGAACTGGAATG 62
QY 457 GAATCTCAACCTTCTCGAATATGAAATTGAAACGGAATTATTCGTAAAGGTTGCTCCT 516
DB 63 GAATCTCAACCTTCTCGAATATGAAATTGAAACGGAATTATTCGTAAAGGTTGCTCCT 122
QY 517 TTTCTCTTCATTTAAAGGAAAGCAATTCACACCTTTCTTTTGAACCGAGCTGT 576
DB 123 TTTCTCTTCATTTAAAGGAAAGCAATTCACACCTTTCTTTTGAACCGAGCTGT 182
QY 577 GACCTGTGTTACGCGCGGACAACTCAAGCTGTAAACCTTCGGAAGCTCGGAACCTG 636
DB 183 GACCTGTGTTACGCGCGGACAACTCAAGCTGTAAACCTTCGGAAGCTCGGAACCTG 242
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DB 243 AACATCAGCAGCATGCTCGGACATGCAAGTGTCCTTCGACACGACCGACCAACTTC 302
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DB 363 ACCTGTAAGCAGAGCAACTACAGAGAGACAGCTGCTCCTTCAAAATGTTCTCA 422
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DB 423 GGGGATTAATTAATGAGCTGTGATGACACTAACACAAGAAAGTGAATGACTAT 482
QY 877 GCGTTAAAGCAGTGACTCCCGTGAGCCGAGCCCATCAAGCCATGSCCATCAAGTG 936
DB 483 GCGTTAAAGCAGTGACTCCCGTGAGCCGAGCCCATCAAGCCATGSCCATCAAGTG 542
QY 937 CCACTGTATGATATCGGCATTCCGAGAGCTCTTCACTGTGATGTCGCGGAAGAGCA 996
DB 543 CCACTGTATGATATCGGCATTCCGAGAGCTCTTCACTGTGATGTCGCGGAAGAGCA 602
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DB 603 CAAGAAATATATATTCATTTAGATGAAGAGAGCTGTGAGTCTTCACTACACTGCA 662
QY 1057 GCACTCCCAAGAGAGAGCTCCGCGCGCGGCGGAAGGTCTTTCTGTCTATTCAGTAA 1116
DB 663 GCACTCCCAAGAGAGAGCTCCGCGCGCGGCGGAAGGTCTTTCTGTCTATTCAGTAA 722
QY 1117 GATGCGCAAGATCACATGAATGTCGTCAGTGTTCGCTACTTCCTTCCAGAGACTTCTGT 1176
DB 723 GATGCGCAAGATCACATGAATGTCGTCAGTGTTCGCTACTTCCTTCCAGAGACTTCTGT 782
QY 1177 GCGCTGAGGTGGCTCTGAGACCTGTGGGAAGACTTCAGGCTCTGTAGAGAGGCGAGAGA 1236
DB 783 GCGCTGAGGTGGCTCTGAGACCTGTGGGAAGACTTCAGGCTCTGTAGAGAGGCGAGAGA 842
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DB 843 GAATGGGTATATCAGAGAGATCCAGAGTCCAGTTCATCATTTGTGTTTTCAAAGGT 902
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DB 1083 GGAAGAGTCCCGGATATCTTAAGCTGAGTACCAAGTACAGACTCATGACATCTCCT 1142
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DB 1203 CGACAGGCGAGAGAAAGAACTAATTCGAGAGAGTACGAGCGGGTCCCTATACGTCGC 1262
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DB 1323 CCTTCATCTCTCTCACTGCGGCTACCGGAGGCAAGTCTTGGAAATTTGATTCGGGC 1382
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DB 1503 GGCCTGACCAAGACGGGAGGGCCCGGCTGCTGACGATGAGCGCGCCTGCAACC 1562
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RESULT 12

ID ADM43761 standard; cDNA; 3948 BP.

XX AC ADM43761;

XX DT 03-JUN-2004 (first entry)

XX DE Novel human arginine-rich protein cDNA #125.

XX KM ss; gene; human; arginine-rich protein; cancer; inflammation;

XX KM genetic disorder.

XX OS Homo sapiens.

XX PN US2004053250-A1.

XX PD 18-MAR-2004.

XX PF 21-NOV-2002; 2002US-00302172.

XX PR 05-MAR-2001; 2001US-00799451.

XX PR 05-MAR-2002; 2002WO-US005095.

XX PR 20-AUG-2002; 2002US-00225251.

XX PA (TANG/) TANG Y T.

XX PA (XUEA/) XUE A.

XX PA (DRMA/) DRMANAC R T.

XX PI Tang YT, Xue A, Drmanac RT;

XX DR WPI: 2004-238579/22.

XX PT New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and inflammation.

XX PS Disclosure; SEQ ID NO 125; 51bp; English.

CC The invention relates to an isolated polynucleotide. The methods and
CC compositions of the present invention are useful for the diagnosis and/or
CC treatment of diseases or conditions associated with aberrant expression
CC or activity of the arginine-rich protein-like polypeptides, such as
CC cancer and inflammation. They can also be used in forensics, gene
CC mapping, identification of mutations responsible for genetic disorders,
CC and in assessing biodiversity. The present sequence represents a novel
CC human arginine-rich protein cDNA.

SQ Sequence 3948 BP; 1013 A; 938 C; 975 G; 1022 T; 0 U; 0 Other;

Query Match 78.7%; Score 2426.4; DB 12; Length 3948;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2430; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 397 CAACAACGATTTCTAAGATCCGAGACGCTCAACAGTACTTCAAAAGAACTGAAAG 456
DB 3 CCACAACGATTTCTAAGATCCGAGACGCTCAACAGTACTTCAAAAGAACTGAAAG 62
QY 457 GAATCTCAACCTTCTGTAATGAAATTTGAAAGGATTAATTTGTAAGGTTGCCCT 516
DB 63 GAATCTCAACCTTCTGTAATGAAATTTGAAAGGATTAATTTGTAAGGTTGCCCT 122
QY 517 TTTCCTTCAATTAAGAAAGCAATTAACACCTTTCTTTTGAACCCGAGCTGT 576
DB 123 TTTCCTTCAATTAAGAAAGCAATTAACACCTTTCTTTTGAACCCGAGCTGT 182
QY 577 GACCTGTGTTTACACCGGACCAATCTAGCTTGAACCTTTGAAAGCTGGAACCTG 636
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DB 243 AACATCAGCAGCAGTGGCTCGGACATGCAAGGTGCTTTCGACACGACCGCAACTTC 302
QY 697 GGCTTCGCTTCTTCTATCTTCACTACAGCTCAAGCTCAAGCAAGCACTTTCAAGCAAG 756
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1263 ATTGGAATATGCAACAAGTTTATGACGAGAGCCGAGCTGGTTCGAAAAGCAAGTTCGTT 1322
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1743 GAACCTCTGCTCCCTCTTCAAGCTCTCTCTTCTGAGTCAAGAGAGATCTTGGT 1802
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2557 GAAATACCTGCACTAATCAATTCAGACTTCATTGAGCTCTGCAAACTTTGCTGTTGCT 2616
2163 GAAATACCTGCACTAATCAATTCAGACTTCATTGAGCTCTGCAAACTTTGCTGTTGCT 2222
2617 ATGGCTACCTGATTTGAATGCTTTTGTGAAAAGCACTTTTAACTATACATACACACA 2676
2223 ATGGCTACCTGATTTGAATGCTTTTGTGAAAAGCACTTTTAACTATACATACACACA 2282
2677 GAAATCAAGTGCAGTCTTATCTGGAATCCATGTTGATTTGAGATATGTTCTCAATTA 2736
2283 GAAATCAAGTGCAGTCTTATCTGGAATCCATGTTGATTTGAGATATGTTCTCAATTA 2342
2737 TTTGATGATGAATTTTACATTCGATGGGTGTTAATAAGCTTGAATCAAAAGTCAAGA 2796
2343 TTTGATGATGAATTTTACATTCGATGGGTGTTAATAAGCTTGAATCAAAAGTCAAGA 2402
2797 AAGTGACTGAATATACAGTACCTTTTATGAAATGA 2832
2403 AAGTGACTGAATATACAGTACCTTTTATGAAATGA 2438

RESULT 13
ABX71363
ID ABX71363 standard; cDNA; 2406 BP.
XX
AC ABX71363;
XX
DT 14-APR-2003 (first entry)
XX
XX Human transmembrane protein cDNA from clone DKZphes3_2013.
DE
XX Human; gene; gene therapy; vaccine; disease treatment; detection; ss.
KW
XX Homo sapiens.
OS
XX WO200112659-A2.
PN
XX 22-FEB-2001.
PD
XX
XX 18-AUG-2000; 2000MO-IB001496.
PF
XX
XX 18-AUG-1999; 99US-0149499P.
PR
XX 28-SEP-1999; 99US-0156503P.
XX
XX (GENU-) GERMAN HUMAN GENOME PROJECT.
PA
XX Wiemann S;
XX
XX PI
XX DR MPI; 2001-327840/34.
XX
XX P-PSDB; ABUS3091.
XX
XX Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies.
XX
XX Claim 1: Page 698; 1095pp; English.
PS
XX This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases

associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence encodes a polypeptide described in the disclosure of the invention

Sequence 2406 BP; 633 A; 650 C; 589 G; 534 T; 0 U; 0 Other;

Query Match 74.8%; Score 2307.6; DB 5; Length 2406;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2113; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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135 CTGTGGCTGAGGAGGAGTGGGGCCAGCCAGCAAGAAACATGGGCTGTACAACTCACTT 194
27 CAGTGAAGACAGGAGTGGGGCCAGCCAGCAAGAAACATGGGCTGTACAACTCACTT 86
195 CAATATGACAAATTTGACCACTTCTGATCCAGTGGGGAAGCATGTGATTTGCTGAGC 254
87 CAATATGACAAATTTGACCACTTCTGATCCAGTGGGGAAGCATGTGATTTGCTGAGC 146
255 CAGAAATATCACCATGAGCCAGTATGCTTGCATGACCAAGTGGCAGTCACTTTTGG 314
147 CAGAAATATCACCATGAGCCAGTATGCTTGCATGACCAAGTGGCAGTCACTTTTGG 206
315 GTCCCAAGGGGCTCTGGCATGCAATCTTGAAGAAATTTGGGTAACTGAGAGAGCT 374
207 GTCCCAAGGGGCTCTGGCATGCAATCTTGAAGAAATTTGGGTAACTGAGAGAGCT 266
375 GAAGTGAGGAGGAGCAGTGGCAACATGATTTGAAAGATCCGAGCAGTCAACAG 434
267 GAAGTGAGGAGGAGCAGTGGCAACATGATTTGAAAGATCCGAGCAGTCAACAG 326
435 TAGCTTCAAAAGAACTGAATGGAATCTCAACCTTTCTGAATATGAAATTTGAAACGA 494
327 TAGCTTCAAAAGAACTGAATGGAATCTCAACCTTTCTGAATATGAAATTTGAAACGA 386
495 TTATTTCTGAAAGGTTTCTCTTCTTCTTCAATTTAAAGAAAGAAAGAAATTTACCCCTT 554
387 TTATTTCTGAAAGGTTTCTCTTCTTCTTCAATTTAAAGAAAGAAAGAAATTTACCCCTT 446
555 CTCTTTTGAAGCCGAGCCGTGACCTGTGTTTGAAGCCGAGCAATCTGACTTGAAGCC 614
447 CTCTTTTGAAGCCGAGCCGTGACCTGTGTTTGAAGCCGAGCAATCTGACTTGAAGCC 506
615 CTCTTGAAGCCCTGGAACCTGAACATCAGCAGCAGTGGCTGCAATCAGAGTGTCTT 674
507 CTCTTGAAGCCCTGGAACCTGAACATCAGCAGCAGTGGCTGCAATCAGAGTGTCTT 566
675 CGACCAACGACCGCAACATCTTGAGCTTCCGTTTCTTCTATCTTCACTAAGCTCAAGCA 734
567 CGACCAACGACCGCAACATCTTGAGCTTCCGTTTCTTCTATCTTCACTAAGCTCAAGCA 626
735 CGAAGAACCTTTCAAGCCGAAAGACCTGTAGAGCAGGCAAACTACAGAAATGACAGCTG 794
627 CGAAGAACCTTTCAAGCCGAAAGACCTGTAGAGCAGGCAAACTACAGAAATGACAGCTG 686
795 CCTCTTCAAAATGTTTCTCAGGGGATATATATTTAGCTGTGATGACACTAATAC 854
687 CCTCTTCAAAATGTTTCTCAGGGGATATATATTTAGCTGTGATGACACTAATAC 746
855 AACAAAGAAAGTATGATGATTAATGAGCCAGTGCCTCCCGTGGCCGGGCCCAT 914
747 AACAAAGAAAGTATGATGATTAATGAGCCAGTGCCTCCCGTGGCCGGGCCCAT 806
915 CAGAGCAGGAGCATGACAGTGGCACTGGTATGATGAGCAATGGGCAAGCTCTTTCAC 974
807 CAGAGCAGGAGCATGACAGTGGCACTGGTATGATGAGCAATGGGCAAGCTCTTTCAC 866
975 TGTGATGTCGCCGAGAGCAACAAAGAAATATATTTCACTTTAGATGAAGAGCTC 1034
867 TGTGATGTCGCCGAGAGCAACAAAGAAATATATTTCACTTTAGATGAAGAGCTC 926
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1035 TGAATCTTCCATACATACATGACAGTCCCAAGAGAGAGAGGCTCCGGCCGGCCCAAGGT 1094
927 TGAATCTTCCATACATACATGACAGTCCCAAGAGAGAGAGGCTCCGGCCGGCCCAAGGT 986
1095 CTTTCTGCTATTTTCAGTAAAGATGACCAAGATCAATGAATGTCTCACTGTTTGGC 1154
987 CTTTCTGCTATTTTCAGTAAAGATGACCAAGATCAATGAATGTCTCACTGTTTGGC 1046
1155 CTACTTCTCCAGAGCTTCTGTGCTGTGAGAGTGTCTGAGCCTGTGGAAGACTTCAG 1214
1047 CTACTTCTCCAGAGCTTCTGTGCTGTGAGAGTGTCTGAGCCTGTGGAAGACTTCAG 1106
1215 CCTGTGAGAGAGGAGAGAGATGGGTCTATCCAGAGATCCAGAGTCCAGTTCAT 1274
1107 CCTGTGAGAGAGGAGAGAGATGGGTCTATCCAGAGATCCAGAGTCCAGTTCAT 1166
1275 CATTTGTTTGTTCCAAGATGATGAATCTTTGTGACCAAGAAACTACAAACAA 1334
1167 CATTTGTTTGTTCCAAGATGATGAATCTTTGTGACCAAGAAACTACAAACAA 1226
1335 AGAGGTGGCCGAGGCTGGGGAAAGAGAGCTTTCTGTGTGGCTGTCAAGCAATTC 1394
1227 AGAGGTGGCCGAGGCTGGGGAAAGAGAGCTTTCTGTGTGGCTGTCAAGCAATTC 1286
1395 CGAAAGCTCCGCGCAAGCCAGAGTTCGTCGCGGGGCTCAGCAAGTTATGCGGT 1454
1287 CGAAAGCTCCGCGCAAGCCAGAGTTCGTCGCGGGGCTCAGCAAGTTATGCGGT 1346
1455 CTACTTGTATTTCTCTGAGAGGAGAGAGTCCCGGTATCTTGAACCTGAGTACCAAGTA 1514
1347 CTACTTGTATTTCTCTGAGAGGAGAGAGTCCCGGTATCTTGAACCTGAGTACCAAGTA 1406
1515 CAGACTCATGACAACTTTCTCTCACTCTGTTCCACTGCACTCCGAGACAGAGGCTT 1574
1407 CAGACTCATGACAACTTTCTCTCACTCTGTTCCACTGCACTCCGAGACAGAGGCTT 1466
1575 CGAGAGCCGGGGCAGCAACGCGCAGGGCAGAGAAAGAACTACTCCGAGCAAGTC 1634
1467 CGAGAGCCGGGGCAGCAACGCGCAGGGCAGAGAAAGAACTACTCCGAGCAAGTC 1526
1635 AGCCGGTCCCTATAGTGTGCTGCAATTTGCAACATGACAGAGTATTTAGAGAGCCGA 1694
1527 AGCCGGTCCCTATAGTGTGCTGCAATTTGCAACATGACAGAGTATTTAGAGAGCCGA 1586
1695 CTGTTTCAAAAGCAAGTGTCTTCCCTTCATCTCTTCACTGCGCTACCGGAGCACT 1754
1587 CTGTTTCAAAAGCAAGTGTCTTCCCTTCATCTCTTCACTGCGCTACCGGAGCACT 1646
1755 CTGGAAGAAATTTGATGGGGCTTGGTTTAAATGATGATGATGCAAAACAGAGGCTTGA 1814
1647 CTGGAAGAAATTTGATGGGGCTTGGTTTAAATGATGATGATGCAAAACAGAGGCTTGA 1706
1815 GAGTGACTTCTGACCTTAAAGTGAAGGCTGTTCTTGGGGCAACGCGACAGAGCACTC 1874
1707 GAGTGACTTCTGACCTTAAAGTGAAGGCTGTTCTTGGGGCAACGCGACAGAGCACTC 1766
1875 CCAGCAGCAGAGTCAAGATGGGGGCTTGAACCAAGAGAGGCTCCGCTGCTTGA 1934
1767 CCAGCAGCAGAGTCAAGATGGGGGCTTGAACCAAGAGAGGCTCCGCTGCTTGA 1826
1935 CGGTAGCCGCGCTGCAACCTCTGCTGCAACCGGTGAAGGCTCCGCTGCTTGA 1994
1827 CGGTAGCCGCGCTGCAACCTCTGCTGCAACCGGTGAAGGCTCCGCTGCTTGA 1886
1995 GCGCGGGGACTCAGGCACTTATGACTGCTGTGCTCATCTGAGCTGTCTCTGCACT 2054
1887 GCGCGGGGACTCAGGCACTTATGACTGCTGTGCTCATCTGAGCTGTCTCTGCACT 1946
2055 GATGGAAGACTCTGAGAGGACAGACAGAAAGCTTTCTCTGACGAGAGGCTGTCTC 2114
1947 GATGGAAGACTCTGAGAGGACAGACAGAAAGCTTTCTCTGACGAGAGGCTGTCTC 2006
2115 CTCTTCAAGGCTGGGTGAGAGGAACCTCTGCTCTTCTTCAAGCTCTCTCTTCTGG 2174
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QY 901 TGGGCGGCGCCATCAGAGCCATGSCCATGACAGTGCCTGAGTACATATGCGCATTC 960
 Db 965 TGGGCGGCGCCATCAGAGCCATGSCCATGACAGTGCCTGAGTACATATGCGCATTC 1024
 QY 961 GCGACGCTCTTCACTGTGATGTGCGCGAAGAGCAAGAAAATATATATTCACATTTA 1020
 Db 1025 GCGACGCTCTTCACTGTGATGTGCGCGAAGAGCAAGAAAATATATATTCACATTTA 1084
 QY 1021 GATGAAGAGAGCTCTGAGTCTTCCACATACATGACAGCTCTCCAGAGAGAGGCTCCG 1080
 Db 1085 GATGAAGAGAGCTCTGAGTCTTCCACATACATGACAGCTCTCCAGAGAGAGGCTCCG 1144
 QY 1081 CCGGCGCGGAGGCTCTTCTGTGTATTCAGATGAAGATGSCCAAGATTCAGAAATGTC 1140
 Db 1145 CCGGCGCGGAGGCTCTTCTGTGTATTCAGATGAAGATGSCCAAGATTCAGAAATGTC 1204
 QY 1141 GTCGAGTGTTCGCTACTTCTCTCAGAGACTTCTGTGCTGTGAGTGTGCTTGCACCTG 1200
 Db 1205 GTCGAGTGTTCGCTACTTCTCTCAGAGACTTCTGTGCTGTGAGTGTGCTTGCACCTG 1264
 QY 1201 TGGGAAAGCTTCAAGCTCTGTGAAGAGGCAAGAGATGSGTCATCCAGAAATGCAC 1260
 Db 1265 TGGGAAAGCTTCAAGCTCTGTGAAGAGGCAAGAGATGSGTCATCCAGAAATGCAC 1324
 QY 1261 GAGTCCGAGTTCATCATTTGTGTGTTGTTCCAAAGATGAAAGTACTTGTGACAGAAAG 1320
 Db 1325 GAGTCCGAGTTCATCATTTGTGTGTTGTTCCAAAGATGAAAGTACTTGTGACAGAAAG 1384
 QY 1321 AACTACAAACAAAGAGGTTGGCCGAGGCTCGGCGGAAAGAGAGCTCTTCTGTGTGGG 1380
 Db 1385 AACTACAAACAAAGAGGTTGGCCGAGGCTCGGCGGAAAGAGAGCTCTTCTGTGTGGG 1444
 QY 1381 GTGTGAGCCATGCGGAAAGCTCCGCGAGGCCAAGAGATTCGTCCGCGGCGCTCAGC 1440
 Db 1445 GTGTGAGCCATGCGGAAAGCTCCGCGAGGCCAAGAGATTCGTCCGCGGCGCTCAGC 1504
 QY 1441 AAGTTATTCGCGCTTACTTGTATATTTCTGTGAGGAGAAAGTCCCGGTATCTAGAC 1500
 Db 1505 AAGTTATTCGCGCTTACTTGTATATTTCTGTGAGGAGAAAGTCCCGGTATCTAGAC 1564
 QY 1501 CTGAGTACCAAGTACAGACTCATGGAACAATCTTCTCAGCTCTGTTCCGACTGCCTCC 1560
 Db 1565 CTGAGTACCAAGTACAGACTCATGGAACAATCTTCTCAGCTCTGTTCCGACTGCCTCC 1624
 QY 1561 CGAGACCAAGGCTCTCAGAGCGGCGGAGCAACGCGAAGGAGCAGAGAGAACTAC 1620
 Db 1625 CGAGACCAAGGCTCTCAGAGCGGCGGAGCAACGCGAAGGAGCAGAGAGAACTAC 1684
 QY 1621 TTCGAGAGCAAGTCAAGGCGGCTCTTATACGTGCGCATTTTGCAATGCAACAGTTTAT 1680
 Db 1685 TTCGAGAGCAAGTCAAGGCGGCTCTTATACGTGCGCATTTTGCAATGCAACAGTTTAT 1744
 QY 1681 GAGGAGGAGCGGAGTGTGGAAGAGCAAGTGTCTTCCATCTCTCCAGCTGCGC 1740
 Db 1745 GAGGAGGAGCGGAGTGTGGAAGAGCAAGTGTCTTCCATCTCTCCAGCTGCGC 1804
 QY 1741 TACCGGAGGAGCTTGTGAGAAATTTGATTCGCGCTTGTGTTTAAATGATCATATGTC 1800
 Db 1805 TACCGGAGGAGCTTGTGAGAAATTTGATTCGCGCTTGTGTTTAAATGATCATATGTC 1864
 QY 1801 AAACCAAGGCTGTGAGAGTGAATTTCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGCGAAC 1860
 Db 1865 AAACCAAGGCTGTGAGAGTGAATTTCTGCTTAAAGGTAGAGGCGCTGTTCTTGGGCGAAC 1924
 QY 1861 GGCACGAGCGAATCCAGAGCAAGATGACATAGGCGCTTGAACCAAGCGGAGAGCC 1920
 Db 1925 GGCACGAGCGAATCCAGAGCAAGATGACATAGGCGCTTGAACCAAGCGGAGAGCC 1984
 QY 1921 CGGCTGCTGCTTGAAGGTAAGCGCGCTCTCAACCTCTGTGCAACAGGTAAGCGCGC 1980
 Db 1985 CGGCTGCTGCTTGAAGGTAAGCGCGCTCTCAACCTCTGTGCAACAGGTAAGCGCGC 2044

QY 1981 AGCCCTCGGACATGCGCGGAGCTCAGGATCTATGACTGTGTGCGCCCTGATCCGAG 2040
 Db 2045 AGCCCTCGGACATGCGCGGAGCTCAGGATCTATGACTGTGTGCGCCCTGATCCGAG 2104
 QY 2041 CTGCTCTGCACTGATGAGAGACTCTCGACGACCAAGCAAGAAAGTCTTCTCTGACG 2100
 Db 2105 CTGCTCTGCACTGATGAGAGACTCTCGACGACCAAGCAAGAAAGTCTTCTCTGACG 2164
 QY 2101 GAGAGGCTGTCTCTCTCTTCAAGGCTCGGAGAGAGAACTCTGCGCTTCTTCCAG 2160
 Db 2165 GAGAGGCTGTCTCTCTCTTCAAGGCTCGGAGAGAGAACTCTGCGCTTCTTCCAG 2224
 QY 2161 CTGCTCTCTTGTGATGACAAAGAGATCTTGTGTGCGGAGCTTACATGATGATC 2220
 Db 2225 CTGCTCTCTTGTGATGACAAAGAGATCTTGTGTGCGGAGCTTACATGATGATC 2284
 QY 2221 CAGCGGCTGCGCCCTTGTGACAAAGAGAGTGAAGATTCGACATTTAGCTG 2277
 Db 2285 CAGCGGCTGCGCCCTTGTGACAAAGAGAGTGAAGATTCGACATTTAGCTG 2341

RESULT 15

ABA95031
 ID ABA95031 standard; DNA; 2383 BP.

AC ABA95031;

DT 20-MAY-2002 (first entry)

XX Human cytokine receptor, Zcytor18 nucleotide sequence.

XX Cytokine receptor, Zcytor18, cell proliferation; antiproliferative; human;

KM pulmonary alveolar proteinosis; familial periodic fever; antitumor;

XX erythroleukemia; chromosome 3p14.3; gene therapy; ds.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 86..2347

FT /tag= a

FT /product= "Zcytor18"

PN W0200208259-A2.

PD 31-JAN-2002.

XX 23-JUL-2001; 2001W0-US023253.

PF 26-JUL-2000; 2000US-0220747P.

PR (ZYMO) ZYMOGENETICS INC.

XX Presnell SR, Kuestner RE, Gao Z;

PI WPI; 2002-217048/27.

DR P-SDB; ABB07626.

XX New cytokine receptor polypeptide designated zcytor18, useful for

PT inhibiting cell proliferation associated with psoriasis or tumor growth,

PT and modulating immune system by binding to endogenous zcytor18 ligand.

XX Claim 5; Page 85-90; 119pp; English.

PS The invention relates to an isolated cytokine receptor polypeptide

CC designated Zcytor18. The Zcytor18 polypeptides can be expressed by

CC standard recombinant methodology. The polypeptides can be used to inhibit

CC cell proliferation associated with psoriasis or tumor growth. The

Linkage-based testing of pulmonary alveolar proteinosis, familial
periodic fever and erythroleukemia, and erythroleukemia associated with
CC polymorphisms of cytokine receptors. The present sequence represents a
human Zeytoris nucleotide sequence

Sequence 2383 BP; 558 A; 679 C; 638 G; 508 T; 0 U; 0 Other;

Query Match 71.9%; Score 2215.4; DB 6; Length 2383;
Best Local Similarity 97.9%; Pred. No. 0;
Matches 2271; Conservative 0; Mismatches 6; Indels 4; Gaps 1;

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Oy 1 TGGCTGGGCGAGCGCAGCGGCGATGAGCCCGTGGCTGCACTGCTCCGTTCTTTAG 60
Db 65 TGGCTGGGCGAGCGCAGCGGCGATGAGCCCGTGGCTGCACTGCTCCGTTCTTTAG 124
Oy 61 GTCAACGCTGCTCAACGGCTTGGCACTGTGTGGCCGCTGGCCGGGTCGGCCGGG 120
Db 125 GTCAACGCTGCTCAACGGCTTGGCACTGTGTGGCCGCTGGCCGGGTCGGCCGGG 184
Oy 121 TGGGGGCTGCAACCTGTGGCTGGAG----- 146
Db 185 CGGGGCGCGACCTGTGGCTGGAGAGTGAAGCGGCTGCCGACCCGGCTTTGT 244
Oy 147 -----GGAGTGGGGCCAGCCAGCAGAAAGTGGGCTGTACAACATCACTTTCAA 198
Db 245 GCTAATGAGGAGTGGGGCCAGCCAGCAGAAAGTGGGCTGTACAACATCACTTTCAA 304
Oy 199 TATGACATTTGACCACTTAATTGAAATCCAGTGGGGAAGCATGTGTTGTGACGCCG 258
Db 305 TATGACATTTGACCACTTAATTGAAATCCAGTGGGGAAGCATGTGTTGTGACGCCG 364
Oy 259 AATATCAGCATGAGCAGTATGCTTGCATGACCAAGTGGCAGTCACTTTCTTGTGTC 318
Db 365 AATATCAGCATGAGCAGTATGCTTGCATGACCAAGTGGCAGTCACTTTCTTGTGTC 424
Oy 319 CAGGGGCGCTGGCTGCAATTCCTGAAAGATTTGGGTAATACTGAGAGACTGAAG 378
Db 425 CAGGGGCGCTGGCTGCAATTCCTGAAAGATTTGGGTAATACTGAGAGACTGAAG 484
Oy 379 TGGAGGGAAGACATGTCACCACTGATTTTAAAGATTCGAGACGCTCAACAGTAGC 438
Db 485 TGGAGGGAAGACATGTCACCACTGATTTTAAAGATTCGAGACGCTCAACAGTAGC 544
Oy 439 TTCAAAAGACATGGAATGGAATCTCAACCTTCTGAAATATGAATTTGAAACGATAT 498
Db 545 TTCAAAAGACATGGAATGGAATCTCAACCTTCTGAAATATGAATTTGAAACGATAT 604
Oy 499 TTCTGAAGGTTGTCCCTTTCTTTCATTTAAAGAAAGCAATTACACCTTTCTTC 558
Db 605 TTCTGAAGGTTGTCCCTTTCTTTCATTTAAAGAAAGCAATTACACCTTTCTTC 664
Oy 559 TTTAAGACCGGAGCTGTGACCTGTGTTTAAAGCCGGAACATTAAGCTTTAAACCTTC 618
Db 665 TTTAAGACCGGAGCTGTGACCTGTGTTTAAAGCCGGAACATTAAGCTTTAAACCTTC 724
Oy 619 TGGAGGCTTGGAACTGAACATCAGCGCAATGAGCTGGGCACTGAAGGTCCTTGGAC 678
Db 725 TGGAGGCTTGGAACTGAACATCAGCGCAATGAGCTGGGCACTGAAGGTCCTTGGAC 784
Oy 679 CAGGCAACCGCACAACCTTGGCTTCGTTTCTTCTATCTTCACTCAAGCTCAAGACGAA 738
Db 785 CAGGCAACCGCACAACCTTGGCTTCGTTTCTTCTATCTTCACTCAAGCTCAAGACGAA 844
Oy 739 GGAACCTTTAAGGGAAGACCTGTAAAGCAGAGCAAACTACAGAGACGACAGCTCTTC 798
Db 845 GGAACCTTTAAGGGAAGACCTGTAAAGCAGAGCAAACTACAGAGACGACAGCTCTTC 904
Oy 799 CTTCAAAAGTTTCTTCAAGGGAATTAATTAATTGAAGTGTGATGAACAACAACA 858
Db 905 CTTCAAAAGTTTCTTCAAGGGAATTAATTAATTGAAGTGTGATGAACAACAACA 964
Oy 859 AGAAAAGTATGATATATGCTTTAAAGCAGTGCATCTCCCGTGGCCGGCCATCAGA 918

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Db 965 AGAAAAGTATGATATATGCTTTAAAGCAGTGCATCTCCCGTGGCCGGCCATCAGA 1024
Oy 919 GGCATGGCCATGACATGTCCTGTGAAGTCAATATGGGATTTGGCGAGCTCTTCACTGAG 978
Db 1025 GCGTGGCCATGACATGTCCTGTGAAGTCAATATGGGATTTGGCGAGCTCTTCACTGAG 1084
Oy 979 ATGTGCCGGAAGACACAAATAATATATTTCACTTATGATGAGAGAGCTGTAG 1038
Db 1085 ATGTGCCGGAAGACACAAATAATATATTTCACTTATGATGAGAGAGCTGTAG 1144
Oy 1039 TCTTCAATACATGTCAGCACTCCCAAGAGAGGCTCCGCGCGGAGAGGTCTTT 1098
Db 1145 TCTTCAATACATGTCAGCACTCCCAAGAGAGGCTCCGCGCGGAGAGGTCTTT 1204
Oy 1099 CTCTGATTTCCAGTAAGATGGCCGAATCAATGAATGTGTCAAGTTCGCTAC 1158
Db 1205 CTCTGATTTCCAGTAAGATGGCCGAATCAATGAATGTGTCAAGTTCGCTAC 1264
Oy 1159 TCTCTCAGGACTTCTGTGGCTGTGAGGTGCTGTGACCTGTGGGAAGACTTACGCTC 1218
Db 1265 TCTCTCAGGACTTCTGTGGCTGTGAGGTGCTGTGACCTGTGGGAAGACTTACGCTC 1324
Oy 1219 TGTAGAAAGGCGAGAGAGATGGGTCATCCAGAAATCCAGATCCCATTTCAATTT 1278
Db 1325 TGTAGAAAGGCGAGAGAGATGGGTCATCCAGAAATCCAGATCCCATTTCAATTT 1384
Oy 1279 GTGTTTGTTCAGAGATGTAATGTAATCTTGTGGAACAAGAACTACAAACAACAAGGA 1338
Db 1385 GTGTTTGTTCAGAGATGTAATGTAATCTTGTGGAACAAGAACTACAAACAACAAGGA 1444
Oy 1339 GGTGGCCGAGGCTCGGGGAAGAGAGCTTTCGTGTGGCCGCTGACCAATGCCGA 1398
Db 1445 GGTGGCCGAGGCTCGGGGAAGAGAGCTTTCGTGTGGCCGCTGACCAATGCCGA 1504
Oy 1399 AAGCTCCGCGAGCCAGACAGATGTCCTCGCGGCGCTCAGCAAGTTATCCGCGTAC 1458
Db 1505 AAGCTCCGCGAGCCAGACAGATGTCCTCGCGGCGCTCAGCAAGTTATCCGCGTAC 1564
Oy 1459 TTTGATTAATCTTGGAGGGAAGAGTCCCGGTATCTAGACTAGATCAAGATACAGA 1518
Db 1565 TTTGATTAATCTTGGAGGGAAGAGTCCCGGTATCTAGACTAGATCAAGATACAGA 1624
Oy 1519 CTATAGCAATCTTCTCAGCTGTGTTCCACTGCACTCCGAGACCAAGCCCTCCAG 1578
Db 1625 CTATAGCAATCTTCTCAGCTGTGTTCCACTGCACTCCGAGACCAAGCCCTCCAG 1684
Oy 1579 GAGCCGGGGCAGCACCGGACAGGGCAGAGAGAACTACTTCCGAGCAAGTCAAGGC 1638
Db 1685 GAGCCGGGGCAGCACCGGACAGGGCAGAGAGAACTACTTCCGAGCAAGTCAAGGC 1744
Oy 1639 CGGTCCCTATAGTGGCCATTTGGCAATGCACTGATTTTGAAGAGGCCGCACTGG 1698
Db 1745 CGGTCCCTATAGTGGCCATTTGGCAATGCACTGATTTTGAAGAGGCCGCACTGG 1804
Oy 1699 TTCGAAAGCAGTGTGTTCCCTTCACTCTCTCACTGCGCTAACCGGAGCAGTCTTG 1758
Db 1805 TTCGAAAGCAGTGTGTTCCCTTCACTCTCTCACTGCGCTAACCGGAGCAGTCTTG 1864
Oy 1759 GAGAAATTTGATTCGGGCTTGGTTTAAATGATGTCAATGTGCAAAACAGGCGCTGAGT 1818
Db 1865 GAGAAATTTGATTCGGGCTTGGTTTAAATGATGTCAATGTGCAAAACAGGCGCTGAGT 1924
Oy 1819 GACTTCTGCTTAAAGTATAGGCGCTGTCTTGGGGCAACCGGACCAAGCCGACTCCAG 1878
Db 1925 GACTTCTGCTTAAAGTATAGGCGCTGTCTTGGGGCAACCGGACCAAGCCGACTCCAG 1984
Oy 1879 CACGAGATCAGATGGGGGCTGTGACCAAGACGAGGAGAGCCGCGCTGCAAGCGT 1938
Db 1985 CACGAGATCAGATGGGGGCTGTGACCAAGACGAGGAGAGCCGCGCTGCAAGCGT 2044
Oy 1939 AGCGCCGCTTGCACCCCTGTGTGACACGATGAAGCCGAGCCCTTGGACATGCCG 1998
Db 2045 AGCGCCGCTTGCACCCCTGTGTGACACGATGAAGCCGAGCCCTTGGACATGCCG 2104

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Query Match 100.0%; Score 3083; DB 6; Length 3083;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3083; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 TGGCTGGGCGAGCGCGGCAATGGCCCGCTGGCTGCACTGCTCGCTCTTTTACG 60
Db      1 TGGCTGGGCGAGCGCGGCAATGGCCCGCTGGCTGCACTGCTCGCTCTTTTACG 60
Qy      61 GTCAACGCTGCTCAACGGCTCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db      61 GTCAACGCTGCTCAACGGCTCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy      121 TGGGGCGTGCACACCTGTGGCTGAGGGGAGTGGGGCGAGCGAGAAAGTGGGCTG 180
Db      121 TGGGGCGTGCACACCTGTGGCTGAGGGGAGTGGGGCGAGCGAGAAAGTGGGCTG 180
Qy      181 TACCAATCACTTCAAAATATGACAAATGTACCACTTACCTTGAATCAGTGGGAAAGCAT 240
Db      181 TACCAATCACTTCAAAATATGACAAATGTACCACTTACCTTGAATCAGTGGGAAAGCAT 240
Qy      241 GTGATTTGCTGAGCGCCGAAATATCACATCAAGCAGTATGCTTGGCATGACCAAGTGGCA 300
Db      241 GTGATTTGCTGAGCGCCGAAATATCACATCAAGCAGTATGCTTGGCATGACCAAGTGGCA 300
Qy      301 GTACCACTTCTTGGTCCCGAGGGGCGCTGGGATCGAATTCCTGAAGGATTTGGGGTA 360
Db      301 GTACCACTTCTTGGTCCCGAGGGGCGCTGGGATCGAATTCCTGAAGGATTTGGGGTA 360
Qy      361 ATAATGAGAGAGCTGAGAGTGGAGGGAGAGAGTGGCAACAACTGATTTTAAAGATCCG 420
Db      361 ATAATGAGAGAGCTGAGAGTGGAGGGAGAGAGTGGCAACAACTGATTTTAAAGATCCG 420
Qy      421 AAGCAGCTCAACAGTATGCTTCAAAAGAACTGGAAATGCAACTTCTGAAATATG 480
Db      421 AAGCAGCTCAACAGTATGCTTCAAAAGAACTGGAAATGCAACTTCTGAAATATG 480
Qy      481 AAATTTGAAAGGATTAATTTGTAAGAGTTGTCCCTTTCTTCACTTAAAGAAAGAGC 540
Db      481 AAATTTGAAAGGATTAATTTGTAAGAGTTGTCCCTTTCTTCACTTAAAGAAAGAGC 540
Qy      541 AATTACCAACCTTTCTTTTGAAGAACCCGAGCCTGAGCTGTGTTTACAGCCGAGCAAT 600
Db      541 AATTACCAACCTTTCTTTTGAAGAACCCGAGCCTGAGCTGTGTTTACAGCCGAGCAAT 600
Qy      601 CTAGCTTTGTAACCCCTTCTGGAAGCCTCGGAACCTGAAACATCAGGCAGCATGCTCGGAC 660
Db      601 CTAGCTTTGTAACCCCTTCTGGAAGCCTCGGAACCTGAAACATCAGGCAGCATGCTCGGAC 660
Qy      661 ATGCAGGTGTCTTGCAGCAGCGACCGGCAAACTTCGAGCTTCGGTTTCTTATCTTAC 720
Db      661 ATGCAGGTGTCTTGCAGCAGCGACCGGCAAACTTCGAGCTTCGGTTTCTTATCTTAC 720
Qy      721 TACAAGCTCAAGCAGAGGAGCCTTTCAAGCGAAAGACCTGTAGCAGAGGAGAACTACA 780
Db      721 TACAAGCTCAAGCAGAGGAGCCTTTCAAGCGAAAGACCTGTAGCAGAGGAGAACTACA 780
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ORIGIN

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 ACCESSION AX392973
 VERSION AX392973.1 GI:19701020
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 Homnidae; Homo.
 REFERENCE
 1 Edmonds, B.T., Micanovic, R., Ou, W., Su, B.W., Tschang, S.H. and Wang, H.
 Novel secreted proteins and their uses
 Patent: WO 0214358-A 15 21-FEB-2002;
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VERSION     CS135272.1  GI:72067723
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens

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1 Gorman, D.M.
AUTHORS    Mammalian receptor proteins; related reagents and methods
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JOURNAL    Schering Corporation (US)
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Query Match      87.5%; Score 2696.6; DB 6; Length 2786;
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ACCESSION AX350979.1 GI:18616355
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AUTHORS Gorman, D.M.
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 REFERENCE 1 (bases 1 to 4478)
 Xiong, S., Zhao, Q., Kong, Z., Huang, G., Huang, Y., Chen, P., Zhang, S.,
 Liu, L., and Chang, Z.
 hsf1 inhibits PC-12 Cell Differentiation by interfering with
 Ras-Mitogen-activated Protein Kinase MAPK Signaling
 J. Biol. Chem. 278 (50), 50273-50282 (2003)
 JOURNAL 12958313
 PUBMED 2 (bases 1 to 4478)
 Xiong, S., Zhao, Q., Huang, G., Chen, P., Rong, Z., Ye, X., Chen, Y.,
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 Direct Submission
 Submitted (22-MAR-2002) Tsinghua Institute of Genome Research,
 Department of Biological Sciences and Biotechnology, and School of
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 ACCESSION AF458067
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TITLE Direct Submission
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ACCESSION AX747904
VERSION AX747904.1 GI:32132292
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ORGANISM Homo sapiens
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Homnidae; Homo.
REFERENCE
AUTHORS 1
Isozaki, T., Sugiyama, T., Otsuki, T., Makematsu, A., Sato, H., Ishii, S.,
Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R.,
Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and
Masuno, Y.
TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1308459-A 1429 07-MAY-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)
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ORIGIN

Query Match 86.9%; Score 2678.6; DB 8; Length 2894;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2684; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Altechul,S.P., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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CONSRTM Mammalian Gene Collection Program Team
TITLE Generation and initial analysis of more than 15,000 full-length
JOURNAL human and mouse cDNA sequences
PUBMED Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
REFERENCE 12477932
2 (bases 1 to 4490)
AUTHORS NIH MGC Project
CONSRTM Direct Submission
JOURNAL Submitted (01-OCT-2002) National Institutes of Health, Mammalian
TITLE Gene Collection (MGC), Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nhl.nih.gov
COMMENT Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiroaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleeged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNLT at: http://image.llnl.gov
Series: IRAX Plate: 72 Row: h Column: 6
This clone was selected for full length sequencing because it
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DEFINITION Sequence 125 from patent US 6783969.

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VERSION AR577949.1 GI:56580745

KEYWORDS

SOURCE

ORGANISM

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1 (bases 1 to 3948)

Tang, Y.T., Goodrich, R.W., Abundl, V. and Drmanac, R.T.

Cathelapsin V-like polypeptides

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Nuvelo, Inc.; Sunnyvale, CA

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 Human dna sequences
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2235 TTTTGA CAAAGCAGGAGTCTAAGCAT TGGC CATTAGCTGTGCTCTCTCTGATTT 2294
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2187 CCAAGCTCATCTCCTG GTTGCATG GCGCCCACTTGA GCTGAGGTCTCATACAGGATAT 2246
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RESULT 14
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (15-NOV-1999) MIPS, Am Klopferpitze 18a, D-82152
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp434N1928) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

[illegible]

Query Match	73.5%	Score 2267.4	DB 6	Length 2341
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Db	305	GTGATTTGCTGAGCGCCGACGATATCAACATCAAGCAGATATGCTTGCATGACCAAGTGGCA	364	
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Qy	361	ATATCTGAGAGCTGAAGTGGAGGGGAGACAGTGGCCAAACATGATCTTAAAGATCCG	420	
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Qy	481	AAATTTGAAACGGAATTTGCTTAAAGGTTGTCCTTTTCTTCCATTTAAAGCAAGC	540	
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Qy	781	GAGACGACACGAGCTGCTCTCTCCAAATTTTCTCAAGGGAGATTATATTAATTGAGCTGTG	840
Db	845	GAGACGACACGAGCTGCTCTCTCCAAATTTTCTCAAGGGAGATTATATTAATTGAGCTGTG	904
Qy	841	GATACACATTAACA CAACAAGAAAAGTAGTCATTATGCTTTAAAGCCAGTGCATCCCG	900
Db	905	GATACACATTAACA CAACAAGAAAAGTAGTCATTATGCTTTAAAGCCAGTGCATCCCG	964
Qy	901	TGGGCGGGGCCCATCAGAGCCATGGCCATCA CAGTGCCACTGTAATCATATCGCATTC	960
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Db	1925	GGACCAACCCGACATCCCAAGCAGAGAGTCAATAGGGGGCCCTGGACCAAGACGGGGAAGCC	1984
Oy	1921	CGGCTTCGCCCTTGAACGGGTAGCGCCGCCCTGCAACCCTGCTGCAACGGGTAAAGCCGGC	1980
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Oy	2041	CTGTCTCTGCGCATGATGGAAGGACTCTCGACGGACAGAGAAAGTCTTCCCTGACG	2100
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Oy	2161	CTCTCTCTTCTGAGGTATGCAAAAGCAGATCTTGTTGCGGCAAGCTACATGATGAATC	2220
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Oy	2221	CAGCGCGGTCCGCTTTTGTAAACAAAGAAAGATCTAAGCATTTGCCACTTTACTG	2277
Db	2285	CAGCGCGGTCCGCTTTTGTAAACAAAGAAAGATCTAAGCATTTGCCACTTTACTG	2341

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Job time : 14967 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2006, 05:13:33 ; Search time 11789 Seconds
(without alignments)
12235.523 Million cell updates/sec

Title: US-10-616-788-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_est2:.*
3: gb_est3:.*
4: gb_hcc:.*
5: gb_est4:.*
6: gb_est5:.*
7: gb_est6:.*
8: gb_est7:.*
9: gb_gse1:.*
10: gb_gse2:.*
11: gb_gse3:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2307.6	74.8	2406	4 HSM805220	AL833913 Homo sapi
2	1541.2	50.0	1677	10 AY408489	AY408489 Homo sapi
3	1512.6	49.1	1677	10 AY408490	AY408490 Pan trogl
4	1032.2	33.5	1674	10 AY408491	AY408491 Mus muscu
5	766.2	24.9	908	7 CJ025168	CJ025168 CU025168
6	734.4	23.8	856	8 DN282586	DN282586 1182679 M
7	730	23.7	851	8 DN283973	DN283973 1184215 M
8	608.4	19.7	724	3 BP154750	BP154750 BP154750
9	578.8	18.8	583	3 BP275741	BP275741 BP275741
10	570.4	18.5	679	5 BM965550	BM965550 BM965550
11	527	17.1	609	8 DN391145	DN391145 L183925-0
12	523.6	17.0	629	7 CN302484	CN302484 170005314
13	496	16.1	7	CJ024557	CJ024557 CJ024557
14	490	15.9	494	8 DR003317	DR003317 TC100455
15	479.8	15.6	547	2 BE750478	BE750478 201867 MA
16	476.8	15.5	665	2 BB641245	BB641245 BB641245
17	471	15.3	748	7 CV126214	CV126214 AGENCOURT
18	468	15.2	754	1 AU124473	AU124473 AU124473
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22	424.4	13.8	692	5 BU212978	BU212978 603105617

23	421.8	13.7	717	5 BU479802	BU479802 603843254
24	416	13.5	907	5 BU909956	BU909956 AGENCOURT
25	415	13.5	667	5 BU726061	BU726061 BU726061
26	413.2	13.4	886	5 BX750910	BX750910 BX750910
27	411.2	13.3	548	5 BQ830554	BQ830554 L1612050
28	408.8	13.3	891	5 BX754503	BX754503 BX754503
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31	385	12.5	889	6 CA787708	CA787708 AGENCOURT
32	381	12.4	474	6 CA879041	CA879041 KO971D08-
33	374.2	12.1	390	1 AA778029	AA778029 zE42E08..8
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36	339	11.0	718	10 CG465953	CG465953 FHCRG-GT-
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38	327.2	10.6	627	1 AM645591	AM645591 CMS4107.w
39	326.8	10.6	434	10 CG603524	CG603524 OST78253
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ALIGNMENTS

RESULT 1	HSM805220	2406 bp	mRNA	linear	HTC 20-JAN-2005
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ACCESSION	AL833913				
VERSION	AL833913.1	GI:21739453			
KEYWORDS	HTC.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 2406)				
AUTHORS	Ostenwaelder,B., Obermaier,B., Deutschenbauf,S., Schajp,A., Mewes,H.W., Weil,B., Amid,C., Oeinger,A., Fobo,G., Han,M. and Wiemann,S.				
CONSRWT	The German cDNA Consortium				
TITLE	Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764				
JOURNAL	Neuberberg, GERMANY				
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp434L0320) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp434L0320 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.				
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	/dev_stage="adult"				
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	/gene="DKFZp434L0320"				
CDS	346..2133				

[illegible]

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Matches 2313;	Conservative 0;	Mismatches 9;	Indels 0;	Gaps 0;

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QY	975	TGTGTATGTGCGCGCAAGACCAAGAAATATATATTCACATTTAGATGAAAGAGCTC	1034
Db	867	TGTGTATGTGCGCGCAAGACCAAGAAATATATATTCACATTTAGATGAAAGAGACTC	926
QY	1035	TGAGCTTCCACATACACTGACAGACTCCCAAGAGAGAGGCTCCGGCGCGGCCGAAGGT	1094
Db	927	TGAGCTTCCACATACACTGACAGACTCCCAAGAGAGAGGCTCCGGCGCGGCCGAAGGT	986
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QY	1215	CCTCTGTAGAGAAAGGCGAGAGAAATGGGTCAATCCAAAGATCCACAGATCCCGATTCAT	1274
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QY	1275	CATTGTGGTTTGTCCAAAAGGTATGAGATCTTTGTGTGACAAAGAAAGACTTCAACAACAA	1334
Db	1167	CATTGTGGTTTGTCCAAAAGGTATGAGATCTTTGTGTGACAAAGAAAGACTTCAACAACAA	1226
QY	1335	AGAGAGTGGCCGAGGCTTCGGGGAAAGAGAGCTCTTCTGTGGTGGGTGTCAAGCCATTGC	1394
Db	1227	AGAGAGTGGCCGAGGCTTCGGGGAAAGAGAGCTCTTCTGTGGTGGGTGTCAAGCCATTGC	1286
QY	1395	CGAAAGCTCCGCGACAGCCCAAGCAGAGATTCGTCCGCGCGCTGCAGAAAGTTATTCGCGCT	1454
Db	1287	CGAAAGCTCCGCGACAGCCCAAGCAGAGATTCGTCCGCGCGCTGCAGAAAGTTATTCGCGCT	1346
QY	1455	CTACTTTGATTATTCCTGCGAGGAGAGAGTCCCGGATTCCTAGACCTGAGTACCAAGTA	1514
Db	1347	CTACTTTGATTATTCCTGCGAGGAGAGAGTCCCGGATTCCTAGACCTGAGTACCAAGTA	1406
QY	1515	CAGACTACATGACAAATCTTCTCTAGCTCTGTTCCCACTGACACTCCGAGACCAAGGCT	1574
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QY	1575	CCAGAGATCCGGGGCAGACACAGCGCACAGGGCAGACAAAGAACTATCTCCGAGACAAATGC	1634
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QY	1635	AGGCCTGGCTCCCTATACGTCCGCACTTTGCAACATGCAACAAGTTTATGACGAGAGCCGGA	1694
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QY	1695	CTGGTTCGAAAAGCAGTTCGTTCCCTTCATCTCTCCACTGCGCTAACCGGGAGCCAGT	1754
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QY	1755	CTTGGAGAAATTTGATTCGGGCTTGTTTAAATGATGTCAATGTGCAAAACAGGCGCTTGA	1814
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QY	1815	GAGTGACTTTCGCTTAAAGTAAAGTAAAGGGCGCTCTTGGGGCAACCGGACCAAGCGACTC	1874
Db	1707	GAGTGACTTTCGCTTAAAGTAAAGTAAAGGGCGCTCTTGGGGCAACCGGACCAAGCGACTC	1766
QY	1875	CCAGACGAGAGTCAAGCATGTGGGGGCTTGGAACAAAGACGGGGAGGCGCGCTGCGCTTGA	1934
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Db	1327	CGGTAGCCGCCCTCTGCACACCCCTGTCTGCACAGGTAAACCCGGACACCCCTTGGACAT	1886
Qy	1995	GCCGCGGAGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTCTTGCCACT	2054
Db	1887	GCCGCGGGAGCTCAAGGCATCTATGACTGTGTGTGCCCTCATCCGAGCTGTCTGTGCCACT	1946
Qy	2055	GATGGAAAGGACTCTTCAGCGGACACGACAGAAACGTCTTCCCTGACCGAGAGCGTGTCTC	2114
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Qy	2355	TGGAGTGAATGTGCGCCAGTACTGTGTCTCCCTTGCCCAACCTTTACCGGATATCTT	2414
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LOCUS	AY408489
DEFINITION	AY408489 1677 bp DNA linear GSS 12-DEC-2003
ACCESSION	Homo sapiens HCN3241 gene, VIRTUAL TRANSCRIPT, partial sequence,
VERSION	AY408489
KEYWORDS	genomic survey sequence.
ORGANISM	AY408489.1 GI:39764460
SOURCE	GSS.
REFERENCE	Homo sapiens (human)
AUTHORS	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominoidea; Homo.
	1 (bases 1 to 1677)
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
	Todd,M.A., Tenenbaum,D.M., Ciyello,D.R., Lu,F., Murphy,B.,
	Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
	Adams,M.D. and Cargill,M.
	Interferring nonneutral evolution from human-chimp-mouse orthologous
	gene trios
	Science 302 (5652), 1960-1963 (2003)
	14671302
	2 (bases 1 to 1677)
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
	Todd,M.A., Tenenbaum,D.M., Ciyello,D.R., Lu,F., Murphy,B.,
	Perriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
	Adams,M.D. and Cargill,M.
	Direct Submission
	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
	Rockville, MD 20850, USA
	This sequence was made by sequencing genomic exons and ordering
	them based on alignment.
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Db	119 TGTGACCTGTGTGTACAGCCGAGCAATCTAGCTTGTAAACCTTCTGGAACCTCGAATC	135
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Qy      1774 GCGTTGGTTTAAATGATGTCATGTGCAACCAAGGCTTGAAGTGAATCTTCTGCTTAAAG 1833
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RESULT 3
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LOCUS Pan troglodytes HCM3241 gene, VIRUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY408490
VERSION AY408490.1 GI:39764461
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
1 (bases 1 to 1677)
Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejaritwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,

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PUBMED
REFERENCE
AUTHORS
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Best Local Similarity 92.4%; Pred. No. 0;
Matches 1652; Conservative 0; Mismatches 25; Indels 111; Gaps 2;

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Dp	610	TGTGGCTGTGAGTGGCTCTGGACCTGTGGGAAGACTTCAGCTCTGTAGAAAGGAGC	669
Qy	1234	AGAGAAATGGGTATCTCAGAAAGATCCAGAGTCCAGTTCAATATGTGGTTTGTCCAA	1295
Dp	670	AGAGAAATGGGTATCTCAGAAAGATCCAGAGTCCAGTTCAATATGTGGTTTGTCCAA	729
Qy	1294	GGAATGAAGTACTTTGTGGACAAGAAAGTACAACAAGAGAGTGGCCGAGGCTCG	1355
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Qy	1354	GGAAGAAAGAGAGCTCTTCTGTGGCGGTGTGAGCAATTCGCGAAGAGCTCCGCGAGCC	1413
Dp	790	GGAAGAAAGAGAGCTCTTCTGTGGCGGTGTGAGCAATTCGCGAAGAGCTCCGCGAGCC	849
Qy	1414	AAGCAGATGTCGTCCGCGAGCTCAGCAAGTTATGCGCTGTACTTTGATTATTCCTGC	1473
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Qy	1474	GAGGGAAGAGTCCCGGTATCTTGACCTGAGTACCAAGTACAGACTCATGGAACAATCTT	1533
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Qy	1534	CCTGAGCTCTGTTCCCACTGCACTCCCGAAGACAAGGCTCTCAGAGAGCGGGGAGAGC	1593
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Qy	1594	ACGGGACAGGGCAGCAGAAAGAACTACTTCCGGAGCAAGTCAAGCGGTCCCTATAGCTC	1653
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LOCUS	AY408491		linear
DEFINITION	Mus musculus HCM3241 gene, VIRUTUAL TRANSCRIPT, partial sequence,		
ACCESSION	AY408491		
VERSION	AY408491.1		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1674) Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tenenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M. inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
TITLE	Science 302 (5652), 1960-1963 (2003)		
JOURNAL	14671302		
PUBMED	2 (bases 1 to 1674)		
REFERENCE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tenenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.		
AUTHORS	Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.		
COMMENT	Location/Qualifiers		
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Matches 1360; Conservative	0; Mismatches 308; Indels 126; Gaps 5		
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Db	1324	CAGCATGAGCCCTGGACCAAGACACTGAGAGGCCAGCCCTCTGTGATGATGAGCCCTGACC	1383
Qy	1348	CTGCAACCCCTGCTGCGACACGGTGAAGCCGGAGCCCTCTCGACATGCGCGGGGACATCA	2007
Db	1384	TTGAGGCCCTCTGTATACAGCAGTGAAGCTGGCAGTCCCTCTGAGATGACCAGGGACATCA	1443
Qy	2008	GGCATCTATGACTGTCTGTGACCCTCATCCGAGCTGTCTCTGACCATGATGGAAGACTC	2067
Db	1444	GGCATATATGATTTCTTCTGTACCCCTCATCAGAGCTCTCTGCTCTGATGGAAGGACTC	1503
Qy	2068	TTCAGACGACGACAGAAAGCTTTCCCTACAGGAGAGCGATGCTCCTCTTACAGGACTG	2127
Db	1504	TCCCCGATCAGATGAGAAACTTCTCTCTGACGAGAGGTATTTTCTCTCTCTGGCCTTA	1563
Qy	2128	GGTAGAGAGAACTCTGCTGCTTCTCTTCCAAAGCTCTCTTCTGTGGGTCAATGCAAGCA	2187
Db	1564	GGTAGAGAGAGACCCCTTACCTCTCCCTTCCAAAGCTCTTGTCTCTGGGGTGTCCA---GA	1620
Qy	2188	GATTTGTTGGCGGACGCTACACTGATGAATCTCAGCGGGCGGCTTTTGTA	2241
Db	1621	GACATGTTGGCCACAGCCACACTGAGAACTGCAAGCGCTTGTCTTTTGTA	1674

RESULT 5	
CJ025168	
LOCUS	CJ025168
DEFINITION	908 bp mRNA linear EST 22-OCT-2004
ACCESSION	CJ025168 full-length enriched swine cDNA library, adult cricchea Sus
VERSION	CJ025168
KEYWORDS	scrofa clone TCHO1B080037 5', mRNA sequence.
SOURCE	CJ025168.1 GI:54533576
ORGANISM	EST.
	Sus scrofa (pig)
	Sus scrofa

REFERENCE	1 (bases 1 to 908)
AUTHORS	Uenishi,H., Eguchi,T., Suzuki,K., Sawasaki,T., Toki,D., Shinkai,H., Okumura,N., Hamaeima,N. and Awata,T.
TITLE	PE3E (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries
JOURNAL	Nucleic Acids Res. 32 (1), D484-D488 (2004)
PubMed	14681463
COMMENT	Contact: Hirohide Uenishi

Email: huenishi@affrc.go.jp
ESR project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.

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FEATURES
SOURCE
    Location/Qualifiers
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            /clone="TCH01B080037"
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            /dev_stage="adult"
            /clone_lib="full-length enriched swine cDNA library, adult
trachea"

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Query Match	24.9%	Score 766.2;	DB 7;	Length 908;
Best Local Similarity	90.4%	Pred. No. 2.1e-189;		
Matches 81;	Conservative	87;	Indels	0;
			Gaps	0;

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61  CCTCAAGGCTGGCAAGCTGGCTGGCCCGTGGAGCTGGCTGGCCCGTGGAGCTGCA 120
132  CACCTGGCTGGAGGGAGTGGGGCCAGCCAGCAGAAACAGTGGCTGTACAACTCAC 191
121  CACCTGGCTGGAGGGAGTGGGGCCAGCCAGCAGAAACAGTGGCTGTACAACTCAC 180
192  CTTCAAAATGACAAATGACAACTGACAACTGACAACTGACAACTGACAACTGACAA 251
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481  AGATTAATTTGTAAGAGTTGTCCCTTTCTTCCATTAATAAGAAAGCAATTAACACCC 540
552  TTTCTTCTTTAAGAACCCGAGCTGTGACCTGTTGTTTACAGCCGAGCAATCTAGCTTGA 611
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612  ACCCTTCTGGAAGCTCGGAACCTGAAACATGAGCCAGCATGCTGGAACATGAGAGTGC 671
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672  CTTTGAACAGCAGCAGCAACTTGGCTTCCGTTCTTCTTCAATCTTCACTACAGCTCAA 731
661  CTTTGAACAGCAGCAGCAACTTGGCTTCCGTTCTTCTTCAATCTTCACTACAGCTCAA 720
732  GCAAGAGAGCTTTCAAGCAGAAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 791
721  GCAAGAGAGCTTTCAAGCAGAAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
792  CTGCTCTCTTCAAAATGTTCTTCAGGGGATTAATATTAATGAGCTGTGATGACACNT 851
781  CTGCTCTCTTCAAAATGTTCTTCAGGGGATTAATATTAATGAGCTGTGATGACACNT 840
852  CACAAACAAGAAAGTATGATCAATATGCTTAAAGCAGTGCATCCCGTGGCCGGGCC 911
841  AATCAACAAGAAAGTATGATCAATATGCTTAAAGCAGTGCATCCCGTGGCCGGGCC 900
912  CAT 914
901  CAT 903

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RESULT 6
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LOCUS DN282586 1182679 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
DEFINITION DN282586
ACCESSION DN282586
VERSION DN282586.1 GI:60451196
KEYWORDS EST.

```

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SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
AUTHORS Wray,J.E. and Keele,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RIK8015 row: B column: 19
Seq primer: TAGAAGGACAGCTGAGG.
Location/Qualifiers
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/mol_type="mRNA"
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/lab_host="DH10B"
/clone_lib="MARC 7BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."
ORIGIN
Query Match 23.8%; Score 734.4; DB 8; Length 856;
Best Local Similarity 91.1%; Pred. No. 4.7e-181;
Matches 780; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
137 GTGGCTGAGGGAGTGGGGCCAGCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
856 GTGGCTGAGGGAGTGGGGCCAGCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 797
197 AATATGACAAATGTACCACTTCTGTAATCCAGTGGGAGAGAGAGAGAGAGAGAGAG 256
796 GATATGACAAATGTACCACTTCTGTAATCCAGTGGGAGAGAGAGAGAGAGAGAGAG 737
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736 AGAATATGACCACTTCAAGCAGTATGCTGCAAGACCAAGTGGCAGTCACTTCTTGGT 677
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377 AGTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 436
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437 GCTTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 496
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497 ATTGCTAAAGAGTGTGCTTCTTCTTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAG 556
496 ACTTTGTAAGAGATGCTTCTTCTTCTTCAATTAAGAGAGAGAGAGAGAGAGAGAGAG 437
557 TCTTTAGAACCCGAGCTGTGACCTGTTGTTACAGCCGAGCAATCTTACTGTAACCTT 616
436 TCTTCAAGAACCCGAGCTGTGACCTGTTGTTACAGCCGAGCAATCTTACTGTAACCTT 377
617 TCTGAGAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 676

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Db 376 TCTGAGAGCTCGGAACTTCACATCATCTCAGACGAGTTCGACATGACAGTGTCTTTTG 317
 Qy 677 ACCAGCAGCCGACGACATTCGAGCTCGTTTCTTATCTTCACTCAAGCTCAAGCAGC 736
 Db 316 ACCATGCGCCGACGACATTCGAGCTCGTTTCTTATCTTCACTCAAGCTTAAAGCAGT 257
 Qy 737 AAGGACCTTTCAGACGAAAGACCTGTAAAGCAGAGGAACTACAGAGCAGCAGCTGCG 796
 Db 256 AAGGACCTTTCAGACGAAAGACCTGTAAAGCAGAGGAACTACAGAGTAAACAGCTGCG 197
 Qy 797 TCCCTCAAAATGTTTCTCCAGGGATTTATTAATTGAGCTGTGATGACATCAACAA 856
 Db 196 TCTTCAAAATGTTTCTCCAGGGATTTATTAATTGAGCTGTGATGACATCAACAA 137
 Qy 857 CAGAAAGATGATGATTAATGCTTAAAGCAGTGCATCCCGTGGGCGGGCCCATCA 916
 Db 136 CAGAAAGATGATGATTAATGCTTAAAGCAGTGCATCCCGTGGGCGGGCCCATCA 77
 Qy 917 GAGCCATGCGCATCAAGTGCATGCTGTATGATCATTCGAGCTTCGAGCCTTCACTG 976
 Db 76 GAGCTGTGCGCATCACTGTGCGCATTCGTGTCTATTCGCGATTCGCGAGCCTTCACTG 17
 Qy 977 TGATGTGCGCGAAGAA 992
 Db 16 TGATGTGCGCGAAGAA 1

RESULT 7
 DN283973 851 bp mRNA linear EST 02-MAR-2005
 LOCUS 1184215 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
 DEFINITION
 ACCESSION DN283973
 VERSION DN283973.1 GI:60452583
 KEYWORDS
 SOURCE EST.
 ORGANISM Bos taurus (cow)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 851)
 Smith,T.P., Roberts,A.J., Echerkamp,S.E., Chitko-Mckown,C.G.,
 Wray,J.E. and Keeler,J.W.
 A second set of bovine ESTs from pooled-tissue normalized libraries
 Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alit option. Vector identified with
 cross_match v0.990329.
 Plate: RLK8015 row: E column: 19
 Seq primer: GTAATACGACTCATTATAGGG.
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 /clone_id="MARC 7BOV"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with RNA pooled from multiple tissues
 including ovary, hindbrain, uterus, and day-30 whole
 embryos."

ORIGIN
 Query Match 23.7%; Score 730; DB 8; Length 851;
 Best Local Similarity 91.1%; Pred. No. 6,7e-180;
 Matches 775; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

FEATURES
 source

ORIGIN

Query Match 23.7%; Score 730; DB 8; Length 851;
 Best Local Similarity 91.1%; Pred. No. 6,7e-180;
 Matches 775; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 137 GTGGCTGAGGGAGTGGGGCCAGCCAGAGAAAGATGGGCTGTACAACTACCTTCA 196
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 Qy 197 AATTGACAAATTGTACACCTTCTTGAATCCAGTGGGGAAGATGTGATGCTGACGCC 256
 Db 61 GATTATGACAACTGACACACTTACTTGAATCCAGTGGGGAAGATGTGATGCTGACGCC 120
 Qy 257 AAGATATGACCACTGACCGCAGTATGCTGAGCAAGCAAGATGGCACTTCTTTGGT 316
 Db 121 AAGACATGACCACTGACCGCAGTATGCTGAGCAAGCAAGATGGCACTTCTTTGGT 180
 Qy 317 CCCAGAGGGCCCTCGGCATCGAATTCCTGAAGATTTCCGGTAAATCTGAGAGCTGA 376
 Db 181 CCCCCGGGGCCCTCGGCATCGAATTCCTGAAGATTTCCGGTAAATCTGAGAGCTGA 240
 Qy 377 AGTCGAGGGAAGACAGTGCACAACTGATTTCTAAAGATTCGAGACGCTCAACATGA 436
 Db 241 AGTCAGAGGGAAGACAGTGCACAACTGATTTCTAAAGATTCGAGACGCTCAACATGA 300
 Qy 437 GCTTCAAAAGAACTGGAATGGAATCTCAACCTTCTGAAATGAAATTTGAAAGGAT 496
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 Qy 497 ATTGCTAAAGGTTGTCTCTTCTTCCATTAAGAAAGCAATTAACACCTTTCT 556
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 Db 541 ACCATGCGCCGACGACATTCGAGCTCGTTTCTTATCTTCACTCAAGCTTAAAGCAGT 600
 Qy 737 AAGGACCTTTCAGACGAAAGACCTGTAAAGCAGAGCAAACTACAGATTAACACCTGCC 796
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 Qy 857 CAGAAAGATGATGATTAATGCTTAAAGCAGTGCATCCCGTGGGCGGGCCCATCA 916
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 Qy 917 GAGCCATGCGCATCAAGTGCATGCTGTATGATCAATTCGAGCTTCGAGCCTTCACTG 976
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 Qy 977 TGATGTGCGCG 987
 Db 841 TGATGTGCGCG 851

RESULT 8
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 LOCUS BP154750 full-length enriched swine cDNA library, adult ovary Sus
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 ACCESSION BP154750
 VERSION BP154750.1 GI:40404223
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 SOURCE EST.
 ORGANISM Sus scrofa (pig)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;

Query Match 23.7%; Score 730; DB 8; Length 851;
 Best Local Similarity 91.1%; Pred. No. 6,7e-180;
 Matches 775; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 724)
 AUTHORS Unishih.H., Eguchi.T., Suzuki.K., Sawazaki.T., Toki.D., Shinkai.H.,
 Okumura.N., Hamashima.N. and Awata.T.
 TITLE PEDF (Pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)
 PUBMED 14681463
 COMMENT Contact: Hirohide Unishih
 National Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishih@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in
 Animal Genome Research Program (Japan) by National Institute of
 Agrobiological Sciences and STAFF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.
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 /tissue_type="ovary"
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 Matches 665; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
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 Db 18 GGCTGGCGAGCGCAGCGCCATGCCCCGCTGGCTGACGCTCTCCGCTCTTTACCG 77
 Oy 62 TCACACCTGCTCTCAACGGCTGCGAGCTGCTGCGCTGCGCGGCTCCGCGCGCT 121
 Db 78 TCACACCTGCTCTCAACGGCTGCGAGCTGCTGCGCGGCTGCGCGGCTCCAGAGCTC 137
 Oy 122 GGGGCGTCCAGACCTGTGCTGAGAGGGAGTGGGCGCAGCAGCAGAAAGTGGCTGT 181
 Db 138 GGGGCGGCGCAGACCTGTGCTGAGAGGGAGTGGGCGCAGCAGCAGAAAGTGGCTGT 197
 Oy 182 ACAACATCACTTCAATATATGACATTTGACACTTAATTGATTCAGTGGGAGCATG 241
 Db 198 ACAACATCACTTCAATATATGACATTTGACACTTAATTGATTCAGTGGGAGCATG 257
 Oy 242 TGATTGCTGACGGCCAGAAATATGACATTCAGCAATGCTTTCAGTACCAAGTGGCAG 301
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 Oy 302 TCACCACTTCTTGGTCCCGAGGGGCGCTCGGCAATTCCTGAAAGATTTCCGGTTAA 361
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Db 498 AATTGAAACAGATTAATTGTCAGAGTGTCCCTTCTTCATTAAGAAAGCA 557
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 Oy 602 TGGCTTGAACCGCTCTGGAAGCCCTGGAACTGGAACCTGGAACCTGGAACCTGGAAC 661
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 Oy 662 TGCAGGTGTCTTTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 708
 Db 678 TGCAGGTGTCTTTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 724
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 BP275741 583 bp mRNA linear EST 16-SEP-2004
 LOCUS BP275741
 DEFINITION BP275741 Sugano cDNA library, kidney Homo sapiens cDNA clone
 KDN04362, mRNA sequence.
 ACCESSION BP275741 GI:52189473
 VERSION BP275741.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCES 1 (bases 1 to 583)
 Suzuki.Y., Yamashita.R., Shiota.M., Sakakibara.Y., Chiba.J.,
 Mizushima-Sugano.J., Nakai.K. and Sugano.S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)
 JOURNAL 15342556
 PUBMED
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers
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 Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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 Db 1 GTACAGATCAATGACAAATCTTCTGAGTCTGTTCCACCTGACATCCCGAGACCA 60
 Oy 1572 CCTCCAGAGCGCGGCGCAGACACGCGACAGGCGCAGAGGAACTACTTCCGAGCAA 1631
 Db 61 CCTCCAGAGCGCGGCGCAGACACGCGACAGGCGCAGAGGAACTACTTCCGAGCAA 120
 Oy 1632 GTCCAGCGCGTCTTAATAGTGCATTTGCAACATGACCAAGTTATTTAGCAGAGAGCC 1691
 Db 121 GTCCAGCGCGTCTTAATAGTGCATTTGCAACATGACCAAGTTATTTAGCAGAGAGCC 180
 Oy 1692 CGACTGTTTCAAAAGCAATGTTCTTCCATCTCTCTCACTGCGCTACCGGAGGCC 1751
 Db 181 CGACTGTTTCAAAAGCAATGTTCTTCCATCTCTCTCACTGCGCTACCGGAGGCC 240
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 Db 241 AGTCTTGAGAAATTTGATTCGGGCTTGGTTTAAATGATGATGATGCAACAGAGGCC 300
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QY 1812 TGAGAGTGAATCTTCTGCTAAAGGATAGAGGCGCTGTCTTGGGGCAACCGGACCAAGCCGA 1871
DB 301 TGAAGAGTGAATCTTCTGCTAAAGGATAGAGGCGCTGTCTTGGGGCAACCGGACCAAGCCGA 360
QY 1872 CTCGCCAGCAGAGAGTACAGATGAGGGGCTTGACCAAGACGAGGAGCCCGCTGCTCCCT 1931
DB 361 CTCGCCAGCAGAGAGTACAGATGAGGGGCTTGACCAAGACGAGGAGCCCGCTGCTCCCT 420
QY 1932 TGACCGTGAAGCGCGCTGCAACCCCTGTGCAACAGGTGAAGACCGGAGCCCGCTGCGGA 1991
DB 421 TGACCGTGAAGCGCGCTGCAACCCCTGTGCAACAGGTGAAGACCGGAGCCCGCTGCGGA 480
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DB 481 CATGCCGCGGAGCTCAGGAGATCTATGATCTGTCTGTGCTCATCCGAGCTGTCTGCTCC 540
QY 2052 ACTGATGAGGAGACTCTGCAACGAGACCAAGACGCTCTTCC 2094
DB 541 ACTGATGAGGAGACTCTGCAACGAGACCAAGACGCTCTTCC 583
RESULT 10
BM965550 679 bp mRNA linear EST 08-AUG-2005
LOCUS BM965550 full-length enriched swine cDNA library, adult ovary Sus
DEFINITION Bm965550
ACCESSION Bm965550
VERSION Bm965550.1 GI:71964881
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
Sus.
REFERENCE 1 (bases 1 to 679)
AUTHORS Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Okumura,N., Hamashima,N. and Awata,T.
TITLE PEDF (pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
JOURNAL Nucleic Acids Res. 32 (1), D484-D488 (2004)
PUBMED 14681463
COMMENT Contact: Hirohide Uenishi
Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-28-838-8627
Fax: +81-28-838-8627
Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried out in
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STRP-Insitute
Single pass sequencing of clones derived from oligo-capped cDNA
library
Vector sequences were eliminated by RepeatMasker version 2002/07/13
and crossmatch version 0.990319
Low quality bases were trimmed based on the quality values.
FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="OVR010067A07"
/issue_type="ovary"
/dev_stage="adult"
/clone_1b="full-length enriched swine cDNA library, adult
ovary"

Query Match 18.5%; Score 570.4; DB 5; Length 679;
Best Local Similarity 90.9%; Pred. No. 5.3e-138;
Matches 607; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 2 GGCTGGGCGAGGCGACGGGCAATGAGCCCGTGAGCTCAAGCTGTCTCCCTCTTCTTTATCG 61
DB 12 GGCTGGGCGAGGCGACGGGCAATGAGCCCGTGAGCTCAAGCTGTCTCTTCTTCAACCG 71
QY 62 TCACAGCTGTGCTTCAACGGCTTGACAGCTGTGTGTGGCGCTGTGGCGGCTGCGCGCT 121
DB 72 TCACAGCTGTGCTTCAACGGCTTGACAGCTGTGTGTGGCGCTGTGGCGGCTGCGCGCT 131
QY 122 GGGGCGTGACACATGTGTGCTGAGAGGAGTGGGGCCAGCCAGCAAGAAACAGTGGGCTGT 181
DB 132 GGGGCGTGACACATGTGTGCTGAGAGGAGTGGGGCCAGCCAGCAAGAAACAGTGGGCTGT 191
QY 182 ACAACATCACTTCAATATATGACAAATTTGACCACTTCAATTCAGTGGGAAAGCATG 241
DB 192 ACAACATCACTTCAATATATGACAAATTTGACCACTTCAATTCAGTGGGAAAGCATG 251
QY 242 TGATTGTGAGCGGCCAGAAATATACCAATACAGCAATATGCTTCCATGACCAAGTGGCG 301
DB 252 TGATTGTGAGCGGCCAGAAATATACCAATACAGCAATATGCTTCCATGACCAAGTGGCG 311
QY 302 TCACCATTTCTTGTGTCCCGAGGGGCTCTGCGCATGCAATTCCTGAAAGGATTTCCGGGTGA 361
DB 312 TCACCATTTCTTGTGTCCCGAGGGGCTCTGCGCATGCAATTCCTGAAAGGATTTCCGGGTGA 371
QY 362 TACTGAGAGAGCTGAGTTCGAGGAGAGACAGTGCACCACTGATTTCTTAAAGATCCGA 421
DB 372 TACTGAGAGAGCTGAGTTCGAGGAGAGACAGTGCACCACTGATTTCTTAAAGATCCGA 431
QY 422 AGCAGCTCAACATGATGCTTCAAAAGAACTGCAATGAAATCTTACCTTTCTGAAATATGA 481
DB 432 AGCAGCTCAACATGATGCTTCAAAAGAACTGCAATGAAATCTTACCTTTCTGAAATATGA 491
QY 482 AATTTGAAACGGAATATTTGTAAGTGTGTCCTTTCTTCATTAAGAAAGCAAGCA 541
DB 492 AATTTGAAACGGAATATTTGTAAGTGTGTCCTTTCTTCATTAAGAAAGCAAGCA 551
QY 542 ATTACACCCCTTTCTTCTTTAGAACCCGAGCTGTGACCTGTGTGTAACCGCGACAATC 601
DB 552 ATTACACCCCTTTCTTCTTTAGAACCCGAGCTGTGACCTGTGTGTAACCGCGACAATC 611
QY 602 TAGCTTGTAACCTTTCTTGTGAAGCTCGGACCTGACATGACCGACATGCTGCTGACGA 661
DB 612 CGGCTGTGAACCTTTCTTGTGAAGCTCGGACCTGACATGACCGACATGCTGCTGACGA 671
QY 662 TGCAGGTG 669
DB 672 TGCAGGTG 679
RESULT 11
DN391145 609 bp mRNA linear EST 07-MAR-2005
LOCUS DN391145
DEFINITION LIB3925-001-Q1-B10 LIB3925 Canis familiaris cDNA clone
LIB8802925, mRNA sequence.
ACCESSION DN391145
VERSION DN391145.1 GI:60572366
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 609)
AUTHORS Staten,N.R.
TITLE Direct Submission (Staten,N.R.)
JOURNAL Unpublished (2005)
COMMENT Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@fizer.com.
FEATURES
source Location/Qualifiers
1..609
/organism="Canis familiaris"
/mol_type="mRNA"

ACCESSION	C0024557	GI:54532279
VERSION	CJ024557.1	
KEYWORDS	EST.	
SOURCE	Sus scrofa (pig)	
ORGANISM	Sus scrofa	
REFERENCE	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Sus.	
AUTHORS	Unishih,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hamasima,N. and Awata,T.	
TITLE	PBE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries	
JOURNAL	Nucleic Acids Res. 32 (1), D484-D488 (2004)	
FIGURED	14681463	
COMMENT	Contact: Hirohide Unishih Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan Tel.: +81-29-838-8627 Fax: +81-29-838-8627 Email: huenishi@affrc.go.jp EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STRP-Institute Single pass sequencing of clones derived from oligo-capped cDNA library Vector sequences were eliminated by RepeatMasker version 2002/07/13/ and crossmatch version 0.990319 Low quality bases were trimmed based on the quality values. Location/Qualifiers 1..803 /organism="Sus scrofa" /mol_type="mRNA" /db_xref="taxon:3823" /clone="TCH01A100029" /rissue_type="trachea" /dev_stage="adult" /clone_idb="full-length enriched swine cDNA library, adult trachea"	
FEATURES		
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Best Local Similarity	92.1%; Pred. No. 2e-118;	
Matches 523;	Conservative 0;	Mismatches 45; Indels 0; Gaps 0;
Dy	2 GGCTGGGAGCAGCAGCGCCATGCGGCCGTGGAGCTGCCTCGCTTTCTTAACG 61	
Dy	56 GGGTGGGAGCAGCAGCGCCATGCGGCCGTGGAGCTGCCTCGCTTTCTTAACG 115	
Dy	62 TCACGCGCTGCTCAACGCGCTGCGAGCTGTGGCCGCTGGCGCGCGCGCT 121	
Dy	116 TCACGCGCTGCTCAACGCGCTGCGAGCTGTGGCCGCTGGCGCGCGCGCTC 175	
Dy	122 GGGGCGTGACACTGTGTGGCTGGAGGGGAGTGGGGCCAGCCAGAAACGTGGCTGT 181	
Dy	176 GGGGCGGGAACAATTGGCTGGAGGGGAGTGGGGCCGCGCGCGCGCGCTGC 235	
Dy	182 ACAACATCACCTTCATAATATGACAAATGTACACCTTGAATTCAGGTGGGAAAGCATG 241	
Dy	236 ACAACATCACCTTCATGATATATACATCTGACACCTTACTTGAATCTGTGGGAAAGCATG 295	
Dy	242 TGATTTGTGACGCCAGAAATATCAACATCAGCCAGTATGCTTGGCATGACCAGTGGCAG 301	
Dy	296 TGAATGGCGAGGCCCAAGAATATCAACATCAGTACGTACGCTGCACGACCAAGTGGCAG 355	
Dy	302 TCACCAATTTCTTGGTCCCCAGGGGCGCTGGCATGCAATTCCTGAAAGGATTTGGGTAA 361	
Dy	356 TCACCAATTTCTTGGTCCCCAGGGGCGCTGGCATGCAATTCCTGAAAGGATTTGGGTAA 415	
Dy	362 TACTGGAGAGCTGAAGTCCGAGGGAGAACAGTGCACCAATCTAATCTTAAGATCCGA 421	
Dy	416 TACTGGAGAGCTGAAGTCCGAGGGAGAACAGTGCACCAATCTAATCTTAAGATCCGA 475	

QY	422	AGCAGCTCAACAGACGCTGAAAGAACTGGAAAGAAATCTCAACCTTCTCGAAATATGA	481
Db	476	AGCAGCTCAACAGATGCTTCAAAAAGACTGGAAATGGAATCTCAACCTTCTCGAAATATGA	535
QY	482	AATTGGAAGGAAATATTTGCTAAGGTGTGCTCTTTCCTTCATTAAAAACGAAAGCA	541
Db	536	AATTGGAACGAGATTACTTGTGTCAAGATGTGCCCTTTCCTTCATTAAAAACGAAAGCA	595
QY	542	ATTACCAACCTTTCCTTCTTTAAGAACCGG	569
Db	596	ATTATCAACCTTTCCTTCTTTAAGAACCGG	623
RESULT 14			
LOCUS	DR003317		
DEFINITION	TC100455 Human fetal brain, large insert, PCMV expression library	494 bp	linear
VERSION	Homo sapiens cDNA clone TC100455 5' similar to Homo sapiens		
KEYWORDS	interleukin 17 receptor D (IL17RD), mRNA sequence.		
ACCESSION	DR003317.1	GI:66263190	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
TITLE	Hominae; Homo.		
JOURNAL	1 (bases 1 to 494)		
COMMENT	Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W. High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts Unpublished (2005) Contact: Kovacs, KR High Throughput cDNA Cloning Origene Technologies, Inc. (www.origene.com) 6 Taft Court, Suite 100, Rockville, MD 20850, USA Tel: 301 340 3188 Fax: 301 340 8606 Email: cDNA@origene.com This EST submission is part of an on-going human full-length cloning project at Origene Technologies, Inc. Please contact Origene for access. Origene Technologies, Inc. 6 Taft Ct. Suite 100 Rockville, MD 20850 Tel: (301) 340-3188 http://www.origene.com Seq primer: PCMV6 Sprieme forward vector primer, Origene Technologies Inc. Location/Qualifiers 1..494 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="TC100455" /tissue_type="Fetal Brain" /clone_lib="Human fetal brain, large insert, PCMV expression library" /note="Organ: Fetal Brain; Vector: PCMV6-XL4; Site 1: ECOR1; Site 2: Xho1/SalI compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"		
ORIGIN			
Query Match	15.9%;	Score 490;	DB 8; Length 494;
Best Local Similarity	100.0%;	Pred. NO. 6.4e-117;	Indels 0;
Matches 490;	Conservative 0;	Mismatches 0;	Gaps 0;

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